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(54) Title: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES ENCODED THEREBY		
(57) Abstract <p>The present invention provides DNA molecules that constitute portions of the genome of a plant, and polypeptides encoded thereby. The DNA molecules are useful for expressing a gene product, either as a promoter or as a structural gene or as an UTR or as a 3' termination sequence and are also useful in controlling expression of the target gene or as tools for genetic mapping or identification of a particular individual plant or for clustering of a group of plants with a common trait.</p>		

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**SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING
POLYPEPTIDES ENCODED THEREBY**

FIELD OF THE INVENTION

5 The present invention relates to isolated polynucleotides that encode all, or a portion of, a gene that is expressed and the corresponding polypeptide. The present invention also relates to isolated polynucleotides that encode regulatory regions of genes.

DESCRIPTION OF THE RELATED ART

Efforts to map and sequence the genome of a number of organisms are in progress; a few complete genome sequences, for example those of *E. coli* and *Saccharomyces cerevisiae* are known (Blattner et al., *Science* 277:1453 (1997); Goffeau et al.,
15 *Science* 274:546 (1996)). The complete genome of a multicellular organism, *C. elegans*, has also been sequenced (See, the *C. elegans* Sequencing Consortium, *Science* 282:2012 (1998)). To date, no complete genome of a plant has been sequenced, nor has a complete cDNA complement of any plant been
20 sequenced.

SUMMARY OF THE INVENTION

The present invention comprises polynucleotides, such as complete cDNA sequences and/or sequences of genomic DNA encompassing complete genes, portions of genes, and/or
25 intergenic regions, hereinafter collectively referred to as "Sequence-Determined DNA Fragments" (SDFs), from plants, particularly corn and *Arabidopsis thaliana* and polypeptides derived therefrom. In some instances, the SDFs span the entirety of a protein-coding segment. In some instances, the
30 entirety of an mRNA is represented. Other objects of the invention are the control sequences, such as but not limited to promoters, that are also represented by SDFs of the invention. Complements of any sequence of the invention are also considered part of the invention.

Other objects of the invention are polynucleotides comprising exon sequences, polynucleotides comprising intron sequences, polynucleotides comprising introns together with exons, intron/exon junction sequences, 5' untranslated sequences, and 3' untranslated sequences of the SDFs of the present invention. Polynucleotides representing the joinder of any exons described herein, in any arrangement, for example, to produce a sequence encoding any desirable amino acid sequence are within the scope of the invention.

The present invention also resides in probes useful for isolating and identifying nucleic acids that hybridize to an SDF of the invention. The probes are typically of a length of 12 to 2000 nucleotides long; more typically, 15 to 200 nucleotides long; even more typically, 18 to 100 nucleotides long.

Yet another object of the invention is a method of isolating and/or identifying nucleic acids using the following steps:

- (a) contacting a probe of the instant invention with a polynucleotide sample under conditions that permit hybridization and formation of a polynucleotide duplex; and
- (b) detecting and/or isolating the duplex of step (a).

The conditions for hybridization can be from low to moderate to high stringency conditions. The sample can include a polynucleotide having a sequence unique in a plant genome. Probes and methods of the invention are useful, for example, without limitation, for mapping of genetic traits and/or for positional cloning of a desired portion of genomic DNA.

Probes and methods of the invention can also be used for detecting alternatively spliced messages within a species. Probes and methods of the invention can further be used to detect or isolate related genes in other plant species using genomic DNA (gDNA) and/or cDNA libraries. In some instances, especially when longer probes and low to moderate stringency

hybridization conditions are used, the probe will hybridize to a plurality of cDNA and/or gDNA sequences of a plant. This approach is useful for isolating representatives of gene families which are identifiable by possession of a common functional domain in the gene product or which have common cis-acting regulatory sequences. This approach is also useful for identifying orthologous genes from other organisms, which can be more or less related to corn, *Arabidopsis*, or another plant.

The present invention also resides in constructs for modulating the expression of the genes comprised of all or a portion of an SDF. The constructs comprise all or a portion of the expressed SDF, or of a complementary sequence. Examples of constructs include ribozymes comprising RNA encoded by an SDF or by a sequence complementary thereto, antisense constructs, constructs comprising coding regions or parts thereof, constructs comprising promoters, introns, untranslated regions, etc. When inserted into a host cell the construct is, preferably, functionally integrated with or operatively linked to a heterologous polynucleotide. For instance, a coding region from an SDF might be operably linked to a promoter that is functional in a plant.

The present invention also resides in host cells, including bacterial or yeast cells or plant cells, and transgenic plants that harbor constructs such as described above. Another aspect of the invention relates to methods for modulating expression of specific genes in transgenic plants by expression of the structural gene component of the constructs, by regulation of expression of one or more endogenous genes in a transgenic plant or by suppression of expression of the polynucleotides of the invention in a transgenic plant. Methods of modulation of gene expression include without limitation (1) inserting into a host cell additional copies of a polynucleotide comprising a coding sequence; (2) modulating an endogenous promoter in a host cell; (3) inserting antisense

or ribozyme constructs into a host cell and (4) inserting into a host cell a polynucleotide comprising a sequence encoding a mutant, fragment, or fusion of the native polypeptides of the instant invention.

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BRIEF DESCRIPTION OF THE TABLES

The sequences of exemplary SDFs and polypeptides encoded thereby of the instant invention are listed in SEQ TABLES 1 and 2; annotation relevant to the sequences shown in SEQ
10 TABLES 1 and 2 is presented in REF TABLES 1 and 2. Each sequence corresponds to a Maximum Length cDNA Polynucleotide Sequence. Each Maximum Length cDNA Polynucleotide Sequence (Ac) corresponds to at least one sequence in SEQ TABLE 1 and 2. REF TABLE 1 corresponds with SEQ TABLE 1; REF TABLE 2
15 corresponds with SEQ TABLE 2.

REF TABLES 1 and 2 are Reference Tables which correlate each of the sequences and SEQ ID NOS in SEQ TABLES 1 and 2 with a corresponding Maximum Length cDNA Sequence (Ac), Ceres (Applicant) sequence identifier and other information about
20 the individual sequence. SEQ TABLES 1 and 2 are Sequence Tables containing the sequence of each nucleic acid and amino acid sequence.

In REF TABLES 1 and 2, each section begins by identifying the Maximum Length cDNA Polynucleotide Sequence, indicating a "Clone ID" that is a number used for
25 identification purposes by the applicant and in some instances a "Public Genomic DNA" sequence, indicated by a "gi No". In those instances where a public sequence is recited, there follows information about gene annotations such as predicted exons. In this portion, after the description of
30 the gene's functional unit, the starting and ending nucleotide number of the public sequence and the computer program used to generate the result are listed. "INIT" denotes an initial exon. "INTR" denotes an internal exon.

"TERM" denotes a terminal exon. For those sequences where the computer program is identified as "OCKHAM", "INIT" denotes the first detected exon and "TERM" denotes the last detected exon. "SINGLE" denotes the entire mRNA coding portion is in one exon. Other notations are considered intuitive to the skilled artisan.

In the next section (Ac), the cDNA MLS is identified by its SEQ ID NO ("Pat. Appln. SEQ ID NO") and the Ceres sequence identifier ("Ceres seq_id"), which is also merely an identifier useful for the applicant. The designation of "Alternative transcription start sites" can include both positive and negative numbers. Positive numbers refer to the referenced SEQ ID NO directly. The positions indicated by negative numbers, if any, refer to positions in the public genomic sequences. In instances where there is a "Public Genomic DNA" referenced, the relevant genomic sequence can be found by direct reference to the nucleotide sequence indicated by the "gi" number shown for the Public Genomic DNA. In instances where there is no Public Genomic DNA referenced, the relevant nucleotide sequence for alignment is the nucleotide sequence associated with the amino acid sequence designated by a "gi" number in the section (Dp). In these instances, the nucleotide sequence is found in GENBANK by clicking on the link in the National Center for Biotechnology Information Entrez database. The numbering is relative to position 1 as determined by aligning the first residue of the MLS cDNA sequence (SEQ ID NO *) with the genomic sequence corresponding to the relevant "gi" number.

Subsection (B) lists SEQ ID NOS and Ceres seq_ids for polypeptide sequences encoded by the cDNA sequence and the location of the start codon within the cDNA sequence that codes for the polypeptide. Subsection (B) also describes additional features within the polypeptide sequence.

Subsection (C) provides information regarding identified domains (where present) within the polypeptide and (where present) a name for the polypeptide. Subsection (Dp) provides (where present) information concerning amino acid sequences that are found to be related and have some sequence identity to the polypeptide sequences of SEQ TABLES 1 and 2. Those "related" sequences are identified by a "gi" number and are amino acid sequences in the publicly accessible BLAST databases on the NCBI FTP web site (accessible at ncbi.nlm.gov/blast). The database at the NCBI FTP site utilizes the "gi" identifiers to assign by NCBI a unique identifier for each sequence in the databases, thereby providing a non-redundant database for sequences from various databases, including GenBank, EMBL, DBBJ (DNA Database of Japan) and PDB (Brookhaven Protein Data Bank). Subsection (Ba), when present, describes a sequence as being considered plant-specific (i.e. a gene found only in a plant) or describes a biochemical activity for the protein encoded by the exemplary SDF. Subsection (Dn) provides polynucleotide sequences (where present) related to the Maximum Length cDNA sequence.

DETAILED DESCRIPTION OF THE INVENTION

The invention relates to (I) polynucleotides and methods of use thereof, such as

- 25 IA. Probes, Primers and Substrates;
- IB. Methods of Detection and Isolation;
 - B.1. Hybridization;
 - B.2. Methods of Mapping;
 - B.3. Southern Blotting;
 - 30 B.4. Isolating cDNA from Related Organisms;
 - B.5. Isolating and/or Identifying Orthologous Genes
- IC. Methods of Inhibiting Gene Expression
 - C.1. Antisense

C.2. Ribozyme Constructs;

C.3. Co-Suppression;

C.4. Other Methods to Inhibit Gene Expression

ID. Methods of Functional Analysis;

5 IE. Promoter Sequences and Their Use;

IF. UTR's and/or Intron Sequences and Their Use; and

IG. Coding Sequences and Their Use.

10 The specification also discloses (II) polypeptides including, without limitation, native proteins, mutants, fragments, and fusions. Antibodies to said polypeptides are also disclosed.

15 The specification also discloses (III) methods of modulating polypeptide production or activity. Examples of such methods include (i) suppressed, (ii) enhanced, and (iii) directed expression.

20 The specification also discloses (IV) gene constructs and construction of expression vectors, including (IVA) coding sequences and (IVB) promoters, and (IVC) Signal Peptides, (V) transformation procedures to illustrate the invention by way of examples.

I. Polynucleotides

25 A number of the nucleotide sequences disclosed in SEQ TABLES 1 AND 2 herein as representative of the SDFs of the invention can be obtained by sequencing genomic DNA (gDNA) and/or cDNA from corn plants grown from HYBRID SEED # 35A19, purchased from Pioneer Hi-Bred International, Inc., Supply Management, P.O. Box 256, Johnston, Iowa 50131-0256.

30 Exemplified SDFs of the invention represent portions of the genome of corn or *Arabidopsis* and/or represent mRNA expressed from that genome. The isolated nucleic acid of the invention also encompasses corresponding portions of the genome

and/or cDNA complement of other organisms as described in detail below.

Starting material for cDNA synthesis for the exemplary corn cDNA clones having sequences presented in SEQ TABLES 1 AND 2 was poly(A)-containing polysomal mRNAs from inflorescences and root tissues of corn plants grown from HYBRID SEED # 35A19. Male inflorescences and female (pre-and post-fertilization) inflorescences were isolated at various stages of development. Selection for poly(A) containing polysomal RNA was done using oligo d(T) cellulose columns, as described by Cox and Goldberg, "Plant Molecular Biology: A Practical Approach", pp. 1-35, Shaw ed., c. 1988 by IRL, Oxford.

Tissues were or each organ was individually pulverized and frozen in liquid nitrogen. Next, the samples were homogenized in the presence of detergents and then centrifuged. The debris and nuclei were removed from the sample and more detergents were added to the sample. The sample was centrifuged and the debris was removed. Then the sample was applied to a 2M sucrose cushion to isolate polysomes. The RNA was isolated by treatment with detergents and proteinase K followed by ethanol precipitation and centrifugation. The polysomal RNA from the different tissues was pooled according to the following mass ratios: 15/15/1 for male inflorescences, female inflorescences and root, respectively. The pooled material was then used for cDNA synthesis by the methods described below.

The quality and the integrity of the polyA+ RNAs were evaluated.

A number of the nucleotide sequences disclosed in SEQ TABLES 1 AND 2 herein as representative of the SDFs of the invention can also be obtained by sequencing genomic DNA from *Arabidopsis thaliana*, Wassilewskija ecotype or by sequencing cDNA obtained from mRNA from such plants as described below.

This is a true breeding strain. Seeds of the plant are available from the Arabidopsis Biological Resource Center at the Ohio State University, under the accession number CS2360. Seeds of this plant were deposited under the terms and conditions of the Budapest Treaty at the American Type Culture Collection, Manassas, VA on August 31, 1999, and were assigned ATCC No. PTA-595.

Starting material for cDNA synthesis for the exemplary *Arabidopsis* cDNA clones having sequences presented in SEQ TABLES 1 AND 2 was polysomal RNA isolated from the top-most inflorescence tissues and roots of *Arabidopsis thaliana* Landsberg erecta (L. er.) also obtained from the Arabidopsis Biological Resource Center. Nine parts inflorescence to every part root was used, as measured by mass. Tissue was pulverized and exposed to liquid nitrogen. Next, the sample was homogenized in the presence of detergents and then centrifuged. The debris and nuclei were removed from the sample and more detergents were added to the sample. The sample was centrifuged and the debris was removed and the sample was applied to a 2M sucrose cushion to isolate polysomal RNA. Cox et al., "Plant Molecular Biology: A Practical Approach", pp. 1-35, Shaw ed., c. 1988 by IRL, Oxford. The polysomal RNA was used for cDNA synthesis by the methods described below. Polysomal mRNA was then isolated as described above for corn cDNA. The quality of the RNA was assessed electrophoretically.

Following preparation of the mRNAs from various tissues as described above, selection of mRNA with intact 5' ends and specific attachment of an oligonucleotide tag to the 5' end of such mRNA was performed using either a chemical or enzymatic approach. Both techniques take advantage of the presence of the "cap" structure, which characterizes the 5' end of most intact mRNAs and which comprises a guanosine generally methylated once, at the 7 position.

The chemical modification approach involves the optional elimination of the 2', 3'-cis diol of the 3' terminal ribose, the oxidation of the 2', 3'-cis diol of the ribose linked to the cap of the 5' ends of the mRNAs into a dialdehyde, and the
5 coupling of the such obtained dialdehyde to a derivatized oligonucleotide tag. Further detail regarding the chemical approaches for obtaining mRNAs having intact 5' ends are disclosed in International Application No. WO96/34981 published November 7, 1996.

10 The enzymatic approach for ligating the oligonucleotide tag to the intact 5' ends of mRNAs involves the removal of the phosphate groups present on the 5' ends of uncapped incomplete mRNAs, the subsequent decapping of mRNAs having intact 5' ends and the ligation of the phosphate present at the 5' end of the
15 decapped mRNA to an oligonucleotide tag. Further detail regarding the enzymatic approaches for obtaining mRNAs having intact 5' ends are disclosed in Dumas Milne Edwards J.B. (Doctoral Thesis of Paris VI University, Le clonage des ADNc complets: difficultes et perspectives nouvelles. Apports pour
20 l'etude de la regulation de l'expression de la tryptophane hydroxylase de rat, 20 Dec. 1993), EP0 625572 and Kato et al., *Gene* 150:243-250 (1994).

In both the chemical ~~or~~ and the enzymatic approach, the oligonucleotide tag has a restriction enzyme site (e.g. an
25 EcoRI site) therein to facilitate later cloning procedures. Following attachment of the oligonucleotide tag to the mRNA, the integrity of the mRNA is examined by performing a Northern blot using a probe complementary to the oligonucleotide tag.

For the mRNAs joined to oligonucleotide tags using either
30 the chemical or the enzymatic method, first strand cDNA synthesis is performed using an oligo-dT primer with reverse transcriptase. This oligo-dT primer can contain an internal tag of at least 4 nucleotides, which can be different from one mRNA preparation to another. Methylated dCTP is used for cDNA

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first strand synthesis to protect the internal EcoRI sites from digestion during subsequent steps. The first strand cDNA is precipitated using isopropanol after removal of RNA by alkaline hydrolysis to eliminate residual primers.

5 Second strand cDNA synthesis is conducted using a DNA polymerase, such as Klenow fragment and a primer corresponding to the 5' end of the ligated oligonucleotide. The primer is typically 20-25 bases in length. Methylated dCTP is used for second strand synthesis in order to protect internal EcoRI
10 sites in the cDNA from digestion during the cloning process.

Following second strand synthesis, the full-length cDNAs are cloned into a phagemid vector, such as pBlueScript™ (Stratagene). The ends of the full-length cDNAs are blunted with T4 DNA polymerase (Biolabs) and the cDNA is digested with
15 EcoRI. Since methylated dCTP is used during cDNA synthesis, the EcoRI site present in the tag is the only hemi-methylated site; hence the only site susceptible to EcoRI digestion. In some instances, to facilitate subcloning, an Hind III adapter is added to the 3' end of full-length cDNAs.

20 The full-length cDNAs are then size fractionated using either exclusion chromatography (AcA, Biosepra) or electrophoretic separation which yields 3 to 6 different fractions. The full-length cDNAs are then directionally cloned either into pBlueScript™ using either the EcoRI and SmaI
25 restriction sites or, when the Hind III adapter is present in the full-length cDNAs, the EcoRI and Hind III restriction sites. The ligation mixture is transformed, preferably by electroporation, into bacteria, which are then propagated under appropriate antibiotic selection.

30 Clones containing the oligonucleotide tag attached to full-length cDNAs are selected as follows.

The plasmid cDNA libraries made as described above are purified (e.g. by a column available from Qiagen). A positive selection of the tagged clones is performed as follows.

Briefly, in this selection procedure, the plasmid DNA is converted to single stranded DNA using phage F1 gene II endonuclease in combination with an exonuclease (Chang et al., *Gene* 127:95 (1993)) such as exonuclease III or T7 gene 6 exonuclease. The resulting single stranded DNA is then purified using paramagnetic beads as described by Fry et al., *Biotechniques* 13: 124 (1992). Here the single stranded DNA is hybridized with a biotinylated oligonucleotide having a sequence corresponding to the 3' end of the oligonucleotide tag. Preferably, the primer has a length of 20-25 bases. Clones including a sequence complementary to the biotinylated oligonucleotide are selected by incubation with streptavidin coated magnetic beads followed by magnetic capture. After capture of the positive clones, the plasmid DNA is released from the magnetic beads and converted into double stranded DNA using a DNA polymerase such as ThermoSequenase™ (obtained from Amersham Pharmacia Biotech). Alternatively, protocols such as the Gene Trapper™ kit (Gibco BRL) can be used. The double stranded DNA is then transformed, preferably by electroporation, into bacteria. The percentage of positive clones having the 5' tag oligonucleotide is typically estimated to be between 90 and 98% from dot blot analysis.

Following transformation, the libraries are ordered in microtiter plates and sequenced. The *Arabidopsis* library was deposited at the American Type Culture Collection on January 7, 2000 as "*E-coli* liba 010600" under the accession number ____.

Other methods for cloning full-length cDNA are described, for example, by Seki et al., *Plant Journal* 15:707-720 (1998) "High-efficiency cloning of *Arabidopsis* full-length cDNA by biotinylated Cap trapper"; Maruyama et al., *Gene* 138:171 (1994) "Oligo-capping a simple method to replace the cap structure of eukaryotic mRNAs with oligoribonucleotides"; and WO 96/34981.

It is contemplated that the nucleotide sequences presented herein may contain some small percentage of errors. These errors may arise in the normal course of determination of nucleotide sequences. Sequence errors can be corrected by obtaining seeds deposited under the accession numbers cited above, propagating them, isolating genomic DNA or appropriate mRNA from the resulting plants or seeds thereof, amplifying the relevant portion of the genomic DNA or mRNA using primers having a sequence that flanks the erroneous sequence, and sequencing the amplification product.

I.A. Probes, Primers and Substrates

SDFs of the invention can be applied to substrates for use in array applications such as, but not limited to, assays of global gene expression, for example under varying conditions of development, growth conditions. The arrays can also be used in diagnostic or forensic methods.

Probes and primers of the instant invention will hybridize to a polynucleotide comprising a sequence in SEQ TABLES 1 AND 2. Though many different nucleotide sequences can encode an amino acid sequence, in some instances, the sequences of SEQ TABLES 1 AND 2 are preferred for encoding polypeptides of the invention. However, the sequence of the probes and/or primers of the instant invention need not be identical to those in SEQ TABLES 1 AND 2 or the complements thereof. For example, some variation in probe or primer sequence and/or length can allow additional family members to be detected, as well as orthologous genes and more taxonomically distant related sequences. Similarly probes and/or primers of the invention can include additional nucleotides that serve as a label for detecting the formed duplex or for subsequent cloning purposes.

Probe length will vary depending on the application. For use as PCR primers, probes should be 12-40 nucleotides,

preferably 18-30 nucleotides long. For use in mapping, probes should be 50 to 500 nucleotides, preferably 100-250 nucleotides long. For Southern hybridizations, probes as long as several kilobases can be used as explained below.

5 The probes and/or primers can be produced by synthetic procedures such as the triester method of Matteucci et al. *J. Am. Chem. Soc.* 103:3185(1981); or according to Urdea et al. *Proc. Natl. Acad.* 80:7461 (1981) or using commercially available automated oligonucleotide synthesizers.

10

I.B. Methods of Detection and Isolation

B.1. Hybridization

Probes and/or primers can be used for detection and/or
15 isolation of polynucleotide sequences. Such polynucleotides are included in the subject matter of the invention. Depending on the stringency of the conditions under which these probes and/or primers are used, polynucleotides exhibiting a wide range of similarity to those in SEQ TABLES 1 AND 2 can be
20 detected or isolated.

"Stringency" is a function of probe length, probe composition (G + C content), and salt concentration, organic solvent concentration, and temperature of hybridization or wash conditions. Stringency is typically compared by the parameter
25 " T_m ", which is the temperature at which 50% of the complementary molecules in the hybridization are hybridized, in terms of a temperature differential from T_m . High stringency conditions are those providing a condition of $T_m - 5^\circ\text{C}$ to $T_m - 10^\circ\text{C}$. Medium stringency conditions are those providing $T_m - 20^\circ\text{C}$ to $T_m - 29^\circ\text{C}$. Low stringency conditions are those
30 providing a condition of $T_m - 40^\circ\text{C}$ to $T_m - 48^\circ\text{C}$. The relationship of hybridization conditions to T_m (in $^\circ\text{C}$) is expressed in the mathematical equation

$$T_m = 81.5 - 16.6(\log_{10}[\text{Na}^+]) + 0.41(\%G+C) - (600/N) \quad (1)$$

where N is the length of the probe. This equation works well for probes 14 to 70 nucleotides in length that are identical to the target sequence. The equation below for T_m of DNA-DNA hybrids is useful for probes in the range of 50 to greater than 500 nucleotides, and for conditions that include an organic solvent (formamide).

$$T_m = 81.5 + 16.6 \log \{ [\text{Na}^+] / (1 + 0.7[\text{Na}^+]) \} + 0.41(\%G+C) - 500/L - 0.63(\% \text{formamide}) \quad (2)$$

where L is the length of the probe in the hybrid. (P. Tijessen, "Hybridization with Nucleic Acid Probes" in Laboratory Techniques in Biochemistry and Molecular Biology, P.C. van der Vliet, ed., c. 1993 by Elsevier, Amsterdam.) The T_m of equation (2) is affected by the nature of the hybrid; for DNA-RNA hybrids T_m is 10-15°C higher than calculated, for RNA-RNA hybrids T_m is 20-25°C higher. Because the T_m decreases about 1 °C for each 1% decrease in homology when a long probe is used (Bonner et al., *J. Mol. Biol.* 81:123 (1973)), stringency conditions can be adjusted to favor detection of identical genes or related family members.

Equation (2) is derived assuming equilibrium and therefore, hybridizations according to the present invention are most preferably performed under conditions of probe excess and for sufficient time to achieve equilibrium. The time required to reach equilibrium can be shortened by inclusion of a "hybridization accelerator" such as dextran sulfate or another high volume polymer in the hybridization buffer.

When the practitioner wishes to examine the result of membrane hybridizations under a variety of stringencies, an efficient way to do so is to perform the hybridization under a low stringency condition, then to wash the hybridization membrane under increasingly stringent conditions. With

respect to wash steps, preferred stringencies lie within the ranges stated above; high stringency is 5-8°C below T_m , medium stringency is 26-29°C below T_m and low stringency is 45-48°C below T_m .

5 A number of methods known to those skilled in the art can be used with the probes and/or primers of the invention to isolate and detect polynucleotides, including, without limitation: Southern, Northern, Branched DNA hybridization assays, polymerase chain reaction, and variations thereof.

10 When using SDFs to identify orthologous genes in other species, the practitioner will preferably adjust the amount of target DNA of each species so that, as nearly as is practical, the same number of genome equivalents are present for each species examined. This prevents faint signals from
15 species having large genomes, and thus small numbers of genome equivalents per mass of DNA, from erroneously being interpreted as absence of the corresponding gene in the genome.

A good general discussion of the factors for determining
20 hybridization conditions is provided by Sambrook et al. ("Molecular Cloning, a Laboratory Manual, 2nd ed., c. 1989 by Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY; see esp., chapters 11 and 12). Additional considerations and details of the physical chemistry of hybridization are provided
25 by G.H. Keller and M.M. Manak "DNA Probes", 2nd Ed. pp. 1-25, c. 1993 by Stockton Press, New York, NY.

Hybridization of one nucleic acid to another constitutes a physical property that defines the subject SDF of the invention. Also, such hybridization imposes structural
30 limitations on the pair. For example, for a probe molecule, given that the sequence of the probe nucleic acid is known and fixed, equation (2) indicates that the combined variation in GC content of the target DNA and mismatch between the

probe and the hybridizing DNA is determined for any given hybridization buffer composition and T_m .

The probes and/or primers of the instant invention can be used to detect or isolate nucleotides that are "identical" to the probes or primers. Two nucleic acid sequences or polypeptides are said to be "identical" if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the sequence can form a Watson-Crick base pair with a reference polynucleotide sequence. Complementary sequences can include nucleotides, such as inosine, that neither disrupt Watson-Crick base pairing nor contribute to the pairing.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman *Add. APL. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman and Wunsch *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson and Lipman *Proc. Natl. Acad. Sci. (USA)* 85: 2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, PASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection. Given that two sequences have been identified for comparison, GAP and BESTFIT are preferably employed to determine their optimal alignment. Typically, the default values of 5.00 for gap weight and 0.30 for gap weight length are used.

The probes and/or primers of the invention can also be used to detect and/or isolate polynucleotides exhibiting at least 80% sequence identity with the sequences of SEQ TABLES 1 AND 2 or fragments thereof.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison

window, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (e.g., gaps or overhangs) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the percentage of sequence identity. "Percentage of sequence identity" can be determined by the algorithms described above.

The term "substantial identity" between polynucleotide or polypeptide sequences refers to polynucleotide or polypeptide comprising a sequence that has at least 80% sequence identity, preferably at least 85%, more preferably at least 90% and most preferably at least 95%, even more preferably, at least 96%, 97%, 98% or 99% sequence identity compared to a reference sequence using the programs.

Isolated polynucleotides within the scope of the invention also include allelic variants of the specific sequences presented in SEQ TABLES 1 AND 2. An "allelic variant" is a sequence that is a variant from that of the SDF, but represents the same chromosomal locus in the organism. Allelic variants can arise by normal genetic variation in a population. Allelic variants can also be produced by genetic engineering methods. An allelic variant can be one that is found in a naturally occurring plant, including a cultivar or ecotype. A silent allele can give rise to phenotypic and expression profiles. An allelic variant may or may not give rise to a phenotypic change, and may or may not be expressed. An expressed allele can result in a detectable change in the phenotype of the trait

represented by the locus. Allelic variations can occur in any portion of the gene sequence, including regulatory regions as well as structural regions.

With respect to nucleotide sequences, degeneracy of the genetic code provides the possibility to substitute at least one base of the base sequence of a gene with a different base without causing the amino acid sequence of the polypeptide produced from the gene to be changed. Hence, the DNA of the present invention may also have any base sequence that has been changed from a sequence in SEQ TABLES 1 AND 2 by substitution in accordance with degeneracy of genetic code. References describing codon usage include: Carels et al., *J. Mol. Evol.* 46: 45 (1998) and Fennoy et al., *Nucl. Acids Res.* 21(23): 5294 (1993).

A. B.2. Mapping

The isolated SDF DNA of the invention can be used to create various types of genetic and physical maps of the genome of corn, Arabidopsis or other plants. Some SDFs may be absolutely associated with particular phenotypic traits, allowing construction of gross genetic maps. While not all SDFs will immediately be associated with a phenotype, all SDFs can be used as probes for identifying polymorphisms associated with phenotypes of interest. Briefly, total DNA is isolated from individuals and is subsequently cleaved with one or more restriction enzymes, separated according to mass, transferred to a solid support, hybridized with SDF DNA and the pattern of fragments compared. Polymorphisms associated with a particular SDF are visualized as differences in the size of fragments produced between individual DNA samples after digestion with a particular restriction enzyme and hybridization with the SDF. After identification of polymorphic SDF sequences, linkage studies can be conducted. Recombinants produced are analyzed using the same restriction

enzyme/hybridization procedure. After identification of many polymorphisms using SDF sequences, linkage studies can be conducted by using the individuals showing polymorphisms as parents in crossing programs. F2 progeny recombinants or recombinant inbreds, for example, are then analyzed using the same restriction enzyme/hybridization procedure. The order of DNA polymorphisms along the chromosomes can be inferred based on the frequency with which they are inherited together versus independently. The closer two polymorphisms are together in a chromosome the higher the probability that they are inherited together. Integration of the relative positions of all the polymorphisms and associated marker SDFs produces a genetic map of the species, where the distances between markers reflect the recombination frequencies in that chromosome segment.

The use of recombinant inbred lines for such genetic mapping is described for *Arabidopsis* by Alonso-Blanco et al. (*Methods in Molecular Biology*, vol.82, "Arabidopsis Protocols", pp. 137-146, J.M. Martinez-Zapater and J. Salinas, eds., c. 1998 by Humana Press, Totowa, NJ) and for corn by Burr ("Mapping Genes with Recombinant Inbreds", pp. 249-254. In Freeling, M. and V. Walbot (Ed.), *The Maize Handbook*, c. 1994 by Springer-Verlag New York, Inc.: New York, NY, USA; Berlin Germany; Burr et al. *Genetics* (1998) 118: 519; Gardiner, J. et al., (1993) *Genetics* 134: 917). However, this procedure is not limited to plants and can be used for other organisms (such as yeast) or for individual cells.

The SDFs of the present invention can also be used for simple sequence repeat (SSR) mapping. Rice SSR mapping is described by Morgante et al. (*The Plant Journal* (1993) 3: 165), Panaud et al. (*Genome* (1995) 38: 1170); Senior et al. (*Crop Science* (1996) 36: 1676), Taramino et al. (*Genome* (1996) 39: 277) and Ahn et al. (*Molecular and General*

Genetics (1993) 241: 483-90). SSR mapping can be achieved using various methods. In one instance, polymorphisms are identified when sequence specific probes flanking an SSR contained within an SDF are made and used in polymerase chain reaction (PCR) assays with template DNA from two or more individuals of interest. Here, a change in the number of tandem repeats between the SSR-flanking sequence produces differently sized fragments (U.S. Patent 5,766,847). Alternatively, polymorphisms can be identified by using the PCR fragment produced from the SSR-flanking sequence specific primer reaction as a probe against Southern blots representing different individuals (U.H. Refseth et al., (1997) *Electrophoresis* 18: 1519).

Genetic and physical maps of crop species have many uses. For example, these maps can be used to devise positional cloning strategies for isolating novel genes from the mapped crop species. In addition, because the genomes of closely related species are largely syntenic (that is, they display the same ordering of genes within the genome), these maps can be used to isolate novel alleles from wild relatives of crop species by positional cloning strategies.

The various types of maps discussed above can be used with the SDFs of the invention to identify Quantitative Trait Loci (QTLs). Many important crop traits, such as the solids content of tomatoes, are quantitative traits and result from the combined interactions of several genes. These genes reside at different loci in the genome, oftentimes on different chromosomes, and generally exhibit multiple alleles at each locus. The SDFs of the invention can be used to identify QTLs and isolate specific alleles as described by de Vicente and Tanksley (*Genetics* 134:585 (1993)). In addition to isolating QTL alleles present crop species, the SDFs of the invention can also be used to isolate alleles from the corresponding QTL of wild relatives. Transgenic plants

having various combinations of QTL alleles can then be created and the effects of the combinations measured. Once an ideal allele combination has been identified, crop improvement can be accomplished either through

5 biotechnological means or by directed conventional breeding programs (for review see Tanksley and McCouch, *Science* 277:1063 (1997)).

In another embodiment the SDFs can be used to help create physical maps of the genome of corn, *Arabidopsis* and
10 related species. Where SDFs have been ordered on a genetic map, as described above, then SDFs can be used as probes to discover which clones in large libraries of plant DNA fragments in YACs, BACs, etc. contain the same SDF or similar sequences, thereby facilitating the assignment of the large
15 DNA fragments to chromosomal positions. Subsequently, the large BACs, YACs, etc. can be ordered unambiguously by more detailed studies of their sequence composition (e.g. Marra et al. (1997) *Genomic Research* 7:1072-1084) and by using their end or other sequences to find the identical sequences in
20 other cloned DNA fragments. The overlapping of DNA sequences in this way allows large contigs of plant sequences to be built, that, when sufficiently extended, provide a complete physical map of a chromosome. Sometimes the SDFs themselves will provide the means of joining cloned sequences
25 into a contig.

The patent publication WO95/35505 and U.S. Patents 5,445,943 and 5,410,270 describe scanning multiple alleles of a plurality of loci using hybridization to arrays of oligonucleotides. These techniques are useful for each of the
30 types of mapping discussed above.

Following the procedures described above and using a plurality of the SDFs of the present invention, any individual can be genotyped. These individual genotypes can be used for the identification of particular cultivars,

varieties, lines, ecotypes and genetically modified plants or can serve as tools for subsequent genetic studies involving multiple phenotypic traits.

B. 3 Southern Blot Hybridization

5

The sequences from SEQ TABLES 1 AND 2 can be used as probes for various hybridization techniques. These techniques are useful for detecting target polynucleotides in a sample or for determining whether transgenic plants, seeds or host cells harbor a gene or sequence of interest and thus might be expected to exhibit a particular trait or phenotype.

10

In addition, the hybridization of the SDFs of the invention to nucleic acids obtained from other organisms can be used to identify orthologous genes from other species and/or additional members of gene families either in the same or different species. In regard to identifying genes in other species, a Southern blot of genomic DNA provides description of isolated DNA fragments that comprise the orthologous genes or additional members of the gene families. That is, given such data, one of ordinary skill in the art could distinguish the isolated DNA fragments by their size together with the restriction sites at each end and by the property of hybridizing with the SDF probe under the stated conditions.

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In addition, the SDFs from the invention can be used to isolate additional members of gene families from the same species and/or orthologous genes from different species. This is accomplished by hybridizing an SDF to a Southern blot containing the appropriate genomic DNA or cDNA. Given the resulting hybridization data, one of ordinary skill in the art could distinguish and isolate the correct DNA fragments by size, restriction sites and stated hybridization conditions from a gel or from a library.

30

Identification and isolation of orthologous genes from closely related species and alleles within a species is particularly desirable because of their potential for crop improvement. Many important crop traits, such as the solid content of tomatoes, result from the combined interactions of the products of several genes residing at different loci in the genome. Generally, alleles at each of these loci can make quantitative differences to the trait. By identifying and isolating numerous alleles for each locus from within or different species, transgenic plants having various combinations of alleles can be created and the effects of the combinations measured. Once a more favorable ideal allele combination has been identified, crop improvement can be accomplished either through biotechnological means or by directed conventional breeding programs (Tanksley et al. *Science* 277:1063(1997)).

The results from hybridizations of the SDFs of the invention to Southern blots containing DNA from another species can also be used to generate restriction fragment maps for the corresponding genomic regions. These maps provide ~~map~~ ~~provides~~ additional information about the relative positions of restriction sites within fragments, further distinguishing mapped DNA from the remainder of the genome.

Physical maps can be made by digesting genomic DNA with different combinations of restriction enzymes.

Probes for Southern blotting to distinguish individual restriction fragments can range in size from 15 to 20 nucleotides to several thousand nucleotides. More preferably, the probe is 100 to 1000 nucleotides long for identifying members of a gene family when it is found that repetitive sequences would complicate the hybridization. For identifying an entire corresponding gene in another species, the probe is more preferably the length of the gene,

typically 2000 to 10,000 nucleotides, but probes 50-1,000 nucleotides long might be used. Some genes, however, might require probes up to 15,000 nucleotides long or overlapping probes constituting the full-length sequence to span their lengths.

Also, while it is preferred that the probe be homogeneous with respect to its sequence, that is not necessary. For example, as described below, a probe representing members of a gene family having diverse sequences can be generated using PCR to amplify genomic DNA or RNA templates using primers derived from SDFs that include sequences that define the gene family.

For identifying corresponding genes in another species, the probe for Southern blotting most preferably would be the genomic copy of the probe gene. This allows all elements of the gene to be identified in the other species. The next most preferable probe is a cDNA spanning the entire coding sequence, which allows all of the mRNA-coding portion of the gene to be identified; in this case it is possible that some introns in the gene might be missed. Probes for Southern blotting can easily be generated from SDFs by making primers having the sequence at the ends of the SDF and using corn or *Arabidopsis* genomic DNA as a template. In instances where the SDF includes sequence conserved among species, primers including the conserved sequence can be used for PCR with genomic DNA from a species of interest to obtain a probe. Similarly, if the SDF includes a domain of interest, that portion of the SDF can be used to make primers and, with appropriate template DNA, used to make a probe to identify genes containing the domain. Alternatively, the PCR products can be resolved, for example by gel electrophoresis, and cloned and/or sequenced. In this manner, the variants of the domain among members of a gene family, both within and across species, can be examined.

B.4.1 Isolating DNA from Related Organisms

The SDFs of the invention can be used to isolate the corresponding DNA from other organisms. Either cDNA or genomic DNA can be isolated. For isolating genomic DNA, a
5 lambda, cosmid, BAC or YAC, or other large insert genomic library from the plant of interest can be constructed using standard molecular biology techniques as described in detail by Sambrook et al. 1989 (Molecular Cloning: A Laboratory Manual, 2nd ed. Cold Spring Harbor Laboratory Press, New York) and by Ausubel et al. 1992 (Current Protocols in Molecular
10 Biology, Greene Publishing, New York).

To screen a phage library, recombinant lambda clones are plated out on appropriate bacterial medium using an appropriate *E. coli* host strain. The resulting plaques are
15 lifted from the plates using nylon or nitrocellulose filters. The plaque lifts are processed through denaturation, neutralization, and washing treatments following the standard protocols outlined by Ausubel et al. (1992). The plaque lifts are hybridized to either radioactively labeled or non-
20 radioactively labeled SDF DNA at room temperature for about 16 hours, usually in the presence of 50% formamide and 5X SSC (sodium chloride and sodium citrate) buffer and blocking reagents. The plaque lifts are then washed at 42°C with 1% Sodium Dodecyl Sulfate (SDS) and at a particular
25 concentration of SSC. The SSC concentration used is dependent upon the stringency at which hybridization occurred in the initial Southern blot analysis performed. For example, if a fragment hybridized under medium stringency (e.g., $T_m - 20^\circ\text{C}$), then this condition is maintained or
30 preferably adjusted to a less stringent condition (e.g., $T_m - 30^\circ\text{C}$) to wash the plaque lifts. Positive clones show detectable hybridization e.g., by exposure to X-ray films or chromogen formation. The positive clones are then

subsequently isolated for purification using the same general protocol outlined above. Once the clone is purified, restriction analysis can be conducted to narrow the region corresponding to the gene of interest. The restriction analysis and succeeding subcloning steps can be done using procedures described by, for example Sambrook et al. (1989) cited above.

To screen a YAC library, the procedures outlined for the lambda library are essentially similar except the YAC clones are harbored in bacterial colonies. The YAC clones are plated out at reasonable density on nitrocellulose or nylon filters supported by appropriate bacterial medium in petri plates. Following the growth of the bacterial clones, the filters are processed through the denaturation, neutralization, and washing steps following the procedures of Ausubel et al. 1992. The same hybridization procedures for lambda library screening are followed.

To isolate cDNA, similar procedures using appropriately modified vectors are employed. For instance, the library can be constructed in a lambda vector appropriate for cloning cDNA such as λ gt11. Alternatively, the cDNA library can be made in a plasmid vector. cDNA for cloning can be prepared by any of the methods known in the art, but is preferably prepared as described above. Preferably, a cDNA library will include a high proportion of full-length clones.

B. 5. Isolating and/or Identifying Orthologous Genes

Probes and primers of the invention can be used to identify and/or isolate polynucleotides related to those in SEQ TABLES 1 AND 2. Related polynucleotides are those that are native to other plant organisms and exhibit either similar sequence or encode polypeptides with similar biological activity. One specific example is an orthologous gene, a gene that has a high degree of sequence similarity, often along the

entire length of the coding portion of the gene, and also encodes a gene product that performs a similar function in the organism. Orthologous genes may be distinguished from homologous genes in that homologous genes share sequence similarity but often only in a portion of the sequence, which often represents a functional domain such as a tyrosine kinase activity, a DNA binding domain, or the like. The functional activities of homologous genes are not necessarily the same, but are the same for orthologous genes. The degree of identity is a function of evolutionary separation and, in closely related species, the degree of identity can be 98 to 100%. The amino acid sequence of a protein encoded by an orthologous gene can be less than 75% identical, but tends to be at least 75% or at least 80% identical, more preferably at least 90%, most preferably at least 95% identical to the amino acid sequence of the reference protein.

To find orthologous genes, the probes are hybridized to nucleic acids from a species of interest under low stringency conditions and blots are then washed under conditions of increasing stringency. It is preferable that the wash stringency be such that sequences that are 85 to 100% identical will hybridize. More preferably, sequences 90 to 100% identical will hybridize and most preferably only sequences greater than 95% identical will hybridize. The low stringency condition is preferably one where sequences containing as much as 40-45% mismatches will be able to hybridize. This condition is established by $T_m - 40^{\circ}\text{C}$ to $T_m - 48^{\circ}\text{C}$ (see below). One of ordinary skill in the art will recognize that, due to degeneracy in the genetic code, amino acid sequences that are identical can be encoded by DNA sequences as little as 67% identical. Thus, it is preferable to make an overlapping series of shorter probes, on the order of 24 to 45 nucleotides, and individually hybridize them to the same arrayed library to

avoid the problem of degeneracy introducing large numbers of mismatches.

As evolutionary divergence increases, genome sequences also tend to diverge. Thus, one of skill will recognize that searches for orthologous genes between more divergent species will require the use of lower stringency conditions compared to searches between closely related species. Also, degeneracy is more of a problem for searches in the genome of a species more distant evolutionarily from the species that is the source of the SDF probe sequences.

Therefore the method described in Bouckaert et al., U.S. Ser. No. 60/121,700 Atty. Dkt. No. 2750-117P, Client Dkt. No. 00010.001, filed February 25, 1999, hereby incorporated in its entirety by reference, can be applied to the SDFs of the present invention to isolate related genes from plant species which do not hybridize to the corn or *Arabidopsis* sequences of SEQ TABLES 1 AND 2.

Identification of the relationship of nucleotide or amino acid sequences among plant species can be done by comparison of the subject nucleotide or amino acid sequence to the sequences of SDFs of the present application presented in SEQ TABLES 1 and 2.

The SDFs of the invention can also be used as probes to search for genes that are related to the SDF within a species. Such related genes are typically considered to be members of a "gene family." In such a case, the sequence similarity will often be concentrated into one or a few portions of the sequence. The portions of similar sequence that define the gene family typically encode a portion of a protein or RNA that has an enzymatic or structural function. The degree of identity in the amino acid sequence of the domain that defines the gene family is preferably at least 70%, more preferably 80 to 95%, most preferably 85 to 99%. To search for members of a gene family within a species, a

"low stringency" hybridization is usually performed, but this will depend upon the size, distribution and degree of sequence divergence of domains that define the gene family. SDFs encompassing regulatory regions can be used to identify "coordinately expressed" genes by using the regulatory region portion of the SDF as a probe.

In the instances where the SDFs are identified as being expressed from genes that confer a particular phenotype, then the SDFs can also be used as probes to assay plants of different species for those phenotypes.

I.C. Methods to Inhibit Gene Expression

In some instances it is desirable to suppress expression of an endogenous or exogenous gene. A well-known instance is the FLAVOR-SAVOR™ tomato, in which the gene encoding ACC synthase is inactivated by an antisense approach, thus delaying softening of the fruit after ripening. See for example, U.S. Patent No. 5,859,330; U.S. Patent No. 5,723,766; Oeller, et al, *Science*, 254:437-439(1991); and Hamilton et al, *Nature*, 346:284-287 (1990). Also, timing of flowering can be controlled by suppression of the *FLOWERING LOCUS C*; high levels of this transcript are associated with late flowering, while absence of *FLC* is associated with early flowering (S.D. Michaels et al., *Plant Cell* 11:949 (1999). Also, the transition of apical meristem from production of leaves with associated shoots to flowering is regulated by *TERMINAL FLOWER1*, *APETALA1* and *LEAFY*. Thus, when it is desired to induce a transition from shoot production to flowering, it is desirable to suppress *TFL1* expression (S.J. Liljegren, *Plant Cell* 11:1007 (1999)). As another instance, it has been found that suppression of the ethylene forming enzyme results in arrested ovule development and female sterility that can be reversed by application of ethylene (D. De Martinis et al., *Plant Cell* 11:1061 (1999)). The ability

to manipulate fertility of female plants is useful in ~~the~~ increasing fruit production and creating hybrids.

In an instance when it is desired to express a dominant negative mutation, it often helpful to suppress expression of the endogenous, native protein. Expression of dominant negative mutant proteins is a useful tool for research, for example when a dominant negative mutation of a receptor is used to constitutively activate or suppress a signal transduction cascade, allowing examination of the phenotype and thus the trait(s) controlled by that receptor and pathway.

C.1 Antisense

In the case of polynucleotides used to inhibit expression of an endogenous gene, the introduced sequence need not be perfectly identical to a sequence of the target endogenous gene. The introduced polynucleotide sequence will typically be at least substantially identical (as determined above) to the target endogenous sequence.

Some polynucleotide SDFs in SEQ TABLES 1 AND 2 represent sequences that are expressed in corn and/or *Arabidopsis*. Thus the invention includes using these sequences to generate antisense constructs to inhibit transcription and/or translation of said SDFs, typically in a plant cell.

To accomplish this, a polynucleotide segment from the desired gene that can hybridize to the mRNA expressed from the desired gene (the "antisense segment") is operably linked to a promoter such that the antisense strand of RNA will be transcribed when the construct is present in a host cell. A regulated promoter can be used in the construct to control transcription of the antisense segment so that transcription occurs only under desired circumstances.

The antisense segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not

be perfectly identical to inhibit expression. Further, the antisense product may hybridize to the untranslated region instead of or in addition to the coding portion of the gene. The vectors of the present invention can be designed such that
5 the inhibitory effect applies to other proteins within a family of genes exhibiting homology or substantial homology to the target gene.

For antisense suppression, the introduced antisense segment sequence also need not be full length relative to
10 either the primary transcription product or fully processed mRNA. Generally, higher sequence identity can be used to compensate for the use of a shorter sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally
15 effective. Normally, a sequence of between about 30 or 40 nucleotides and the full length of the transcript should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of at least about 500
20 nucleotides is especially preferred.

C.2. Ribozymes

It is also contemplated that gene constructs representing ribozymes and based on the SDFs in SEQ TABLES 1 AND 2 are an object of the invention. Ribozymes can also be
25 used to inhibit expression of genes by suppressing the translation of the mRNA into a polypeptide. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In
30 carrying out this cleavage, the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences

within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of ribozymes is derived from a number of small circular RNAs, which are capable of self-cleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, luceme transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haselhoff et al. *Nature*, 334:585 (1988).

Like the antisense constructs above, the ribozyme sequence portion necessary for pairing need not be identical to the target nucleotides to be cleaved, nor identical to the sequences in SEQ TABLES 1 AND 2. Generally, the sequence in the ribozyme capable of binding to the target sequence exhibits substantial sequence identity to a sequence in SEQ TABLES 1 AND 2 or the complement thereof, or to a portion of said sequence or complement. Further, the ribozyme sequence also need not be full length relative to either the primary transcription product or fully processed mRNA. The ribozyme can be equally effective in inhibiting mRNA translation by cleaving either in the untranslated or coding regions. Generally, higher sequence identity can be used to compensate for the use of a shorter sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective.

C.3. Sense Suppression

Another method of suppression is by introducing an exogenous copy of the gene to be suppressed. Introduction of

expression cassettes in which a nucleic acid is configured in the sense orientation with respect to the promoter into the chromosome of a plant or by a self-replicating virus has been shown to be an effective means by which to induce degradation of mRNAs of target genes. For an example of the use of this method to modulate expression of endogenous genes see, Napoli et al., *The Plant Cell* 2:279 (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184. Generally, where inhibition of expression is desired, some transcription of the introduced sequence is probably necessary. The effect may occur where the introduced sequence contains no coding sequence *per se*, but comprises only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The introduction of only regulatory promoter sequences can also cause interference with the activity of endogenous promoters possessing the same sequence. Thus, the described SDFs can also be used to control transcription. In all of these procedures, the introduced sequence generally will be substantially identical to the endogenous sequence intended to be inactivated. The minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Sequence identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with antisense regulation, the effect would likely apply to any other proteins within a similar family of genes exhibiting homology or substantial homology to the suppressing sequence.

C.4. Other Methods to Inhibit Gene Expression

Yet another means of suppressing gene expression is to insert a polynucleotide into the gene of interest to disrupt transcription or translation of the gene.

Low frequency homologous recombination can be used to target a polynucleotide insert to a gene by flanking the polynucleotide insert with sequences that are substantially similar to the gene to be disrupted. Sequences from SEQ TABLES 1 AND 2, fragments thereof, and substantially similar sequence thereto can be used for homologous recombination.

In addition, random insertion of polynucleotides into a host cell genome can also be used to disrupt the gene of interest. Azpiroz-Leehan et al., *Trends in Genetics* 13:152 (1997). In this method, screening for clones from a library containing random insertions is preferred to identifying those that have polynucleotides inserted into the gene of interest. Such screening can be performed using probes and/or primers described above based on sequences from SEQ TABLES 1 AND 2, fragments thereof, and substantially similar sequence thereto. The screening can also be performed by selecting clones or R₁ plants having a desired phenotype.

I.D. Methods of Functional Analysis

The constructs described in the methods under I.C. above can be used to determine the function of the polypeptide encoded by the gene that is targeted by the constructs.

Down-regulating the transcription and translation of the targeted gene, the host cell or organisms, such as a plant, may produce phenotypic changes as compared to a wild-type cell or organism. In addition, *in vitro* assays can be used to determine if any biological activity, such as calcium flux, DNA transcription, nucleotide incorporation, etc., are being modulated by the down-regulation of the targeted gene.

Coordinated regulation of sets of genes, e.g., those contributing to a desired polygenic trait, is sometimes necessary to obtain a desired phenotype. SDFs of the invention representing transcription activation and DNA binding domains can be assembled into hybrid transcriptional

activators. These hybrid transcriptional activators can be used with their corresponding DNA elements (i.e., those bound by the DNA-binding SDFs) to effect coordinated expression of desired genes (J.J. Schwarz et al., *Mol. Cell. Biol.* 12:266 (1992), A. Martinez et al., *Mol. Gen. Genet.* 261:546 (1999)).

The SDFs of the invention can also be used in the two-hybrid genetic systems to identify networks of protein-protein interactions (L. McAlister-Henn et al., *Methods* 19:330 (1999), J.C. Hu et al., *Methods* 20:80 (2000), M. Golovkin et al., *J. Biol. Chem.* 274:36428 (1999), K. Ichimura et al., *Biochem. Biophys. Res. Comm.* 253:532 (1998)). The SDFs of the invention can also be used in various expression display methods to identify important protein-DNA interactions (e.g. B. Luo et al., *J. Mol. Biol.* 266:479 (1997)).

I.E. Promoters

The SDFs of the invention are also useful as structural or regulatory sequences in a construct for modulating the expression of the corresponding gene in a plant or other organism, e.g. a symbiotic bacterium. For example, promoter sequences represented in SEQ TABLES 1 AND 2 can be useful in directing expression of coding sequences either as constitutive promoters or to direct expression in particular cell types, tissues, or organs or in response to environmental stimuli.

The term "promoter" refers to a region of sequence determinants located upstream or downstream from the start of transcription and which are involved in recognition and binding of RNA polymerase and other proteins to initiate transcription. A "plant promoter" is a promoter capable of initiating transcription in plant cells and can be used to drive expression of a translated portion of an SDF. Such promoters need not be of plant origin. For example, promoters derived from plant viruses, such as the CaMV35S promoter or from

Agrobacterium tumefaciens such as the T-DNA promoters, can be plant promoters. A typical example of a constitutive promoter of plant origin is the promoter of the cowpea trypsin inhibitor gene. Typical examples of temporal and/or tissue specific promoters of plant origin that can be used with the polynucleotides of the present invention, are: PTA29, a promoter which is capable of driving gene expression specifically in tapetum and only during anther development (Koltonow et al., *Plant Cell* 2:1201 (1990); RCc2 and RCc3, promoters that direct root-specific gene expression in rice (Xu et al., *Plant Mol. Biol.* 27:237 (1995); TobRB27, a root-specific promoter from tobacco (Yamamoto et al., *Plant Cell* 3:371 (1991)).

By "specific promoters" is meant promoters that have a high preference of driving gene expression in the specified tissue and/or at the specified time during the concerned tissue or organ development. By "high preference" is meant at least 3-fold, preferably 5-fold, more preferably at least 10-fold still more preferably at least 20-fold, 50-fold or 100-fold increase in expression in the desired tissue over the expression in any undesired tissue.

A typical example of an inducible promoter, which can be utilized with the polynucleotides of the present invention, is PARSK1, the promoter from the *Arabidopsis* gene encoding a serine-threonine kinase enzyme, and which promoter is induced by dehydration, abscissic acid and sodium chloride (Wang and Goodman, *Plant J.* 8:37 (1995)).

With respect to the SDFs of the present invention a promoter is likely to be a relatively small portion of a genomic DNA (gDNA) sequence located in the first 2000 nucleotides upstream from an initial exon identified in a gDNA sequence or initial "ATG" or methionine codon in a corresponding cDNA or mRNA sequence. Such promoters are more likely to be found in the first 1000 nucleotides upstream of an

initial ATG or methionine codon of a cDNA sequence corresponding to a gDNA sequence. In particular, the promoter is usually located upstream of the transcription start site. Such a start site is located at the first exon predicted in the OCKHAM-cDNA predictions. In such an instance, the transcription start site is the first nucleotide of the 5' most exon, if the predictions are in the plus (+) strand, or the 3' most if the predictions are in the minus (-) strand. Alternative transcription start sites may be located between the first nucleotide of the 5' most exon (or the 3' most exon in the minus (-) strand) and the initial ATG or methionine codon in the cDNA sequence. The portions of a particular gDNA sequence that function as a promoter in a plant cell will preferably be found to hybridize at medium or high stringency to gDNA sequences presented in SEQ TABLES 1 AND 2.

Promoters are generally modular in nature. Short DNA sequences representing binding sites for proteins can be separated from each other by intervening sequences of varying length. For example, within a particular functional module protein binding sites may be constituted by regions of 5 to 60, preferably 10 to 30, more preferably 10 to 20 nucleotides. Within such binding sites, there are typically 2 to 6 nucleotides that specifically contact amino acids of the nucleic acid binding protein. The protein binding sites are usually separated from each other by 10 to several hundred nucleotides, typically by 15 to 150 nucleotides, often by 20 to 50 nucleotides. DNA binding sites in promoter elements often display dyad symmetry in their sequence. Often elements binding several different proteins, and/or a plurality of sites that bind the same protein, will be combined in a region of 100 to 1000 basepairs.

Elements that have transcription regulatory function can be isolated from their corresponding endogenous gene, or the desired sequence can be synthesized, and recombined in

constructs to direct expression of a structural gene in a desired tissue-specific, temporal-specific or other desired manner of inducibility or suppression. When hybridizations are performed to identify or isolate elements of a promoter by hybridization to the long sequences presented in SEQ TABLES 1 AND 2, conditions should be adjusted to account for the above-described nature of promoters. For example short probes, constituting the element sought, should be used under low temperature and/or high salt conditions. When long probes, which might include several promoter elements are used, low to medium stringency conditions are preferred when hybridizing to promoters across species.

Promoters can consist of a "basal promoter" that functions as a site for assembly of a transcription complex comprising an RNA polymerase, for example RNA polymerase II. A typical transcription complex will include additional factors such as TF_{II}B, TF_{II}D, and TF_{II}E. Of these, TF_{II}D appears to be the only one to bind DNA directly. Basal promoters frequently include a "TATA box" element usually located between 20 and 35 nucleotides upstream from the site of initiation of transcription. Basal promoters also sometimes include a "CCAAT box" element (typically a sequence CCAAT) and/or a GGGCG sequence, usually located between 40 and 200 nucleotides, preferably 60 to 120 nucleotides, upstream from the start site of transcription.

The promoter might also contain one or more "enhancers" and/or "suppressors" that function as binding sites for additional transcription factors that have the function of modulating the level of transcription with respect to tissue specificity of transcription, transcriptional responses to particular environmental or nutritional factors, and the like.

If a nucleotide sequence of an SDF, or part of the SDF, functions as a promoter or portion of a promoter, then nucleotide substitutions, insertions or deletions that do not

substantially affect the binding of relevant DNA binding proteins would be considered equivalent to the exemplified nucleotide sequence. It is envisioned that there are instances where it is desirable to decrease the binding of relevant DNA binding proteins to "silence" or "down-regulate" a promoter, or conversely to increase the binding of relevant DNA binding proteins to "enhance" or "up-regulate" a promoter. In such instances, polynucleotides representing changes to the nucleotide sequence of the DNA-protein contact region by insertion of additional nucleotides, changes to identity of relevant nucleotides, including use of chemically-modified bases, or deletion of one or more nucleotides are considered encompassed by the present invention.

Promoter function can be assayed by methods known in the art, preferably by measuring activity of a reporter gene operatively linked to the sequence being tested for promoter function. Examples of reporter genes include those encoding luciferase, green fluorescent protein, GUS, neo, cat and bar.

I.F. UTRs and Junctions

Polynucleotides comprising untranslated (UTR) sequences and intron/exon junctions are also within the scope of the invention. UTR sequences include introns and 5' or 3' untranslated regions (5' UTRs or 3' UTRs). Portions of the sequences shown in SEQ TABLES 1 AND 2 can comprise UTRs and introns or intron/exon junctions.

These portions of SDFs, especially UTRs, can have regulatory functions related to, for example, translation rate and mRNA stability. Thus, these portions of SDFs can be isolated for use as elements of gene constructs for expression of polynucleotides encoding desired polypeptides.

Introns of genomic DNA segments might also have regulatory functions. Sometimes promoter elements,

especially transcription enhancer or suppressor elements, are found within introns. Also, elements related to stability of heteronuclear RNA and efficiency of transport to the cytoplasm for translation can be found in intron elements.

5 Thus, these segments can also find use as elements of expression vectors intended for use to transform plants.

Just as with promoters, introns and UTR sequences and intron/exon junctions can vary from those shown in SEQ TABLES 1 AND 2. Such changes from those sequences preferably will
10 not affect the regulatory activity of the UTRs or intron or intron/exon junction sequences on expression, transcription, or translation. However, in some instances, down-regulation of such activity may be desired to modulate traits or phenotypic or *in vitro* activity.

15 I.G. Coding Sequences

Isolated polynucleotides of the invention can include coding sequences that encode polypeptides comprising an amino acid sequence encoded by a sequences in SEQ TABLES 1 AND 2 or an amino acid sequence presented in SEQ TABLES 1 AND 2.

20 A nucleotide sequence "encodes" a polypeptide if a cell (or a cell free *in vitro* system) expressing that nucleotide sequence produces a polypeptide having the recited amino acid sequence when the nucleotide sequence is transcribed and the primary transcript is subsequently processed and translated
25 by a host cell (or a cell free *in vitro* system) harboring the nucleic acid. Thus, an isolated nucleic acid that "encodes" a particular amino acid sequence can be a genomic sequence comprising exons and introns or a cDNA sequence that represents the product of splicing thereof. An isolated
30 nucleic acid "encoding an amino acid sequence" also encompasses heteronuclear RNA, which contains sequences that are spliced out during expression, and mRNA, which lacks those sequences.

Coding sequences can be constructed using chemical synthesis techniques or by isolating coding sequences or by modifying such synthesized or isolated coding sequences as described above.

5 In addition to encoding the polypeptide sequences of SEQ TABLES 1 AND 2, which are native to corn or *Arabidopsis*, the isolated polynucleotides can be variant polynucleotides that encode mutants, fragments, and fusions of those native proteins. Such polypeptides are described below in part II.

10 In variant polynucleotides generally, the number of substitutions, deletions or insertions is preferably less than 20%, more preferably less than 15%; even more preferably less than 10%, 5%, 3% or 1% of the number of nucleotides comprising a particularly exemplified sequence. It is generally expected
15 that non-degenerate nucleotide sequence changes that result in 1 to 10, more preferably 1 to 5 and most preferably 1 to 3 amino acid insertions, deletions or substitutions will not greatly affect the function of an encoded polypeptide. The most preferred embodiments are those wherein 1 to 20, preferably 1
20 to 10, most preferably 1 to 5 nucleotides are added to, deleted from and/or substituted in the sequences specifically disclosed in SEQ TABLES 1 AND 2.

Insertions or deletions in polynucleotides intended to be used for encoding a polypeptide should preserve the reading
25 frame. This consideration is not so important in instances when the polynucleotide is intended to be used as a hybridization probe.

II. Polypeptides

Polypeptides within the scope of the invention include
30 both native proteins as well as mutants, fragments, and fusions thereof. Polypeptides of the invention are those encoded by any of the six reading frames of sequences shown

in SEQ TABLES 1 AND 2, preferably encoded by the three frames reading in the 5' to 3' direction of the sequences as shown.

Native polypeptides include the proteins encoded by the sequences shown in SEQ TABLES 1 AND 2. Such native
5 polypeptides include those encoded by allelic variants.

Variants, including mutants, will exhibit at least 80% sequence identity to those native polypeptides of SEQ TABLES 1 AND 2. Sequence identity is used for polypeptides as defined above for polynucleotides. More preferably, the variants will
10 exhibit at least 85% sequence identity; even more preferably, at least 90% sequence identity; more preferably at least 95%, 96%, 97%, 98%, or 99% sequence identity. "Fragments" of polypeptide or "portions" of polypeptides will exhibit similar degrees of identity to the relevant portions of the native
15 polypeptide. Fusions will exhibit similar degrees of identity in that portion of the fusion represented by the variant of the native peptide.

Furthermore, variants will exhibit at least one of the functional properties of the native protein. Such properties
20 include, without limitation, protein interaction, DNA interaction, biological activity, immunological activity, receptor binding, signal transduction, transcription activity, growth factor activity, secondary structure, three-dimensional structure, etc. As to properties related to *in vitro* or *in*
25 *vivo* activities, the variants preferably exhibit at least 60% of the activity of the native protein; more preferably at least 70%, even more preferably at least 80%, 85%, 90% or 95% of at least one activity of the native protein.

A type of mutant of the native polypeptides comprises
30 amino acid substitutions. "Conservative substitutions" are preferred to maintain the function or activity of the polypeptide. Such substitutions include conservation of charge, polarity, hydrophobicity, size, etc. For example, one or more amino acid residues within the sequence can be

substituted with another amino acid of similar polarity that acts as a functional equivalent, for example providing a hydrogen bond in an enzymatic catalysis. Substitutes for an amino acid within an exemplified sequence are preferably made among the members of the class to which the amino acid belongs. For example, the nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan and methionine. The polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine. The positively charged (basic) amino acids include arginine, lysine and histidine. The negatively charged (acidic) amino acids include aspartic acid and glutamic acid.

Within the scope of sequence identity described above, a polypeptide of the invention may have additional individual amino acids or amino acid sequences inserted into the polypeptide in the middle thereof and/or at the N-terminal and/or C-terminal ends thereof. Likewise, some of the amino acids or amino acid sequences may be deleted from the polypeptide.

Antibodies

Isolated polypeptides can be utilized to produce antibodies. Polypeptides of the invention can generally be used, for example, as antigens for raising antibodies by known techniques. The resulting antibodies are useful as reagents for determining the distribution of the antigen protein within the tissues of a plant or within a cell of a plant. The antibodies are also useful for examining the expression level of proteins in various tissues, for example in a wild-type plant or following genetic manipulation of a plant, by methods such as Western blotting.

Antibodies of the present invention, both polyclonal and monoclonal, may be prepared by conventional methods. In

general, the polypeptides of the invention are first used to immunize a suitable animal, such as a mouse, rat, rabbit, or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies as detection reagents. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 μ g/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization.

Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating the blood at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000xg for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the method of Kohler and Milstein, *Nature* 256: 495 (1975), or modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells can be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate, or well, coated with the protein antigen. B-cells expressing membrane-bound immunoglobulin specific for the antigen bind to the plate, and are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen

cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are
5 assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected Mab-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in
10 mice).

Other methods for sustaining antibody-producing B-cell clones, such as by EBV transformation, are known.

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques.
15 Suitable labels include fluorophores, chromophores, radioactive atoms (particularly ^{32}P and ^{125}I), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to
20 convert 3,3',5,5'-tetramethylbenzidine (TNB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other
25 specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct modes. For example, ^{125}I may serve as a
30 radioactive label or as an electron-dense reagent. HRP may serve as an enzyme or as an antigen for a Mab. Further one may combine various labels for desired effect. For example, Mabs and avidin also require labels in the practice of this invention: thus, one might label a Mab with biotin, and detect

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its presence with avidin labeled with ^{125}I , or with an anti-biotin Mab labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

In Vitro Applications of Polypeptides

Some polypeptides of the invention will have enzymatic activities that are useful *in vitro*. For example, the soybean trypsin inhibitor (Kunitz) family is one of the numerous families of proteinase inhibitors. It comprises plant proteins which have inhibitory activity against serine proteinases from the trypsin and subtilisin families, thiol proteinases and aspartic proteinases. Thus, these peptides find *in vitro* use in protein purification protocols and perhaps in therapeutic settings requiring topical application of protease inhibitors.

Delta-aminolevulinic acid dehydratase (EC 4.2.1.24) (ALAD) catalyzes the second step in the biosynthesis of heme, the condensation of two molecules of 5-aminolevulinate to form porphobilinogen. Thus, ALAD proteins can be used as catalysts in synthesis of heme derivatives. Enzymes of biosynthetic pathways generally can be used as catalysts for *in vitro* synthesis of the compounds representing products of the pathway.

Polypeptides encoded by SDFs of the invention can be engineered to provide purification reagents to identify and purify additional polypeptides that bind to them. This allows one to identify proteins that function as multimers or elucidate signal transduction or metabolic pathways. In the case of DNA binding proteins, the polypeptide can be used in a similar manner to identify the DNA determinants of specific binding (S. Pierrou et al., *Anal. Biochem.* 229:99 (1995), S.

Chusacultanachai et al., *J. Biol. Chem.* 274:23591 (1999), Q.
Lin et al., *J. Biol. Chem.* 272:27274 (1997)).

II.A. MUTANTS, FRAGMENTS, AND FUSIONS

Generally, mutants, fragments, or fusions of the
5 polypeptides encoded by the maximum length sequence (MLS) can
exhibit at least one of the activities of the identified
domains and/or related polypeptides described in Sections (C)
and (D) of REF TABLES 1 and 2 corresponding to the MLS of
interest.

II.A.(1) Mutants

A type of mutant of the native polypeptides
comprises amino acid substitutions. "Conservative
substitutions", described above (see II.), are preferred to
maintain the function or activity of the polypeptide.

15 polypeptide. Such substitutions include conservation of
charge, polarity, hydrophobicity, size, etc. For example, one
or more amino acid residues within the sequence can be
substituted with another amino acid of similar polarity that
acts as a functional equivalent, for example providing a
20 hydrogen bond in an enzymatic catalysis. Substitutes for an
amino acid within an exemplified sequence are preferably made
among the members of the class to which the amino acid belongs.
For example, the nonpolar (hydrophobic) amino acids include
alanine, leucine, isoleucine, valine, proline, phenylalanine,
25 tryptophan and methionine. The polar neutral amino acids
include glycine, serine, threonine, cysteine, tyrosine,
asparagine, and glutamine. The positively charged (basic)
amino acids include arginine, lysine and histidine. The
negatively charged (acidic) amino acids include aspartic acid
30 and glutamic acid.

Within the scope of sequence identity described above, a
polypeptide of the invention may have additional individual

amino acids or amino acid sequences inserted into the polypeptide in the middle thereof and/or at the N-terminal and/or C-terminal ends thereof. Likewise, some of the amino acids or amino acid sequences may be deleted from the polypeptide. Amino acid substitutions may also be made in the sequences; conservative substitutions being preferred.

One preferred class of mutants are those that comprise (1) the domain of a MLS encoded polypeptide and/or (2) residues conserved between the MLS encoded polypeptide and related polypeptides of the MLS. For this class of mutants, the MLS encoded polypeptide sequence is changed by insertion, deletion, or substitution at positions flanking the domain and/or conserved residues.

Another class of mutants includes those that comprise a MLS encoded polypeptide sequence that is changed in the domain or conserved residues by a conservative substitution.

Yet another class of mutants includes those that lack one of the *in vitro* activities, or structural features of the MLS encoded polypeptides. One example is dominant negative mutants. Such a mutant may comprise an MLS encoded polypeptide sequence with non-conservative changes in a particular domain or group of conserved residues.

II.A.(2) FRAGMENTS

Fragments of particular interest are those that comprise a domain identified for a polypeptide encoded by an MLS of the instant invention and mutants thereof. Also, fragments that comprise at least one region of residues conserved between an MLS encoded polypeptide and its related polypeptides are of great interest. Fragments are sometimes useful as dominant negative mutations.

II.A.(3) FUSIONS

Of interest are chimeras comprising (1) a fragment of the MLS encoded polypeptide or mutants thereof of interest and (2) a fragment of a polypeptide comprising the same domain. For example, an AP2 helix encoded by a MLS of the invention fused to second AP2 helix from ANT protein, which comprises two AP2 helices. The present invention also encompasses fusions of MLS encoded polypeptides, mutants, or fragments thereof fused with related proteins or fragments thereof.

10 **DEFINITION OF DOMAINS**

The polypeptides of the invention may possess identifying domains as shown in REF TABLES 1 and 2. Domains are fingerprints or signatures that can be used to characterize protein families and/or motifs. Such fingerprints or signatures can comprise conserved (1) primary sequence, (2) secondary structure, and/or (3) three-dimensional conformation. Generally, each domain has been associated with either a family of proteins or a motif. Typically, these families and/or motifs have been correlated with specific *in-vitro* and/or *in-vivo* activities. A domain can be any length, including the entirety of the sequence of a protein. Detailed descriptions of the domains, associated families and motifs, and correlated activities of the polypeptides of the instant invention are described below. Usually, the polypeptides with designated domain(s) can exhibit at least one activity that is exhibited by any polypeptide that comprises the same domain(s).

Specific domains within the MLS encoded polypeptides are indicated by the reference REF TABLES 1 and 2. In addition, the domains within the MLS encoded polypeptide can be defined by the region that exhibits at least 70% sequence identity with the consensus sequences listed in the detailed description below of each of the domains.

The majority of the protein domain descriptions given below are obtained from Prosite,
(<http://www.expasy.ch/prosite/>), and Pfam,
(<http://pfam.wustl.edu/browse.shtml>).

1. (AAA) AAA-protein family signature

A large family of ATPases has been described [1 to 5] whose key feature is that they share a conserved region of about 220 amino acids that contains an ATP-binding site. This family is now called AAA, for 'A'TPases 'A'ssociated with diverse cellular 'A'ctivities. The proteins that belong to this family either contain one or two AAA domains. Proteins containing two AAA domains:

- Mammalian and drosophila NSF (N-ethylmaleimide-sensitive fusion protein) and the fungal homolog, SEC18. These proteins are involved in intracellular transport between the endoplasmic reticulum and Golgi, as well as between different Golgi cisternae.
- Mammalian transitional endoplasmic reticulum ATPase (previously known as p97 or VCP) which is involved in the transfer of membranes from the endoplasmic reticulum to the golgi apparatus. This protein forms a ring-shaped homooligomer composed of six subunits. The yeast homolog is CDC48 and it may play a role in spindle pole proliferation.
- Yeast protein PAS1, essential for peroxisome assembly and the related protein PAS1 from *Pichia pastoris*.
- Yeast protein AFG2.
- *Sulfolobus acidocaldarius* protein SAV and *Halobacterium salinarium* cdhH which may be part of a transduction pathway connecting light to cell division.

Proteins containing a single AAA domain:

- *Escherichia coli* and other bacteria ftsH (or hflB) protein. FtsH is an ATP-dependent zinc metallopeptidase that seems to degrade the heat-shock sigma-32 factor.

It is an integral membrane protein with a large cytoplasmic C-terminal domain that contain both the AAA and the protease domains.

- Yeast protein YME1, a protein important for maintaining the integrity of the mitochondrial compartment. YME1 is also a zinc-dependent protease.
- Yeast protein AFG3 (or YTA10). This protein also seems to contain a AAA domain followed by a zinc-dependent protease domain.

Subunits from the regulatory complex of the 26S proteasome [6] which is involved in the ATP-dependent degradation of ubiquitinated proteins:

- a) Mammalian subunit 4 and homologs in other higher eukaryotes, in yeast (gene YTA5) and fission yeast (gene mts2).
- b) Mammalian subunit 6 (TBP7) and homologs in other higher eukaryotes and in yeast (gene YTA2).
- c) Mammalian subunit 7 (MSS1) and homologs in other higher eukaryotes and in yeast (gene CIM5 or YTA3).
- d) Mammalian subunit 8 (P45) and homologs in other higher eukaryotes and in yeast (SUG1 or CIM3 or TBY1) and fission yeast (gene let1).

Other probable subunits such as human TBP1 which seems to influence HIV gene expression by interacting with the virus tat transactivator protein and yeast YTA1 and YTA6.

- Yeast protein BCS1, a mitochondrial protein essential for the expression of the Rieske iron-sulfur protein.
- Yeast protein MSP1, a protein involved in intramitochondrial sorting of proteins.
- Yeast protein PAS8, and the corresponding proteins PAS5 from *Pichia pastoris* and PAY4 from *Yarrowia lipolytica*.
- Mouse protein SKD1 and its fission yeast homolog (SpAC2G11.06).
- *Caenorhabditis elegans* meiotic spindle formation protein mei-1.
- Yeast protein SAP1.

- Yeast protein YTA7.
- Mycobacterium leprae hypothetical protein A2126A.

It is proposed that, in general, the AAA domains in these proteins act as ATP- dependent protein clamps [5]. In addition to the ATP-binding 'A' and 'B' motifs, which are located in the N-terminal half of this domain, there is a highly conserved region located in the central part of the domain which was used to develop a signature pattern.

Consensus pattern: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]- D-x-A-[LIFA]-x-R

[1] Froehlich K.-U., Fries H.W., Ruediger M., Erdmann R., Botstein D., Mecke D. J. Cell Biol. 114:443-453(1991).

[2] Erdmann R., Wiebel F.F., Flessau A., Rytka J., Beyer A., Froehlich K.-U., Kunau W.-H. Cell 64:499-510(1991).

[3] Peters J.-M., Walsh M.J., Franke W.W. EMBO J. 9:1757-1767(1990).

[4] Kunau W.-H., Beyer A., Goette K., Marzioch M., Saidowsky J., Skaletz-Rorowski A., Wiebel F.F. Biochimie 75:209-224(1993).

[5] Confalonieri F., Duguet M. BioEssays 17:639-650(1995).

[6] Hilt W., Wolf D.H. Trends Biochem. Sci. 21:96-102(1996).

2. Aminotransferases class-IV signature

Aminotransferases share certain mechanistic features with other pyridoxal-phosphate dependent enzymes, such as the covalent binding of the pyridoxal-phosphate group to a lysine residue. On the basis of sequence similarity, these various enzymes can be grouped [1,2] into subfamilies. One of these, called class-IV, currently consists of the following enzymes:

- Branched-chain amino-acid aminotransferase (EC 2.6.1.42) (transaminase B), a bacterial (gene *ilvE*) and eukaryotic enzyme which catalyzes the reversible

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transfer of an amino group from 4-methyl-2-oxopentanoate to glutamate, to form leucine and 2-oxoglutarate.

- D-alanine aminotransferase (EC 2.6.1.21). A bacterial enzyme which catalyzes the transfer of the amino group from D-alanine (and other D-amino acids) to 2-oxoglutarate, to form pyruvate and D-aspartate.
- 4-amino-4-deoxychorismate (ADC) lyase (gene pabC). A bacterial enzyme that converts ADC into 4-aminobenzoate (PABA) and pyruvate.

The above enzymes are proteins of about 270 to 415 amino-acid residues that share a few regions of sequence similarity. Surprisingly, the best-conserved region does not include the lysine residue to which the pyridoxal-phosphate group is known to be attached, in *ilvE*. The region that has been selected as a signature pattern is located some 40 residues at the C-terminus side of the Plp-lysine

Consensus pattern: E-x-[STAGCI]-x(2)-N-[LIVMFAC]-[FY]-x(6,12)-[LIVMF]-x-T-x(6,8)-[LIVM]-x-[GS]-[LIVM]-x-[KR]-

[1] Green J.M., Merkel W.K., Nichols B.P. J. Bacteriol. 174:5317-5323(1992).

[2] Bairoch A. Unpublished observations (1992).

3. Bacterial mutT domain signature

The bacterial mutT protein is involved in the GO system [1] responsible for removing an oxidatively damaged form of guanine (8-hydroxyguanine or 7,8-dihydro-8-oxoguanine) from DNA and the nucleotide pool. 8-oxo-dGTP is inserted opposite to dA and dC residues of template DNA with almost equal efficiency thus leading to A.T to G.C transversions. MutT specifically degrades 8-oxo-dGTP to the monophosphate with the concomitant release of pyrophosphate. MutT is a small

protein of about 12 to 15 Kd. It has been shown [2,3] that a region of about 40 amino acid residues, which is found in the N-terminal part of mutT, can also be found in a variety of other prokaryotic, viral, and eukaryotic proteins. These proteins are:

- *Streptomyces pneumoniae* mutX.
- A mutT homolog from plasmid pSAM2 of *Streptomyces ambofaciens*.
- *Bartonella bacilliformis* invasion protein A (gene invA).
- *Escherichia coli* dATP pyrophosphohydrolase.
- Protein D250 from African swine fever viruses.
- Proteins D9 and D10 from a variety of poxviruses.
- Mammalian 7,8-dihydro-8-oxoguanine triphosphatase (EC 3.1.6.-) [4].
- Mammalian diadenosine 5',5'''-P₁,P₄-tetrphosphate asymmetrical hydrolase (Ap4Aase) (EC 3.6.1.17) [5], which cleaves A-5'-PPPP-5'A to yield AMP and ATP.
- A protein encoded on the antisense RNA of the basic fibroblast growth factor gene in higher vertebrates.
- Yeast protein YSA1.
- *Escherichia coli* hypothetical protein yfaO.
- *Escherichia coli* hypothetical protein ygdU and HI0901, the corresponding *Haemophilus influenzae* protein.
- *Escherichia coli* hypothetical protein yjaD and HI0432, the corresponding *Haemophilus influenzae* protein.
- *Escherichia coli* hypothetical protein yrfE.
- *Bacillus subtilis* hypothetical protein yqkG.
- *Bacillus subtilis* hypothetical protein yzgD.
- Yeast hypothetical protein YGL067w.

It is proposed [2] that the conserved domain could be involved in the active center of a family of pyrophosphate-releasing NTPases. As a signature pattern the core region of

the domain was selected; it contains four conserved glutamate residues.

Consensus pattern: G-x(5)-E-x(4)-[STAGC]-[LIVMAC]-x-R-E-
5 [LIVMFT]-x-E-E-

[1] Michaels M.L., Miller J.H. J. Bacteriol. 174:6321-6325(1992).

[2] Koonin E.V. Nucleic Acids Res. 21:4847-4847(1993).

10 [3] Mejean V., Salles C., Bullions M.J., Bessman M.J., Claverys J.-P. Mol. Microbiol. 11:323-330(1994).

[4] Sakumi K., Furuichi M., Tsuzuki T., Kakuma T., Kawabata S., Maki H., Sekiguchi M. J. Biol. Chem. 268:23524-23530(1993).

15 [5] Thorne N.M.H., Hankin S., Wilkinson M.C., Nunez C., Barraclough R., McLennan A.G. Biochem. J. 311:717-721(1995).

4. Cystatin domain

20 This is a very diverse family. Attempts to define separate subfamilies have failed. Typically, either the N-terminal or C-terminal end is very divergent. But splitting into two domains would make very short families. Cathelicidins are related to this family but have not been included. Number of members: 147

25 Inhibitors of cysteine proteases [1,2,3], which are found in the tissues and body fluids of animals, in the larva of the worm *Onchocerca volvulus* [4], as well as in plants, can be grouped into three distinct but related families:

- 30 - Type 1 cystatins (or stefins), molecules of about 100 amino acid residues with neither disulfide bonds nor carbohydrate groups.
- Type 2 cystatins, molecules of about 115 amino acid residues which contain one or two disulfide loops near their C-terminus.

- Kininogens, which are multifunctional plasma glycoproteins.

They are the precursor of the active peptide bradykinin and play a role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII. They are also inhibitors of cysteine proteases. Structurally, kininogens are made of three contiguous type-2 cystatin domains, followed by an additional domain (of variable length) which contains the sequence of bradykinin. The first of the three cystatin domains seems to have lost its inhibitory activity.

In all these inhibitors, there is a conserved region of five residues which has been proposed to be important for the binding to the cysteine proteases. The consensus pattern starts one residue before this conserved region.

-Consensus pattern: [GSTEQKRV]-Q-[LIVT]-[VAF]-[SAGQ]-G-x-[LIVMNK]-x(2)-[LIVMFY]-x-[LIVMFYA]-[DENQKRHSIV]

- [1] Barrett A.J. Trends Biochem. Sci. 12:193-196(1987).
- [2] Rawlings N.D., Barrett A.J. J. Mol. Evol. 30:60-71(1990).
- [3] Turk V., Bode W. FEBS Lett. 285:213-219(1991).
- [4] Lustigman S., Brotman B., Huima T., Prince A.M. Mol. Biochem. Parasitol. 45:65-76(1991).

5. Dehydrins signatures

A number of proteins are produced by plants that experience water-stress. Water-stress takes place when the water available to a plant falls below a critical level. The plant hormone abscisic acid (ABA) appears to modulate the response of plant to water-stress. Proteins that are expressed during water-stress are called dehydrins [1,2] or LEA group 2 proteins [3]. The proteins that belong to this family are listed below.

- *Arabidopsis thaliana* XERO 1, XERO 2 (LTI30), RAB18, ERD10 (LTI45) ERD14 and COR47.
- Barley dehydrins B8, B9, B17, and B18.
- Cotton LEA protein D-11.
- 5 - *Craterostigma plantagineum* dessication-related proteins A and B.
- Maize dehydrin M3 (RAB-17).
- Pea dehydrins DHN1, DHN2, and DHN3.
- Radish LEA protein.
- 10 - Rice proteins RAB 16B, 16C, 16D, RAB21, and RAB25.
- Tomato TAS14.
- Wheat dehydrin RAB 15 and cold-shock protein cor410, cs66 and cs120.

Dehydrins share a number of structural features.

15 One of the most notable features is the presence, in their central region, of a continuous run of five to nine serines followed by a cluster of charged residues. Such a region has been found in all known dehydrins so far with the exception of pea dehydrins. A second

20 conserved feature is the presence of two copies of a lysine-rich octapeptide; the first copy is located just after the cluster of charged residues that follows the poly-serine region and the second copy is found at the C-terminal extremity. Signature patterns for both

25 regions were derived.

Consensus pattern: S(5)-[DE]-x-[DE]-G-x(1,2)-G-x(0,1)-[KR](4
 Consensus pattern: [KR]-[LIM]-K-[DE]-K-[LIM]-P-G-

- 30 [1] Close T.J., Kortt A.A., Chandler P.M. Plant Mol. Biol. 13:95-108(1989).
- [2] Robertson M., Chandler P.M. Plant Mol. Biol. 19:1031-1044(1992).

[3] Dure L. III, Crouch M., Harada J., Ho T.-H. D., Mundy J., Quatrano R., Thomas T., Sung Z.R. Plant Mol. Biol. 12:475-486(1989).

5 6. D-isomer specific 2-hydroxyacid dehydrogenases (2 Hacid DH)

This Pfam covers the Formate dehydrogenase, D-glycerate dehydrogenase and D-lactate dehydrogenase families in SCOP. A number of NAD-dependent 2-hydroxyacid dehydrogenases which
10 seem to be specific for the D-isomer of their substrate have been shown [1,2,3,4] to be functionally and structurally related. These enzymes are listed below.

- 15 - D-lactate dehydrogenase (EC 1.1.1.28), a bacterial enzyme which catalyzes the reduction of D-lactate to pyruvate.
- D-glycerate dehydrogenase (EC 1.1.1.29) (NADH-dependent hydroxypyruvate reductase), a plant leaf peroxisomal enzyme that catalyzes the reduction of hydroxypyruvate to glycerate. This reaction is part
20 of the glycolate pathway of photorespiration.
- D-glycerate dehydrogenase from the bacteria *Hyphomicrobium methylovorum* and *Methylobacterium extorquens*.
- 3-phosphoglycerate dehydrogenase (EC 1.1.1.95), a
25 bacterial enzyme that catalyzes the oxidation of D-3-phosphoglycerate to 3-phosphohydroxypyruvate. This reaction is the first committed step in the 'phosphorylated' pathway of serine biosynthesis.
- Erythronate-4-phosphate dehydrogenase (EC 1.1.1.-) (gene *pdxB*), a bacterial enzyme involved in the
30 biosynthesis of pyridoxine (vitamin B6).
- D-2-hydroxyisocaproate dehydrogenase (EC 1.1.1.-) (D-hicDH), a bacterial enzyme that catalyzes the reversible and stereospecific interconversion between

2-ketocarboxylic acids and D-2-hydroxy-carboxylic acids.

- Formate dehydrogenase (EC 1.2.1.2) (FDH) from the bacteria *Pseudomonas* sp. 101 and various fungi [5].
- Vancomycin resistance protein vanH from *Enterococcus faecium*; this protein is a D-specific alpha-keto acid dehydrogenase involved in the formation of a peptidoglycan which does not terminate by D-alanine thus preventing vancomycin binding.
- *Escherichia coli* hypothetical protein ycdW.
- *Escherichia coli* hypothetical protein yiaE.
- *Haemophilus influenzae* hypothetical protein HI1556.
- Yeast hypothetical protein YER081w.
- Yeast hypothetical protein YIL074w.

All these enzymes have similar enzymatic activities and are structurally related. Three of the most conserved regions of these proteins have been selected to develop patterns. The first pattern is based on a glycine-rich region located in the central section of these enzymes; this region probably corresponds to the NAD-binding domain. The two other patterns contain a number of conserved charged residues, some of which may play a role in the catalytic mechanism.

-Consensus pattern: [LIVMA]-[AG]-[IVT]-[LIVMFY]-[AG]-x-G-

[NHKRQGSAC]-[LIV]-G-x(13,14)-[LIVfMT]-x(2)-[FYwCTH]-[DNSTK]

-Consensus pattern: [LIVMFYWA]-[LIVFYWC]-x(2)-[SAC]-[DNQHR]-[IVFA]-[LIVF]-x-[LIVF]-[HNI]-x-P-x(4)-[STN]-x(2)-[LIVMF]-x-[GSDN]

-Consensus pattern: [LMFATC]-[KPQ]-x-[GSTDN]-x-[LIVMFYWR]-

[LIVMFYW](2)-N-x-[STAGC]-R-[GP]-x-[LIVH]-[LIVMC]-[DNV]

[1] Grant G.A. Biochem. Biophys. Res. Commun. 165:1371-1374 (1989).

- [2] Kochhar S., Hunziker P., Leong-Morgenthaler P.M., Hottinger H. Biochem. Biophys. Res. Commun. 184:60-66(1992).
 [3] Ohta T., Taguchi H. J. Biol. Chem. 266:12588-12594(1991).
 [4] Goldberg J.D., Yoshida T., Brick P. J. Mol. Biol. 236:1123-1140(1994).
 [5] Popov V.O., Lamzin V.S. Biochem. J. 301:625-643(1994).

7. dnaJ domains signatures and profile

The prokaryotic heat shock protein dnaJ interacts with the chaperone hsp70-like dnaK protein [1]. Structurally, the dnaJ protein consists of an N- terminal conserved domain (called 'J' domain) of about 70 amino acids, a glycine-rich region ('G' domain') of about 30 residues, a central domain containing four repeats of a CXXCXGXG motif ('CRR' domain) and a C-terminal region of 120 to 170 residues. Such a structure is shown in the following schematic representation:

```

+-----+-----+-----+-----+-----+-----+
-----+ | N-terminal | | Gly-R | | CXXCXGXG | C-
terminal | +-----+-----+-----+-----+-----+
-----+

```

It has been shown [2] that the 'J' domain as well as the 'CRR' domain are also found in other prokaryotic and eukaryotic proteins which are listed below.

a) Proteins containing both a 'J' and a 'CRR' domain:

- Yeast protein MAS5/YDJ1 which seems to be involved in mitochondrial protein import.
- Yeast protein MDJ1, involved in mitochondrial biogenesis and protein folding.
- Yeast protein SCJ1, involved in protein sorting.
- Yeast protein XDJ1.
- Plants dnaJ homologs (from leek and cucumber).
- Human HDJ2, a dnaJ homolog of unknown function.
- Yeast hypothetical protein YNL077w.

b) Proteins containing a 'J' domain without a 'CRR' domain:

63

- *Rhizobium fredii* nolC, a protein involved in cultivar-specific nodulation of soybean.
- *Escherichia coli* cbpA [3], a protein that binds curved DNA.
- 5 - Yeast protein SEC63/NPL1, important for protein assembly into the endoplasmic reticulum and the nucleus.
- Yeast protein SIS1, required for nuclear migration during mitosis.
- 10 - Yeast protein CAJ1.
- Yeast hypothetical protein YFR041c.
- Yeast hypothetical protein YIR004w.
- Yeast hypothetical protein YJL162c.
- *Plasmodium falciparum* ring-infected erythrocyte surface antigen (RESA). RESA, whose function is not known, is associated with the membrane skeleton of newly invaded erythrocytes.
- 15 - Human HDJ1.
- Human HSJ1, a neuronal protein.
- 20 - *Drosophila* cysteine-string protein (csp).

A signature pattern for the 'J' domain was developed, based on conserved positions in the C-terminal half of this domain. A pattern for the 'CRR' domain, based on the first two copies of that motif was also developed. A profile for the 'J' domain was also developed.

Consensus pattern: [FY]-x(2)-[LIVMA]-x(3)-[FYWHNT]-[DENQSA]-x-L-x-[DN]-x(3)-[KR]-x(2)-[FYI]-

Consensus pattern: C-[DEGSTHKKR]-x-C-x-G-x-[GK]-[AGSDM]-x(2)-[GSNKR]-x(4,6)-C-x(2,3)-C-x-G-x-G-

[1] Cyr D.M., Langer T., Douglas M.G. Trends Biochem. Sci. 19:176-181(1994).

[2] Bork P., Sander C., Valencia A., Bukau B. Trends Biochem. Sci. 17:129-129(1992).

[3] Ueguchi C., Kaneda M., Yamada H., Mizuno T. Proc. Natl. Acad. Sci. U.S.A. 91:1054-1058(1994).

5

8. Domain of unknown function

9. Gamma-thionins family signature

10 The following small plant proteins are evolutionary related:

- Gamma-thionins from wheat endosperm (gamma-purothionins) and barley (gamma-hordothionins) which are toxic to animal cells and inhibit protein synthesis in cell free systems [1].
- 15 - A flower-specific thionin (FST) from tobacco [2].
- Antifungal proteins (AFP) from the seeds of Brassicaceae species such as radish, mustard, turnip and Arabidopsis thaliana [3].
- Inhibitors of insect alpha-amylases from sorghum [4].
- 20 - Probable protease inhibitor P322 from potato.
- A germination-related protein from cowpea [5].
- Anther-specific protein SF18 from sunflower [6]. SF18 is a protein that contains a gamma-thionin domain at its N-terminus and a proline-rich C-terminal domain.
- 25 - Soybean sulfur-rich protein SE60 [7].
- Vicia faba antibacterial peptides fabatin-1 and -2.

In their mature form, these proteins generally consist of about 45 to 50 amino-acid residues. As shown in the following schematic representation, these peptides contain
30 eight conserved cysteines involved in disulfide bonds.

```
+-----+ | +-----+
-----+ | | | |
xxCxxxxxxxxxxCxxxxCxxxCxxxxxxxxCxxxxxCxCxxxC
*****|***| | | +---|-----+ | +-----+
35 -----+
```


65

'C': conserved cysteine involved in a disulfide bond.

'*': position of the pattern.

Consensus pattern: [KRG]-x-C-x(3)-[SV]-x(2)-[FYWH]-x-[GF]-x-
5 C-x(5)-C-x(3)-C [The four C's are involved in disulfide
bonds]-

[1] Bruix M., Jimenez M.A., Santoro J., Gonzalez C., Colilla
F.J., Mendez E., Rico M. Biochemistry 32:715-724(1993).

10 [2] Gu Q., Kawata E.E., Morse M.-J., Wu H.-M., Cheung A.Y.
Mol. Gen. Genet. 234:89-96(1992).

[3] Terras F.R.G., Torrekens S., van Leuven F., Osborn R.W.,
Vanderleyden J., Cammue B.P.A., Broekaert W.F. FEBS Lett.
316:233-240(1993).

15 [4] Bloch C. Jr., Richardson M. FEBS Lett. 279:101-104(1991).

[5] Ishibashi N., Yamauchi D., Miniamikawa T. Plant Mol.
Biol. 15:59-64(1990).

[7] Choi Y., Choi Y.D., Lee J.S. Plant Physiol. 101:699-
700(1993).

20

10. haloacid dehalogenase-like hydrolase

This family is structurally different from the alpha/
beta hydrolase family (abhydrolase). This family includes L-
2-haloacid dehalogenase, epoxide hydrolases and phosphatases.

25 The structure of the family consists of two domains. One is
an inserted four helix bundle, which is the least well
conserved region of the alignment, between residues 16 and 96
of Swiss:P24069. The rest of the fold is composed of the core
alpha/beta domain.

30 [1] Hisano T, Hata Y, Fujii T, Liu JQ, Kurihara T, Esaki N,
Soda K, J Biol Chem 1996; 271:20322-20330.

11. Helix-turn-helix (HTH3)

This large family of DNA binding helix-turn helix proteins includes Cro Swiss:P03036 and CI Swiss:P03034.

12. Heme-binding domain in cytochrome b5 and oxidoreductases
5 (heme_1)

Cytochrome b5 is a membrane-bound hemo protein which acts as an electron carrier for several membrane-bound oxygenases [1]. There are two homologous forms of b5, one found in microsomes and one found in the outer membrane of
10 mitochondria. Two conserved histidine residues serve as axial ligands for the heme group. The structure of a number of oxidoreductases consists of the juxtaposition of a heme-binding domain homologous to that of b5 and either a flavodehydrogenase or a molybdopterin domain. These enzymes
15 are:

- Lactate dehydrogenase (EC 1.1.2.3) [2], an enzyme that consists of a flavodehydrogenase domain and a heme-binding domain called cytochrome b2.
- Nitrate reductase (EC 1.6.6.1), a key enzyme involved
20 in the first step of nitrate assimilation in plants, fungi and bacteria [3,4]. Consists of a molybdopterin domain (see <PDOC00484>), a heme-binding domain called cytochrome b557, as well as a cytochrome reductase domain.
- Sulfite oxidase (EC 1.8.3.1) [5], which catalyzes the
25 terminal reaction in the oxidative degradation of sulfur-containing amino acids. Also consists of a molybdopterin domain and a heme-binding domain.

This family of proteins also includes:

- TU-36B, a Drosophila muscle protein of unknown
30 function [6].
- Fission yeast hypothetical protein SpAC1F12.10c.
- Yeast hypothetical protein YMR073c.
- Yeast hypothetical protein YMR272c.

A segment was used which includes the first of the two histidine heme ligands, as a signature pattern for the heme-binding domain of cytochrome b5 family.

5 Consensus pattern: [FY]-[LIVMK]-x(2)-H-P-[GA]-G [H is a heme axial ligand]-

[1] Ozols J. Biochim. Biophys. Acta 997:121-130(1989).

[2] Guiard B. EMBO J. 4:3265-3272(1985).

10 [3] Calza R., Huttner E., Vincentz M., Rouze P., Galangau F., Vaucheret H., Cherel I., Meyer C., Kronenberger J., Caboche M. Mol. Gen. Genet. 209:552-562(1987).

[4] Crawford N.M., Smith M., Bellissimo D., Davis R.W. Proc. Natl. Acad. Sci. U.S.A. 85:5006-5010(1988).

15 [5] Guiard B., Lederer F. Eur. J. Biochem. 100:441-453(1979).

[6] Levin R.J., Boychuk P.L., Croniger C.M., Kazzaz J.A., Rozek C.E. Nucleic Acids Res. 17:6349-6367(1989).

13. KH domain

20 KH motifs probably bind RNA directly. Auto antibodies to Nova, a KH domain protein, cause paraneoplastic opsoclonus ataxia.

[1] Burd CG, Dreyfuss G, Science 1994;265:615-621.

25 [2] Musco G, Stier G, Joseph C, Castiglione Morelli MA, Nilges M, Gibson TJ, Pastore A, Cell 1996;85:237-245.

14. MAPEG family (aka: FLAP/GST2/LTC4S family signature)

The following mammalian proteins are evolutionary related [1]:

30 - Leukotriene C4 synthase (EC 2.5.1.37) (gene LTC4S), an enzyme that catalyzes the production of LTC4 from LTA4.

68

- Microsomal glutathione S-transferase II (EC 2.5.1.18) (GST-II) (gene GST2), an enzyme that can also produces LTC4 from LTA4.
- 5-lipoxygenase activating protein (gene FLAP), a protein that seems to be required for the activation of 5-lipoxygenase.

These are proteins of 150 to 160 residues that contain three transmembrane segments. As a signature pattern, a conserved region between the first and second transmembrane domains was selected.

Consensus pattern: G-x(3)-F-E-R-V-[FY]-x-A-[NQ]-x-N-C

[1] Jakobsson P.-J., Mancini J.A., Ford-Hutchinson A.W. J. Biol. Chem. 271:22203-22210(1996).

15. Pathogenesis-related protein Bet v I family signature

A number of plant proteins, which all seem to be involved in pathogen defense response, are structurally related [1,2,3]. These proteins are:

- Bet v I, the major pollen allergen from white birch. Bet v I is the main cause of type I allergic reactions in Europe, North America and USSR.
- Aln g I, the major pollen allergen from alder.
- Api G I, the major allergen from celery.
- Car b I, the major pollen allergen from hornbeam.
- Cor a I, the major pollen allergen from hazel.
- Mal d I, the major pollen allergen from apple.
- Asparagus wound-induced protein AoPR1.
- Kidney bean pathogenesis-related proteins 1 and 2.
- Parsley pathogenesis-related proteins PR1-1 and PR1-3.
- Pea disease resistance response proteins pI49, pI176 and DRRG49-C.
- Pea abscisic acid-responsive proteins ABR17 and ABR18.

- Potato pathogenesis-related proteins STH-2 and STH-21.
- Soybean stress-induced protein SAM22.

These proteins are thought to be intracellularly located. They contain from 155 to 160 amino acid residues. As a signature pattern, a conserved region located in the third quarter of these proteins has been selected

Consensus pattern: G-x(2)-[LIVMF]-x(4)-E-x(2)-[CSTAEN]-x(8,9)-[GND]-G-[GS]-[CS]-x(2)-K-x(4)-[FY]-

[1] Breiteneder H., Pettenburger K., Bito A., Valenta R., Kraft D., Rumpold H., Scheiner O., Breitenbach M. EMBO J. 8:1935-1938(1989).

[2] Crowell D., John M.E., Russell D., Amasino R.M. Plant Mol. Biol. 18:459-466(1992).

[3] Warner S.A.J., Scott R., Draper J. Plant Mol. Biol. 19:555-561(1992).

16. Photosystem I psaG / psaK (PSI PSAK) proteins signature

Photosystem I (PSI) [1] is an integral membrane protein

complex that uses light energy to mediate electron transfer from plastocyanin to ferredoxin. It is found in the chloroplasts of plants and cyanobacteria. PSI is composed of at least 14 different subunits, two of which PSI-G (gene psaG) and PSI-K (gene psaK) are small hydrophobic proteins of about 7 to 9 Kd and evolutionary related [2]. Both seem to contain two transmembrane regions. Cyanobacteria seem to encode only for PSI-K.

As a signature pattern, the best-conserved region was selected which seems to correspond to the second transmembrane region.

-Consensus pattern: [GT]-F-x-[LIVM]-x-[DEA]-x(2)-[GA]-x-[GTA]-[SA]-x-G-H-x-[LIVM]-[GA]

- [1] Golbeck J.H. Biochim. Biophys. Acta 895:167-204 (1987).
 [2] Kjaerulff S., Andersen B., Nielsen V.S., Moller B.L.,
 Okkels J.S. J. Biol. Chem. 268:18912-18916 (1993).

5 17. Plant lipid transfer protein family signature (LTP)

Plant cells contain proteins, called lipid transfer proteins (LTP) [1,2,3], which are able to facilitate the transfer of phospholipids and other lipids across membranes. These proteins, whose subcellular location is not yet known,
 10 could play a major role in membrane biogenesis by conveying phospholipids such as waxes or cutin from their site of biosynthesis to membranes unable to form these lipids. Plant LTP's are proteins of about 9 Kd (90 amino acids) which contain eight conserved cysteine residues all involved in
 15 disulfide bridges, as shown in the following schematic representation.

```

      +-----+ | +-----+ | | | |
*****
xCxxxxCxxxxxxCCxxxxxxxxxCxCxxxxxxxxxxxxxCxxxxxCxx | | | | +----
20 ----|-----+ | +-----+
'C': conserved cysteine involved in a disulfide bond.
'*': position of the pattern.
```

Consensus pattern: [LIVM]-[PA]-x(2)-C-x-[LIVM]-x-[LIVM]-x-
 25 [LIVMFY]-x-[LIVM]-[ST]-x(3)-[DN]-C-x(2)-[LIVM] [The two C's
 are involved in disulfide bonds]

- [1] Wirtz K.W.A. Annu. Rev. Biochem. 60:73-99 (1991).
 [2] Arondel V., Kader J.C. Experientia 46:579-585 (1990).
 30 [3] Ohlrogge J.B., Browse J., Somerville C.R. Biochim.
 Biophys. Acta 1082:1-26 (1991).

18. Ribosomal protein S7e signature

A number of eukaryotic ribosomal proteins can be grouped on the basis of sequence similarities [1]. One of these families consists of:

- Mammalian S7.
- Xenopus S8.
- Insect S7.
- Yeast probable ribosomal protein S7 (N2212).
- Fission yeast probable ribosomal protein S7 (SpAC18G6.13c).

These proteins have about 200 amino acids. A highly conserved stretch of 14 residues which is located in the central section and which is rich in charged residues was selected as a signature pattern.

Consensus pattern: [KR]-L-x-R-E-L-E-K-K-F-[SAP]-x-[KR]-H

[1] Salazar C.E., Mills-Hamm D.M., Kumar V., Collins F.H. Nucleic Acids Res. 21:4147-4147(1993).

19. Ribosomal protein L34 signature

Ribosomal protein L34 is one of the proteins from the large subunit of the prokaryotic ribosome. It is a small basic protein of 44 to 51 amino-acid residues [1]. L34 belongs to a family of ribosomal proteins which, on the basis of sequence similarities, groups: - Eubacterial L34.

- Red algal chloroplast L34. - Cyanelle L34.

A conserved region that corresponds to the N-terminal half of L34 has been selected

as a signature pattern.

-Consensus pattern: K-[RG]-T-[FYWL]-[EQS]-x(5)-[KRHS]-x(4,5)-G-F-x(2)-R

[1] Old I.G., Margarita D., Saint Girons I. Nucleic Acids Res. 20:6097-6097(1992).

20. Ribosomal protein L6 signatures

Ribosomal protein L6 is one of the proteins from the large ribosomal subunit. In *Escherichia coli*, L6 is known to bind directly to the 23S rRNA and is located at the aminoacyl-tRNA binding site of the peptidyltransferase center. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2,3,4], groups: - Eubacterial L6.

- Algal chloroplast L6.
- Cyanelle L6.
- Archaeobacterial L6.
- *Marchantia polymorpha* mitochondrial L6.
- Yeast mitochondrial YmL6 (gene MRPL6).
- Mammalian L9.
- *Drosophila* L9.
- Plants L9.
- Yeast L9 (YL11).

While all the above proteins are evolutionary related it is very difficult to derive a pattern that will find them all. Two patterns were therefore created, the first to detect eubacterial, cyanelle and mitochondrial L6, the second to detect archaeobacterial L6 as well as eukaryotic L9.

-Consensus pattern: [PS]-[DENS]-x-Y-K-[GA]-K-G-[LIVM]

-Consensus pattern: Q-x(3)-[LIVM]-x(2)-[KR]-x(2)-R-x-F-x-D-G-[LIVM]-Y-[LIVM]-x(2)-[KR]

[1] Suzuki K., Olvera J., Wool I.G. *Gene* 93:297-300(1990).

[2] Schwank S., Harrer R., Schueller H.-J., Schweizer E. *Curr. Genet.* 24:136-140(1993).

[3] Golden B.L., Ramakrishnan V., White S.W. *EMBO J.* 12:4901-4908(1993).

[4] Otaka E., Hashimoto T., Mizuta K., Suzuki K. *Protein Seq. Data Anal.* 5:301-313(1993).

21. Ribosomal protein S14p/S29e (Ribosomal protein S14 signature)

Ribosomal protein S14 is one of the proteins from the small ribosomal subunit. In *Escherichia coli*, S14 is known to be required for the assembly of 30S particles and may also be responsible for determining the conformation of 16S rRNA at the A site. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1,2], groups:

- Eubacterial S14.
- Algal and plant chloroplast S14.
- Cyanelle S14.
- Archaeobacterial *Methanococcus vannielii* S14.
- Plant mitochondrial S14.
- Yeast mitochondrial MRP2.
- Mammalian S29.
- Yeast YS29A/B.

S14 is a protein of 53 to 115 amino-acid residues. Our signature pattern is based on the few conserved positions located in the center of these proteins.

Consensus pattern: [RP]-x(0,1)-C-x(11,12)-[LIVMF]-x-[LIVMF]-[SC]-[RG]-x(3)-[RN]

[1] Chan Y.-L., Suzuki K., Olvera J., Wool I.G. *Nucleic Acids Res.* 21:649-655(1993).

[2] Otaka E., Hashimoto T., Mizuta K. *Protein Seq. Data Anal.* 5:285-300(1993).

22. Ribosomal protein S16 signature

Ribosomal protein S16 is one of the proteins from the small ribosomal subunit. It belongs to a family of ribosomal proteins which, on the basis of sequence similarities [1], groups:

- Eubacterial S16.

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- Algal and plant chloroplast S16.
- Cyanelle S16.
- *Neurospora crassa* mitochondrial S24 (cyt-21).

5 S16 is a protein of about 100 amino-acid residues. A conserved region located in the N-terminal extremity of these proteins has been selected as a signature pattern.

Consensus pattern: [LIVMT]-x-[LIVM]-[KR]-L-[STAK]-R-x-G-[AKR]

10 [1] Otake E., Hashimoto T., Mizuta K. Protein Seq. Data Anal. 5:285-300(1993).

23. Ribosomal protein S21 signature

15 Ribosomal protein S21 is one of the proteins from the small ribosomal subunit. So far S21 has only been found in eubacteria. It is a protein of 55 to 70 amino-acid residues. A conserved region in the N-terminal section of the protein has been selected as a signature pattern.

20 Consensus pattern: [DE]-x-A-[LIY]-[KR]-R-F-K-[KR]-x(3)-[KR]

24. Universal stress protein family (Usp)

By a wide range of stress conditions members of the Usp family are predicted to be related to the MADS-box proteins transcript fact and bind to DNA [2]. Number of members: 39

25

[1] Expression and role of the universal stress protein, UspA, of *Escherichia coli* during growth arrest. Nystrom T, Neidhardt FC; Mol Microbiol 1994; 11:537-544.

30 [2] Sequence analysis of eukaryotic developmental proteins: ancient and novel domains. Mushegian AR, Koonin EV; Genetics 1996; 144:817-828.

III. Methods of Modulating Polypeptide Production

Within the scope of invention are chimeric gene constructs wherein the promoter and the structural coding sequence and/or other regulatory sequences within said
5 constructs are heterologous to each other. "Heterologous sequences" are those that are not operatively linked or are not contiguous to each other in nature. For example, a promoter from corn is considered heterologous to an *Arabidopsis* coding region sequence. Also, a promoter from a gene encoding a
10 growth factor from corn is considered heterologous to a sequence encoding the corn receptor for the growth factor. Regulatory element sequences, such as UTRs or 3' end termination sequences that do not originate in nature from the same gene as the coding sequence originates from, are
15 considered heterologous to said coding sequence. On the other hand, elements operatively linked in nature are not heterologous. Thus, the promoter and coding portion of a corn gene expressing an amino acid transporter are not heterologous to each other.

20 Such chimeric polynucleotides are of particular interest for modulating gene expression in a host cell upon transformation of said cell with said chimeric polynucleotide.

Also within the scope of the invention are DNA molecules, whereof at least a part or portion of these DNA molecules are
25 presented in SEQ TABLES 1 AND 2 of the present application, and wherein the structural coding sequence is under the control of its own promoter and/or its own regulatory elements. Such DNA molecules are useful for transforming the genome of a host cell or an organism regenerated from said host cell.

30 Typically, such polynucleotides, whether chimeric or not, are "exogenous to" the genome of an individual host cell or the organism regenerated from said host cell, such as a plant cell, respectively for a plant, when initially or subsequently introduced into said host cell or organism, by any means other

than by a sexual cross. Examples of means by which this can be accomplished are described below, and include *Agrobacterium*-mediated transformation (of dicots - e.g. Salomon et al. *EMBO J.* 3:141 (1984); Herrera-Estrella et al. *EMBO J.* 2:987 (1983);
5 A.C. Vergunst et al, *Nucleic Acids Res.* 26:11, 2729 (1998); of monocots, representative papers are those by Escudero et al., *Plant J.* 10:355 (1996), Ishida et al., *Nature Biotechnology* 14:745 (1996), May et al., *Bio/Technology* 13:486 (1995)), biolistic methods (Armaleo et al., *Current Genetics* 17:97
10 1990)), electroporation, *in planta* techniques, and the like. Such a plant containing the exogenous nucleic acid is referred to here as an R₁ generation transgenic plant. Transgenic plants which arise from a sexual cross with another parent line or by selfing are "descendants or the progeny" of a R₁ plant and are
15 generally called F_n plants or S_n plants, respectively, n meaning the number of generations.

The SDFs prepared as described herein can be used to prepare expression cassettes useful in a number of techniques for suppressing or enhancing expression.

20 III.A. Suppression

Expression cassettes of the invention can be used to suppress expression of endogenous genes which comprise the SDF sequence. Inhibiting expression can be useful, for instance, to tailor the ripening characteristics of a fruit
25 (Oeller et al., *Science* 254:437 (1991)) or to influence seed size_ (WO98/07842) or or to provoke cell ablation (Mariani et al., *Nature* 357: 384-387 (1992)).

As described above, a number of methods can be used to inhibit gene expression in plants, such as antisense,
30 ribozyme, introduction of "exogenous" genes into a host cell, insertion of a polynucleotide sequence into the coding sequence and/or the promoter of the endogenous gene of interest, and the like.

III.A.1. Antisense

An expression cassette as described above can be transformed into host cell or plant to produce an antisense strand of RNA. In plant cells, it has been suggested that antisense RNA inhibits gene expression by preventing the accumulation of mRNA which encodes the enzyme of interest, see, e.g., Sheehy et al., *Proc. Nat. Acad. Sci. USA*, 85:8805 (1988), and Hiatt et al., U.S. Patent No. 4,801,340.

III.A.2. Ribozymes

Similarly, ribozyme constructs can be transformed into a plant to cleave mRNA and down-regulate translation.

III.A.3. Co-Suppression

Another method of suppression is by introducing an exogenous copy of the gene to be suppressed. Introduction of expression cassettes in which a nucleic acid is configured in the sense orientation with respect to the promoter has been shown to be an effective means by which to block the transcription of target genes. A detailed description of this method is described above.

III.A.4. Insertion of Sequences into the Gene to be Modulated

Yet another means of suppressing gene expression is to insert a polynucleotide into the gene of interest to disrupt transcription or translation of the gene.

Homologous recombination could ~~can~~ be used to target a polynucleotide insert to a gene using the Cre-Lox system (A.C. Vergunst et al., *Nucleic Acids Res.* 26:2729 (1998), A.C. Vergunst et al., *Plant Mol. Biol.* 38:393 (1998), H. Albert et al., *Plant J.* 7:649 (1995)).

In addition, random insertion of polynucleotides into a host cell genome can also be used to disrupt the gene of interest. Azpiroz-Leehan et al., *Trends in Genetics* 13:152 (1997). In this method, screening for clones from a library containing random insertions is preferred for identifying those that have polynucleotides inserted into the gene of interest. Such screening can be performed using probes and/or primers described above based on sequences from SEQ TABLES 1 AND 2, fragments thereof, and substantially similar sequence thereto. The screening can also be performed by selecting clones or R₁ plants having a desired phenotype.

III.A.5. Promoter Modulation

Inactivation of the promoter that drives a gene of interest can modulate transcription and translation, and therefore expression. For example, triple helices can be formed using oligonucleotides based on sequences from SEQ TABLES 1 AND 2, fragments thereof, and substantially similar sequence thereto. The oligonucleotide can be delivered to the host cell can bind to the promoter in the genome to form a triple helix and prevent transcription.

Additionally, a vector capable of producing the oligonucleotide can be inserted into the host cell to deliver the oligonucleotide.

III.A.6. Expression of Mutants

An alternative method for inhibiting gene function is through the use of dominant negative mutations. Dominant negative mutations produce a mutant polypeptide which is capable of competing with the native polypeptide, but which does not produce the native result. Consequently, over expression of these mutations can titrate out an undesired activity of the native protein. For example, the inactive dominant-negative mutant may bind to the same receptor as the

native protein, preventing the native protein from activating a signal transduction pathway. Alternatively, the dominant-negative mutant can be an inactive enzyme still capable of binding to the same substrate as the native protein.

5 Dominant-negative mutants also can act upon the native protein itself to prevent activity. For example, the native protein may be active only as a homo-multimer or as one subunit of a hetero-multimer. Incorporation of an inactive subunit into the multimer with native subunit(s) can inhibit
10 activity.

Thus, gene function can be modulated by insertion of an expression construct encoding a dominant-negative mutant into a host cell of interest.

III.B. Enhanced Expression

15 Enhanced expression of a gene of interest in a host cell can be accomplished by either (1) insertion of an exogenous gene; or (2) promoter modulation.

III.B.1. Insertion of an Exogenous Gene

20 Insertion of an expression construct encoding an exogenous gene can boost the number of gene copies expressed in a host cell.

Such expression constructs can comprise genes that either encode the native protein that is of interest or that encode a variant that exhibits enhanced activity as compared to
25 the native protein. Such genes encoding proteins of interest can be constructed from the sequences from SEQ TABLES 1 AND 2, fragments thereof, and substantially similar sequence thereto.

Such an exogenous gene can include either a constitutive promoter permitting expression in any cell in a
30 host organism or a promoter that directs expression only in particular cells or times during a host cell life cycle or in response to environmental stimuli.

III.B.2. Promoter Modulation

Some promoters require binding of a regulatory protein to be activated. Other promoters may need a protein that signals a promoter binding protein to expose a polymerase
5 binding site. In either case, over-expression of such proteins can be used to enhance expression of a gene of interest by increasing the activation time of the promoter.

Such regulatory proteins are encoded by some of the sequences in SEQ TABLES 1 AND 2, fragments thereof, and
10 substantially similar sequences thereto.

Coding sequences for these proteins can be constructed as described above.

In some cases, duplication of enhancer elements or insertion of exogenous enhancer elements will increase expression of a desired gene from a particular promoter. The useful enhancer elements can be portions of one or more of the SDFs of SEQ TABLES 1 AND 2.

IV. **Gene Constructs and Vector Construction**

15 To use isolated SDFs of the present invention or a combination of them or parts and/or mutants and/or fusions of said SDFs in the above techniques, recombinant DNA vectors which comprise said SDFs and are suitable for transformation of cells, such as plant cells, are usually prepared.

20 The vector backbone can be any of those typical in the art such as plasmids, viruses, artificial chromosomes, BACs, YACs and PACs and vectors of the sort described by **.

Typically, a vector will comprise the exogenous gene, which in its turn comprises an SDF of the present invention to
25 be introduced into the genome of a host cell, and which gene may be an antisense construct, a ribozyme construct, or a structural coding sequence with any desired transcriptional and/or translational regulatory sequences, such as promoters

and 3' end termination sequences. Vectors of the invention can also include origins of replication, markers, homologous sequences, introns, etc.

A DNA sequence coding for the desired polypeptide, for example a cDNA sequence encoding a full length protein, will preferably be combined with transcriptional and translational initiation regulatory sequences which will direct the transcription of the sequence from the gene in the intended tissues of the transformed plant.

For example, for over-expression, a plant promoter fragment may be employed that will direct expression of the gene in all tissues of a regenerated plant. Such promoters are referred to herein as "constitutive" promoters and are active under most environmental conditions and states of development or cell differentiation. Examples of constitutive promoters include the cauliflower mosaic virus (CaMV) 35S transcription initiation region, the 1' or 2' promoter derived from T-DNA of *Agrobacterium tumefaciens*, and other transcription initiation regions from various plant genes known to those of skill.

Alternatively, the plant promoter may direct expression of an SDF of the invention in a specific tissue (tissue-specific promoters) or may be otherwise under more precise environmental control (inducible promoters). Examples of tissue-specific promoters under developmental control include promoters that initiate transcription only in certain tissues, such as root, ovule, fruit, seeds, or flowers. The promoter from a *LEC1* gene, described in copending application U.S. Ser. No. 09/103,478, is particularly useful for directing gene expression so that a desired gene product is located in embryos or seeds. Other suitable promoters include those from genes encoding storage proteins or the lipid body membrane protein, oleosin. A few root-specific promoters are noted above. Examples of environmental conditions that may affect

transcription by inducible promoters include anaerobic conditions, elevated temperature, or the presence of light.

If proper polypeptide expression is desired, a polyadenylation region at the 3'-end of the coding region should be included. The polyadenylation region can be derived from the natural gene, from a variety of other plant genes, or from T-DNA.

The vector comprising the sequences (e.g., promoters or coding regions) from genes of the invention will typically comprise a marker gene that confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or phosphinotricin.

IV.A. Coding Sequences

Generally, the sequence in the transformation vector and to be introduced into the genome of the host cell does not need to be absolutely identical to an SDF of the present invention. Also, it is not necessary for it to be full length, relative to either the primary transcription product or fully processed mRNA. Use of sequences shorter than full-length may be preferred to avoid concurrent production of some plants that are overexpressors. Furthermore, the introduced sequence need not have the same intron or exon pattern as a native gene. Also, heterologous non-coding segments can be incorporated into the coding sequence without changing the desired amino acid sequence of the polypeptide to be produced.

IV.B. Promoters

As explained above, introducing an exogenous SDF from the same species or an orthologous SDF from another species can modulate the expression of a native gene corresponding to

that SDF of interest. Such an SDF construct can be under the control of either a constitutive promoter (e.g., the promoter of the 35S gene of the cauliflower mosaic virus or the promoter of the gene encoding the cowpea trypsin inhibitor) or a highly regulated inducible promoter (e.g., a copper inducible promoter). The promoter of interest can initially be either endogenous or heterologous to the species in question. When re-introduced into the genome of said species, such promoter becomes "exogenous" to said species. The promoter-SDF construct can be made using standard recombinant DNA techniques (Sambrook et al. 1989) and can be introduced to the species of interest by *Agrobacterium*-mediated transformation or by other means of transformation (e.g., particle gun bombardment) as referenced above. Over-expression of an SDF transgene can lead to co-suppression of the homologous gene thereby creating some alterations in the phenotypes of the transformed species as demonstrated by similar analysis of the chalcone synthase gene (Napoli et al., *Plant Cell* 2:279 (1990) and van der Krol et al., *Plant Cell* 2:291 (1990)). If an SDF is found to encode a protein with desirable characteristics, its over-expression can be controlled so that its accumulation can be manipulated in an organ- or tissue-specific manner utilizing a promoter having such specificity.

Likewise, if the promoter of an SDF (or an SDF that includes a promoter) is found to be tissue-specific or developmentally regulated, such a promoter can be utilized to drive the expression of a specific gene of interest (e.g., seed storage protein or root-specific protein). Thus, the level of accumulation of a particular protein can be manipulated or its spatial localization in an organ- or tissue- specific manner can be altered.

IV. C Signal Peptides

In some cases it may be desirable for the protein encoded by an introduced exogenous or orthologous SDF to be targeted (1) to a particular organelle, (2) to interact with a particular molecule or (3) for secretion outside of the cell harboring the introduced SDF. This will be accomplished using a signal peptide.

Signal peptides direct protein targeting, are involved in ligand-receptor interactions and act in cell to cell communication. Many proteins, especially soluble proteins, contain a signal peptide that targets the protein to one of several different intracellular compartments. In plants, these compartments include, but are not limited to, the endoplasmic reticulum (ER), mitochondria, plastids (such as chloroplasts), the vacuole, the Golgi apparatus, protein storage vessicles (PSV) and, in general, membranes . Some signal peptide sequences are conserved, such as the Asn-Pro-Ile-Arg amino acid motif found in the N-terminal propeptide signal that targets proteins to the vacuole (Marty (1999) *The Plant Cell* 11: 587-599). Other signal peptides do not have a consensus sequence *per se*, but are largely composed of hydrophobic amino acids, such as those signal peptides targeting proteins to the ER (Vitale and Denecke (1999) *The Plant Cell* 11: 615-628). Still others do not appear to contain either a consensus sequence or an identified common secondary sequence, for instance the chloroplast stromal targeting signal peptides (Keegstra and Cline (1999) *The Plant Cell* 11: 557-570). Furthermore, some targeting peptides are bipartite, directing proteins first to an organelle and then to a membrane within the organelle (e.g. within the thylakoid lumen of the chloroplast; see Keegstra and Cline (1999) *The Plant Cell* 11: 557-570). In addition to the diversity in sequence and secondary structure, placement of the signal peptide is also varied. Proteins destined for

the vacuole, for example, have targeting signal peptides found at the N-terminus, at the C-terminus and at a surface location in mature, folded proteins.

Signal peptides also serve as ligands for some
5 receptors. Perhaps the best known example of this is the interaction of the ER targeting signal peptide with the signal recognition particle (SRP). Here, the SRP binds to the signal peptide, halting translation, and the resulting SRP complex then binds to docking proteins located on the
10 surface of the ER, prompting the transfer of the protein into the ER.

These characteristics of signal proteins can be used to more tightly control the expression of introduced SDFs. In particular, associating the appropriate signal sequence with
15 a specific SDF can allow sequestering of the protein in specific organelles (plastids, as an example), secretion outside of the cell, targeting interaction with particular receptors, etc. Hence, the inclusion of signal proteins in constructs involving the SDFs of the invention increases the
20 range of manipulation of SDF expression. To carry this out, constructs are made with the nucleotide sequence of a known signal peptide immediately 5' to the initiation of the coding region of an SDF so that the signal peptide is translated in frame with the coding region and immediately precedes it.
25 The nucleotide sequence of the signal peptide can be isolated from characterized genes using common molecular biological techniques or can be synthesized in vitro.

V. Transformation Techniques

A wide range of techniques for inserting exogenous
30 polynucleotides are known for a number of host cells, including, without limitation, bacterial, yeast, mammalian, insect and plant cells.

Techniques for transforming a wide variety of higher plant species are well known and described in the technical and scientific literature. See, e.g. Weising et al., *Ann. Rev. Genet.* 22:421 (1988); and Christou, *Euphytica*, v. 85, n.1-3:13-27, (1995).

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques. For example, the DNA construct may be introduced directly into the genomic DNA of the plant cell using techniques such as electroporation and microinjection of plant cell protoplasts, or the DNA constructs can be introduced directly to plant tissue using ballistic methods, such as DNA particle bombardment. Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional *Agrobacterium tumefaciens* host vector. The virulence functions of the *Agrobacterium tumefaciens* host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria (Vergunst et al., *Nucl. Acids. Res.* 26:2729 (1998) (site-directed integration using a Cre-Lox recombinase system); McCormac et al., *Mol. Biotechnol.* 8:199 (1997); Hamilton, *Gene* 200:107 (1997)); Salomon et al. *EMBO J.* 3:141 (1984); Herrera-Estrella et al. *EMBO J.* 2:987 (1983).

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. *EMBO J.* 3:2717 (1984). Electroporation techniques are described in Fromm et al. *Proc. Natl Acad. Sci. USA* 82:5824 (1985). Ballistic transformation techniques are described in Klein et al. *Nature* 327:773 (1987). *Agrobacterium tumefaciens*-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Hamilton, *CM.*, *Gene* 200:107

(1997); Müller et al. *Mol. Gen. Genet.* 207:171 (1987); Komari et al. *Plant J.* 10:165 (1996); Venkateswarlu et al. *Biotechnology* 9:1103 (1991) and Gleave, AP., *Plant Mol. Biol.* 20:1203 (1992); Graves and Goldman, *Plant Mol. Biol.* 7:34 (1986) and Gould et al., *Plant Physiology* 95:426 (1991).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant that possesses the transformed genotype and thus the desired phenotype such as seedlessness. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium, typically relying on a biocide and/or herbicide marker which has been introduced together with the desired nucleotide sequences. Plant regeneration from cultured protoplasts is described in Evans et al., *Protoplasts Isolation and Culture* in "Handbook of Plant Cell Culture," pp. 124-176, MacMillan Publishing Company, New York, 1983; and Binding, *Regeneration of Plants, Plant Protoplasts*, pp. 21-73, CRC Press, Boca Raton, 1988. Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. *Ann. Rev. of Plant Phys.* 38:467 (1987). Regeneration of monocots (rice) is described by Hosoyama et al. (*Biosci. Biotechnol. Biochem.* 58:1500 (1994)) and by Ghosh et al. (*J. Biotechnol.* 32:1 (1994)). The nucleic acids of the invention can be used to confer desired traits on essentially any plant.

Thus, the invention has use over a broad range of plants, including species from the genera *Asparagus*, *Atropa*, *Avena*, *Brassica*, *Citrus*, *Citrullus*, *Capsicum*, *Cucumis*, *Cucurbita*, *Daucus*, *Fragaria*, *Glycine*, *Gossypium*, *Helianthus*, *Heterocallis*, *Hordeum*, *Hyoscyamus*, *Lactuca*, *Linum*, *Lolium*, *Lycopersicon*, *Malus*, *Manihot*, *Majorana*, *Medicago*, *Nicotiana*, *Oryza*, *Panicum*, *Pennisetum*, *Persea*, *Pisum*, *Pyrus*, *Prunus*, *Raphanus*, *Secale*, *Senecio*, *Sinapis*, *Solanum*, *Sorghum*, *Trigonella*, *Triticum*, *Vitis*, *Vigna*, and, *Zea*.

One of skill will recognize that after the expression cassette is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed.

The particular sequences of SDFs identified are provided in the attached SEQ TABLES 1 AND 2. One of ordinary skill in the art, having this data, can obtain cloned DNA fragments, synthetic DNA fragments or polypeptides constituting desired sequences by recombinant methodology known in the art or described herein.

EXAMPLES

The invention is illustrated by way of the following examples. The invention is not limited by these examples as the scope of the invention is defined solely by the claims following.

EXAMPLE 1: SOUTHERN HYBRIDIZATIONS

The SDFs of the invention can be used in Southern hybridizations as described above. The following describes extraction of DNA from nuclei of plant cells, digestion of the nuclear DNA and separation by length, transfer of the separated fragments to membranes, preparation of probes for hybridization, hybridization and detection of the hybridized probe.

The procedures described herein can be used to isolate related polynucleotides or for diagnostic purposes. Moderate stringency hybridization conditions, as defined above, are described in the present example. These conditions result in detection of hybridization between sequences having at least 70% sequence identity. As described above, the hybridization and wash conditions can be changed to reflect the desired

degree of sequence identity between probe and target sequences that can be detected.

In the following procedure, a probe for ~~the~~ hybridization is produced from two PCR reactions using two primers from genomic sequence of *Arabidopsis thaliana*. As described above, the particular template for generating the probe can be any desired template.

The first PCR product is assessed to validate the size of the primer to assure it is of the expected size. Then the product of the first PCR is used as a template, with the same pair of primers used in the first PCR, in a second PCR that produces a labeled product used as the probe.

Fragments detected by hybridization, or other bands of interest, can be isolated from gels used to separate genomic DNA fragments by known methods for further purification and/or characterization.

Buffers for nuclear DNA extraction

1. 10X HB

	1000 ml	
40 mM spermidine	10.2 g	Spermine (Sigma S-2876) and spermidine (Sigma S-2501)
10 mM spermine	3.5 g	Stabilize chromatin and the nuclear membrane
0.1 M EDTA (disodium)	37.2 g	EDTA inhibits nuclease
0.1 M Tris	12.1 g	Buffer
0.8 M KCl	59.6 g	Adjusts ionic strength for stability of nuclei

Adjust pH to 9.5 with 10 N NaOH. It appears that there is a nuclease present in leaves. Use of pH 9.5 appears to inactivate this nuclease.

90

2. 2 M sucrose (684 g per 1000 ml)

Heat about half the final volume of water to about 50°C.
Add the sucrose slowly then bring the mixture to close
to final volume; stir constantly until it has dissolved.

5 Bring the solution to volume.

3. Sarkosyl solution (lyses nuclear membranes)

1000 ml

N-lauroyl sarcosine (Sarkosyl) 20.0 g

0.1 M Tris 12.1 g

10 0.04 M EDTA (Disodium) 14.9 g

Adjust the pH to 9.5 after all the components are
dissolved and bring up to the proper volume.

4. 20% Triton X-100

80 ml Triton X-100

15 320 ml 1xHB (w/o β -ME and PMSF)

Prepare in advance; Triton takes some time to dissolve

A. Procedure

1. Prepare 1X "H" buffer (keep ice-cold during use)

1000 ml

20 10X HB 100 ml

2 M sucrose 250 ml a non-ionic osmoticum

Water 634 ml

Added just before use:

100 mM PMSF*

10 ml a protease

inhibitor; protects

nuclear membrane proteins

25

91

 β -mercaptoethanol

1 ml inactivates nuclease
by reducing disulfide
bonds

*100 mM PMSF

5 (phenyl methyl sulfonyl fluoride, Sigma P-7626)
(add 0.0875 g to 5 ml 100% ethanol)

2. Homogenize the tissue in a blender (use 300-400 ml of 1xHB per blender). Be sure that you use 5-10 ml of HB buffer per gram of tissue. Blenders generate heat so
10 be sure to keep the homogenate cold. It is necessary to put the blenders in ice periodically.
3. Add the 20% Triton X-100 (25 ml per liter of homogenate) and gently stir on ice for 20 min. This lyses plastid, but not nuclear, membranes.
- 15 4. Filter the tissue suspension through several nylon filters into an ice-cold beaker. The first filtration is through a 250-micron membrane; the second is through an 85-micron membrane; the third is through a 50-micron membrane; and the fourth is through a 20-micron
20 membrane. Use a large funnel to hold the filters. Filtration can be sped up by gently squeezing the liquid through the filters.
5. Centrifuge the filtrate at 1200 x g for 20 min. at 4°C to pellet the nuclei.
- 25 6. Discard the dark green supernatant. The pellet will have several layers to it. One is starch; it is white and gritty. The nuclei are gray and soft. In the early

steps, there may be a dark green and somewhat viscous layer of chloroplasts.

Wash the pellets in about 25 ml cold H buffer (with Triton X-100) and resuspend by swirling gently and pipetting. After the pellets are resuspended.

Pellet the nuclei again at 1200 - 1300 x g. Discard the supernatant.

Repeat the wash 3-4 times until the supernatant has changed from a dark green to a pale green. This usually happens after 3 or 4 resuspensions. At this point, the pellet should be grayish white and very slippery. The Triton X-100 in these repeated steps helps to destroy the chloroplasts and mitochondria that contaminate the prep.

Resuspend the nuclei for a final time in a total of 15 ml of H buffer and transfer the suspension to a sterile 125 ml Erlenmeyer flask.

7. Add 15 ml, dropwise, cold 2% Sarkosyl, 0.1 M Tris, 0.04 M EDTA solution (pH 9.5) while swirling gently. This lyses the nuclei. The solution will become very viscous.

8. Add 30 grams of CsCl and gently swirl at room temperature until the CsCl is in solution. The mixture will be gray, white and viscous.

9. Centrifuge the solution at 11,400 x g at 4°C for at least 30 min. The longer this spin is, the firmer the protein pellicle.

10. The result should be a clear green supernatant over a white pellet, and (perhaps) under a protein pellicle. Carefully remove the solution under the protein pellicle and above the pellet. Determine the density of the solution by weighing 1 ml of solution and add CsCl if necessary to bring to 1.57 g/ml. The solution contains dissolved solids (sucrose etc) and the refractive index alone will not be an accurate guide to CsCl concentration.
11. Add 20 μ l of 10 mg/ml EtBr per ml of solution.
12. Centrifuge at 184,000 x g for 16 to 20 hours in a fixed-angle rotor.
13. Remove the dark red supernatant that is at the top of the tube with a plastic transfer pipette and discard. Carefully remove the DNA band with another transfer pipette. The DNA band should be visible in room light; otherwise, use a long wave UV light to locate the band.
14. Extract the ethidium bromide with isopropanol saturated with water and salt. Once the solution is clear, extract at least two more times to ensure that all of the EtBr is gone. Be very gentle, as it is very easy to shear the DNA at this step. This extraction may take a while because the DNA solution tends to be very viscous. If the solution is too viscous, dilute it with TE.
15. Dialyze the DNA for at least two days against several changes (at least three times) of TE (10 mM Tris, 1mM EDTA, pH 8) to remove the cesium chloride.

16. Remove the dialyzed DNA from the tubing. If the dialyzed DNA solution contains a lot of debris, centrifuge the DNA solution at least at 2500 x g for 10 min. and carefully transfer the clear supernatant to a new tube. Read the A260 concentration of the DNA.
17. Assess the quality of the DNA by agarose gel electrophoresis (1% agarose gel) of the DNA. Load 50 ng and 100 ng (based on the OD reading) and compare it with known and good quality DNA. Undigested lambda DNA and a lambda-HindIII-digested DNA are good molecular weight makers.

Protocol for Digestion of Genomic DNA

Protocol:

1. The relative amounts of DNA for different crop plants that provide approximately a balanced number of genome equivalent is given in Table 3. Note that due to the size of the wheat genome, wheat DNA will be underrepresented. Lambda DNA provides a useful control for complete digestion.
2. Precipitate the DNA by adding 3 volumes of 100% ethanol. Incubate at -20°C for at least two hours. Yeast DNA can be purchased and made up at the necessary concentration, therefore no precipitation is necessary for yeast DNA.
3. Centrifuge the solution at 11,400 x g for 20 min. Decant the ethanol carefully (be careful not to disturb the pellet). Be sure that the residual ethanol is completely removed either by vacuum desiccation or by carefully wiping the sides of the tubes with a clean tissue.

95

4. Resuspend the pellet in an appropriate volume of water. Be sure the pellet is fully resuspended before proceeding to the next step. This may take about 30 min.
5. Add the appropriate volume of 10X reaction buffer provided by the manufacturer of the restriction-enzyme to the resuspended DNA followed by the appropriate volume of enzymes. Be sure to mix it properly by slowly swirling the tubes.
6. Set-up the lambda digestion-control for each DNA that you are digesting.
7. Incubate both the experimental and lambda digests overnight at 37°C. Spin down condensation in a microfuge before proceeding.
8. After digestion, add 2 µl of loading dye (typically 0.25% bromophenol blue, 0.25% xylene cyanol in 15% Ficoll or 30% glycerol) to the lambda-control digests and load in 1% TPE-agarose gel (TPE is 90 mM Tris-phosphate, 2 mM EDTA, pH 8). If the lambda DNA in the lambda control digests are completely digested, proceed with the precipitation of the genomic DNA in the digests.
9. Precipitate the digested DNA by adding 3 volumes of 100% ethanol and incubating in -20°C for at least 2 hours (preferably overnight).

EXCEPTION: *Arabidopsis* and yeast DNA are digested in an appropriate volume; they don't have to be precipitated.

10. Resuspend the DNA in an appropriate volume of TE (e.g., 22 μ l x 50 blots = 1100 μ l) and an appropriate volume of 10X loading dye (e.g., 2.4 μ l x 50 blots = 120 μ l). Be careful in pipetting the loading dye - it is viscous.
- 5 Be sure you are pipetting the correct volume.

Table 3

Some guide points in digesting genomic DNA.

Species	Genome Size	Size Relative to Arabidopsis	Genome Equivalent to 2 μ g Arabidopsis DNA	Amount of DNA per blot
Arabidopsis	120 Mb	1X	1X	2 μ g
Brassica	1,100 Mb	9.2X	0.54X	10 μ g
Corn	2,800 Mb	23.3X	0.43X	20 μ g
Cotton	2,300 Mb	19.2X	0.52X	20 μ g
Oat	11,300 Mb	94X	0.11X	20 μ g
Rice	400 Mb	3.3X	0.75X	5 μ g
Soybean	1,100 Mb	9.2X	0.54X	10 μ g
Sugarbeet	758 Mb	6.3X	0.8X	10 μ g
Sweetclover	1,100 Mb	9.2X	0.54X	10 μ g
Wheat	16,000 Mb	133X	0.08X	20 μ g
Yeast	15 Mb	0.12X	1X	0.25 μ g

10 Protocol for Southern Blot Analysis

The digested DNA samples are electrophoresed in 1% agarose gels in 1x TPE buffer. Low voltage; overnight separations are preferred. The gels are stained with EtBr and photographed.

15

1. For blotting the gels, first incubate the gel in 0.25 N HCl (with gentle shaking) for about 15 min.

2. Then briefly rinse with water. The DNA is denatured by 2 incubations. Incubate (with shaking) in 0.5 M NaOH in 1.5 M NaCl for 15 min.
3. The gel is then briefly rinsed in water and neutralized by incubating twice (with shaking) in 1.5 M Tris pH 7.5 in 1.5 M NaCl for 15 min.
4. A nylon membrane is prepared by soaking it in water for at least 5 min, then in 6X SSC for at least 15 min. before use. (20x SSC is 175.3 g NaCl, 88.2 g sodium citrate per liter, adjusted to pH 7.0.)
5. The nylon membrane is placed on top of the gel and all bubbles in between are removed. The DNA is blotted from the gel to the membrane using an absorbent medium, such as paper toweling and 6x SCC buffer. After the transfer, the membrane may be lightly brushed with a gloved hand to remove any agarose sticking to the surface.
6. The DNA is then fixed to the membrane by UV crosslinking and baking at 80°C. The membrane is stored at 4°C until use.

B. Protocol for PCR Amplification of Genomic Fragments in Arabidopsis

Amplification procedures:

1. Mix the following in a 0.20 ml PCR tube or 96-well PCR plate:

Volume	Stock	Final Amount or Conc.
--------	-------	-----------------------

0.5 μ l	~ 10 ng/ μ l genomic DNA ¹	5 ng
2.5 μ l	10X PCR buffer	20 mM Tris, 50 mM KCl
0.75 μ l	50 mM MgCl ₂	1.5 mM
1 μ l	10 pmol/ μ l Primer 1 (Forward)	10 pmol
1 μ l	10 pmol/ μ l Primer 2 (Reverse)	10 pmol
0.5 μ l	5 mM dNTPs	0.1 mM
0.1 μ l	5 units/ μ l Platinum Taq™ (Life Technologies, Gaithersburg, MD) DNA Polymerase	1 units
(to 25 μ l)	Water	

2. The template DNA is amplified using a Perkin Elmer 9700 PCR machine:

1) 94°C for 10 min. followed by

<u>2)</u> 5 cycles:	<u>3)</u> 5 cycles:	<u>4)</u> 25 cycles:
94 °C - 30 sec	94 °C - 30 sec	94 °C - 30 sec
62 °C - 30 sec	58 °C - 30 sec	53 °C - 30 sec
72 °C - 3 min	72 °C - 3 min	72 °C - 3 min

5) 72°C for 7 min. Then the reactions are stopped by chilling to 4°C.

¹ Arabidopsis DNA is used in the present experiment, but the procedure is a general one.

The procedure can be adapted to a multi-well format if necessary.

Quantification and Dilution of PCR Products:

1. The product of the PCR is analyzed by electrophoresis in a 1% agarose gel. A linearized plasmid DNA can be used as a quantification standard (usually at 50, 100, 200, and 400 ng). These will be used as references to approximate the amount of PCR products. HindIII-digested Lambda DNA is useful as a molecular weight marker. The gel can be run fairly quickly; e.g., at 100 volts. The standard gel is examined to determine that the size of the PCR products is consistent with the expected size and if there are significant extra bands or smeary products in the PCR reactions.
2. The amounts of PCR products can be estimated on the basis of the plasmid standard.
3. For the small number of reactions that produce extraneous bands, a small amount of DNA from bands with the correct size can be isolated by dipping a sterile 10- μ l tip into the band while viewing through a UV Transilluminator. The small amount of agarose gel (with the DNA fragment) is used in the labeling reaction.

C. Protocol for PCR-DIG-Labeling of DNA

Solutions:

- Reagents in PCR reactions (diluted PCR products, 10X PCR Buffer, 50 mM MgCl₂, 5 U/ μ l Platinum Taq Polymerase, and the primers)

10X dNTP + DIG-11-dUTP [**1:5**]: (2 mM dATP, 2 mM dCTP, 2 mM dGTP, 1.65 mM dTTP, 0.35 mM DIG-11-dUTP)

100

10X dNTP + DIG-11-dUTP [1:10]: (2 mM dATP, 2 mM dCTP, 2 mM dGTP, 1.81 mM dTTP, 0.19 mM DIG-11-dUTP)

10X dNTP + DIG-11-dUTP [1:15]: (2 mM dATP, 2 mM dCTP, 2 mM dGTP, 1.875 mM dTTP, 0.125 mM DIG-11-dUTP)

5 TE buffer (10 mM Tris, 1 mM EDTA, pH 8)

Maleate buffer: In 700 ml of deionized distilled water, dissolve 11.61 g maleic acid and 8.77 g NaCl. Add NaOH to adjust the pH to 7.5. Bring the volume to 1 L. Stir for 15 min. and sterilize.

10 10% blocking solution: In 80 ml deionized distilled water, dissolve 1.16g maleic acid. Next, add NaOH to adjust the pH to 7.5. Add 10 g of the blocking reagent powder (Boehringer Mannheim, Indianapolis, IN, Cat. no. 1096176). Heat to 60°C while stirring to dissolve the
15 powder. Adjust the volume to 100 ml with water. Stir and sterilize.

1% blocking solution: Dilute the 10% stock to 1% using the maleate buffer.

Buffer 3 (100 mM Tris, 100 mM NaCl, 50 mM MgCl₂, pH9.5).
20 Prepared from autoclaved solutions of 1M Tris pH 9.5, 5 M NaCl, and 1 M MgCl₂ in autoclaved distilled water.

Procedure:

1. PCR reactions are performed in 25 µl volumes containing:

	PCR buffer	1X
	MgCl ₂	1.5 mM
5	10X dNTP + DIG-11-dUTP	1X (please see the note below)
	Platinum Taq™ Polymerase	1 unit
	10 pg probe DNA	
	10 pmol primer 1	

10

Note:Use for:

<u>10X dNTP + DIG-11-dUTP (1:5)</u>	<u>< 1 kb</u>
10X dNTP + DIG-11-dUTP (1:10)	1 kb to 1.8 kb
10X dNTP + DIG-11-dUTP (1:15)	> 1.8 kb

15

2. The PCR reaction uses the following amplification cycles:

1) 94°C for 10 min.

<u>2)</u> 5 cycles:	<u>3)</u> 5 cycles:	<u>4)</u> 25 cycles:
95°C - 30 sec	95°C - 30 sec	95°C - 30 sec
61°C - 1 min	59°C - 1 min	51°C - 1 min
73°C - 5 min	75°C - 5 min	73°C - 5 min

5) 72°C for 8 min. The reactions are terminated by chilling to 4°C (hold).

20

3. The products are analyzed by electrophoresis- in a 1% agarose gel, comparing to an aliquot of the unlabelled probe starting material.

4. The amount of DIG-labeled probe is determined as follows:

Make serial dilutions of the diluted control DNA in dilution buffer (TE: 10 mM Tris and 1 mM EDTA, pH 8) as shown in the following table:

DIG-labeled control DNA starting conc.	Stepwise Dilution	Final Conc. (Dilution Name)
5 ng/ μ l	1 μ l in 49 μ l TE	100 pg/ μ l (A)
100 pg/ μ l (A)	25 μ l in 25 μ l TE	50 pg/ μ l (B)
50 pg/ μ l (B)	25 μ l in 25 μ l TE	25 pg/ μ l (C)
25 pg/ μ l (C)	20 μ l in 30 μ l TE	10 pg/ μ l (D)

- a. Serial deletions of a DIG-labeled standard DNA ranging from 100 pg to 10 pg are spotted onto a positively charged nylon membrane, marking the membrane lightly with a pencil to identify each dilution.
- b. Serial dilutions (e.g., 1:50, 1:2500, 1:10,000) of the newly labeled DNA probe are spotted.
- c. The membrane is fixed by UV crosslinking.
- d. The membrane is wetted with a small amount of maleate buffer and then incubated in 1% blocking solution for 15 min at room temp.
- e. The labeled DNA is then detected using alkaline phosphatase conjugated anti-DIG antibody (Boehringer Mannheim, Indianapolis, IN, cat. no.

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1093274) and an NBT substrate according to the manufacture's instruction.

- f. Spot intensities of the control and experimental dilutions are then compared to estimate the concentration of the PCR-DIG-labeled probe.

D. Prehybridization and Hybridization of Southern Blots

Solutions:

100% Formamide purchased from Gibco

20X SSC (1X = 0.15 M NaCl, 0.015 M Na₃citrate)

per L: 175 g NaCl
87.5 g Na₃citrate·2H₂O

20% Sarkosyl (N-lauroyl-sarcosine)

20% SDS (sodium dodecyl sulphate)

10% Blocking Reagent: In 80 ml deionized distilled water, dissolve 1.16 g maleic acid. Next, add NaOH to adjust the pH to 7.5. Add 10 g of the blocking reagent powder. Heat to 60°C while stirring to dissolve the powder. Adjust the volume to 100 ml with water. Stir and sterilize.

Prehybridization Mix:

Final Concentration	Components	Volume (per 100 ml)	Stock
50%	Formamide	50 ml	100%
5X	SSC	25 ml	20X
0.1%	Sarkosyl	0.5 ml	20%

0.02%	SDS	0.1 ml	20%
2%	Blocking Reagent	20 ml	10%
	Water	4.4 ml	

General Procedures:

1. Place the blot in a heat-sealable plastic bag and add an appropriate volume of prehybridization solution (30 ml/100cm²) at room temperature. Seal the bag with a heat sealer, avoiding bubbles as much as possible. Lay down the bags in a large plastic tray (one tray can accommodate at least 4-5 bags). Ensure that the bags are lying flat in the tray so that the prehybridization solution is evenly distributed throughout the bag. Incubate the blot for at least 2 hours with gentle agitation using a waver shaker.
2. Denature DIG-labeled DNA probe by incubating for 10 min. at 98°C using the PCR machine and immediately cool it to 4°C.
3. Add probe to prehybridization solution (25 ng/ml; 30 ml = 750 ng total probe) and mix well but avoid foaming. Bubbles may lead to background.
4. Pour off the prehybridization solution from the hybridization bags and add new prehybridization and probe solution mixture to the bags containing the membrane.
5. Incubate with gentle agitation for at least 16 hours.
6. Proceed to medium stringency post-hybridization wash:

105

Three times for 20 min. each with gentle agitation using 1X SSC, 1% SDS at 60°C.

All wash solutions must be prewarmed to 60°C. Use about 100 ml of wash solution per membrane.

5 To avoid background keep the membranes fully submerged to avoid drying in spots; agitate sufficiently to avoid having membranes stick to one another.

7. After the wash, proceed to immunological detection and CSPD development.

10 **E. Procedure for Immunological Detection with CSPD**

Solutions:

Buffer 1: Maleic acid buffer (0.1 M maleic acid, 0.15 M NaCl; adjusted to pH 7.5 with NaOH)

15 Washing buffer: Maleic acid buffer with 0.3% (v/v) Tween 20.

Blocking stock solution 10% blocking reagent in buffer 1. Dissolve (10X concentration): blocking reagent powder (Boehringer Mannheim, Indianapolis, IN, cat. no. 1096176) by constantly stirring on a 65°C heating block or heat in a microwave, autoclave and store at 4°C.

20

25 Buffer 2

106

(1X blocking solution): Dilute the stock solution 1:10 in Buffer 1.

Detection buffer: 0.1 M Tris, 0.1 M NaCl, pH 9.5

Procedure:

- 5 1. After the post-hybridization wash the blots are briefly rinsed (1-5 min.) in the maleate washing buffer with gentle shaking.
2. Then the membranes are incubated for 30 min. in Buffer 2 with gentle shaking.
- 10 3. Anti-DIG-AP conjugate (Boehringer Mannheim, Indianapolis, IN, cat. no. 1093274) at 75 mU/ml (1:10,000) in Buffer 2 is used for detection. 75 ml of solution can be used for 3 blots.
- 15 4. The membrane is incubated for 30 min. in the antibody solution with gentle shaking.
5. The membrane are washed twice in washing buffer with gentle shaking. About 250 mls is used per wash for 3 blots.
- 20 6. The blots are equilibrated for 2-5 min in 60 ml detection buffer.
7. Dilute CSPD (1:200) in detection buffer. (This can be prepared ahead of time and stored in the dark at 4°C).

25 The following steps must be done individually. Bags (one for detection and one for exposure) should be cut and ready before doing the following steps.

8. The blot is carefully removed from the detection buffer and excess liquid removed without drying the membrane. The blot is immediately placed in a bag and 1.5 ml of CSPD solution is added. The CSPD solution can be spread over the membrane. Bubbles present at the edge and on the surface of the blot should be removed by gentle rubbing. The membrane is incubated for 5 min. in CSPD solution.
9. Excess liquid is removed and the membrane is blotted briefly (DNA side up) on Whatman 3MM paper. Do not let the membrane dry completely.
10. Seal the damp membrane in a hybridization bag and incubate for 10 min at 37°C to enhance the luminescent reaction.
11. Expose for 2 hours at room temperature to X-ray film. Multiple exposures can be taken. Luminescence continues for at least 24 hours and signal intensity increases during the first hours.

Example 2: Transformation of Carrot Cells

- Transformation of plant cells can be accomplished by a number of methods, as described above. Similarly, a number of plant genera can be regenerated from tissue culture following transformation. Transformation and regeneration of carrot cells as described herein is illustrative.
- Single cell suspension cultures of carrot (*Daucus carota*) cells are established from hypocotyls of cultivar Early Nantes in B₅ growth medium (O.L. Gamborg et al., *Plant Physiol.* 45:372 (1970)) plus 2,4-D and 15 mM CaCl₂ (B₅ -44 medium) by methods known in the art. The suspension cultures are subcultured by adding 10 ml of the suspension culture to

108

40 ml of B₅-44 medium in 250 ml flasks every 7 days and are maintained in a shaker at 150 rpm at 27 °C in the dark.

The suspension culture cells are transformed with exogenous DNA as described by Z. Chen et al. *Plant Mol. Bio.* 36:163 (1998). Briefly, 4-days post-subculture cells are incubated with cell wall digestion solution containing 0.4 M sorbitol, 2% driselase, 5mM MES (2-[N-Morpholino] ethanesulfonic acid) pH 5.0 for 5 hours. The digested cells are pelleted gently at 60 xg for 5 min. and washed twice in W5 solution containing 154 mM NaCl, 5 mM KCl, 125 mM CaCl₂ and 5mM glucose, pH 6.0. The protoplasts are suspended in MC solution containing 5 mM MES, 20 mM CaCl₂, 0.5 M mannitol, pH 5.7 and the protoplast density is adjusted to about 4 x 10⁶ protoplasts per ml.

15-60 µg of plasmid DNA is mixed with 0.9 ml of protoplasts. The resulting suspension is mixed with 40% polyethylene glycol (MW 8000, PEG 8000), by gentle inversion a few times at room temperature for 5 to 25 min. Protoplast culture medium known in the art is added into the PEG-DNA-protoplast mixture. Protoplasts are incubated in the culture medium for 24 hour to 5 days and cell extracts can be used for assay of transient expression of the introduced gene. Alternatively, transformed cells can be used to produce transgenic callus, which in turn can be used to produce transgenic plants, by methods known in the art. See, for example, Nomura and Komamine, *Plt. Phys.* 79:988-991 (1985), *Identification and Isolation of Single Cells that Produce Somatic Embryos in Carrot Suspension Cultures*.

The invention being thus described, it will be apparent to one of ordinary skill in the art that various modifications of the materials and methods for practicing the invention can be made. Such modifications are to be

considered within the scope of the invention as defined by the following claims.

Each of the references from the patent and periodical literature cited herein is hereby expressly incorporated in its
5 entirety by such citation.

110

REF TABLE 1

Maximum Length Sequence:

related to:

Clone IDs:

5 9581

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1

- Ceres seq_id 1007546

- Alternative transcription start site(s) located in SEQ

10 ID NO 1:

-96,-51,25,27,29,55,64

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 2

15 - Ceres seq_id 1007547

- Location of start within SEQ ID NO 1: at 1 nt.

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 2: at 32 aa.

20 (C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 1

- gi No. 3879939

25 - Description:

- % Identity: 45.9

- Alignment Length: 61

- Location of Alignment in SEQ ID NO 2: from 48 to

108

30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 3

- Ceres seq_id 1007548

- Location of start within SEQ ID NO 1: at 100 nt.

35

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 2

- gi No. 3879939

- Description:

- % Identity: 45.9

- Alignment Length: 61

- Location of Alignment in SEQ ID NO 3: from 15 to

45 75

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4

- Ceres seq_id 1007549

50 - Location of start within SEQ ID NO 1: at 121 nt.

111

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 3

- gi No. 3879939

- Description:

- % Identity: 45.9

- Alignment Length: 61

- Location of Alignment in SEQ ID NO 4: from 8 to 68

(Ba) Polypeptide Activities: Similar to yeast membrane
protein activities

Maximum Length Sequence:

related to:

Clone IDs:

9568

402131

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 5

- Ceres seq_id 1007583

- Alternative transcription start site(s) located in SEQ
ID NO 5:

2,3,4,7,10,11,12,17,42,43,300,505

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 6

- Ceres seq_id 1007584

- Location of start within SEQ ID NO 5: at 55 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- KH domain

- Location within SEQ ID NO 6: from 47 to 95 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 4

- gi No. 133940

- Description:

- % Identity: 75.1

- Alignment Length: 250

- Location of Alignment in SEQ ID NO 6: from 1 to

249

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 7

- Ceres seq_id 1007585

- Location of start within SEQ ID NO 5: at 184 nt.

112

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- KH domain
- Location within SEQ ID NO 7: from 4 to 52 aa.

5

(Dp) Related Amino Acid Sequences

- Alignment No. 5
- gi No. 133940
- Description:
- % Identity: 75.1
- Alignment Length: 250
- Location of Alignment in SEQ ID NO 7: from 1 to

10

206

15 Maximum Length Sequence:

related to:

Clone IDs:

91769

(Ac) cDNA Polynucleotide Sequence

20

- Pat. Appln. SEQ ID NO 8
- Ceres seq_id 1008148
- Alternative transcription start site(s) located in SEQ
ID NO 8:
-19,2,3,4,5,6,7,9,10,11,12,14

25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 9
- Ceres seq_id 1008149
- Location of start within SEQ ID NO 8: at 3 nt.

30

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 6
- gi No. 4539292
- Description:
- % Identity: 89.9
- Alignment Length: 181
- Location of Alignment in SEQ ID NO 9: from 25 to

35

40 203

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 10
- Ceres seq_id 1008150
- Location of start within SEQ ID NO 8: at 75 nt.

45

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 7
- gi No. 4539292

50

113

- Description:
- % Identity: 89.9
- Alignment Length: 181
- Location of Alignment in SEQ ID NO 10: from 1 to

5 179

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 11
- Ceres seq_id 1008151
- Location of start within SEQ ID NO 8: at 210 nt.

10

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

15

- Alignment No. 8
- gi No. 4539292
- Description:
- % Identity: 89.9
- Alignment Length: 181
- Location of Alignment in SEQ ID NO 11: from 1 to

20

134

(Ba) Polypeptide Activities: Similar to 40S Ribosomal
protein activities, and glycine rich RNA binding protein
activities.

25

Maximum Length Sequence:

related to:

30

Clone IDs:

8898

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 12
- Ceres seq_id 1008334
- Alternative transcription start site(s) located in SEQ
ID NO 12:
-12,29,30

35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 13
- Ceres seq_id 1008335
- Location of start within SEQ ID NO 12: at 2 nt.

40

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 9
- gi No. 3602948
- Description:
- % Identity: 43.7
- Alignment Length: 71

50

114

- Location of Alignment in SEQ ID NO 13: from 178
to 248

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 14
- Ceres seq_id 1008336
- Location of start within SEQ ID NO 12: at 59 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 14: at 22 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 10
- gi No. 3602948
- Description:
- % Identity: 43.7
- Alignment Length: 71
- Location of Alignment in SEQ ID NO 14: from 159
to 229

(Ba) Polypeptide Activities: Plant specific gene, Chloroplast
specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

8286

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 15
- Ceres seq_id 1008701
- Alternative transcription start site(s) located in SEQ
ID NO 15:
-6,2,3,5,6,7,18,24,25,28,31,33,35,37,42,50

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 16
- Ceres seq_id 1008702
- Location of start within SEQ ID NO 15: at 1 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 11
- gi No. 1083282
- Description:
- % Identity: 41.4
- Alignment Length: 106
- Location of Alignment in SEQ ID NO 16: from 23 to

115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 17
- Ceres seq_id 1008703
- Location of start within SEQ ID NO 15: at 67 nt.

5

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 12
- gi No. 1083282
- Description:
- % Identity: 41.4
- Alignment Length: 106
- Location of Alignment in SEQ ID NO 17: from 1 to

10

15 99

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 18
- Ceres seq_id 1008704
- Location of start within SEQ ID NO 15: at 2 nt.

20

(Ba) Polypeptide Activities: Similar to cytochrome C oxidase activities.

25

Maximum Length Sequence:

related to:

Clone IDs:

7792

30 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 19
- Ceres seq_id 1009003
- Alternative transcription start site(s) located in SEQ ID NO 19:

35

2,374

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 20
- Ceres seq_id 1009004
- Location of start within SEQ ID NO 19: at 48 nt.

40

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 13
- gi No. 3582320
- Description:
- % Identity: 32.6
- Alignment Length: 44
- Location of Alignment in SEQ ID NO 20: from 51 to

45

50

93

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 21
- Ceres seq_id 1009005
- 5 - Location of start within SEQ ID NO 19: at 57 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 10 - Alignment No. 14
- gi No. 3582320
- Description:
- % Identity: 32.6
- Alignment Length: 44
- 15 - Location of Alignment in SEQ ID NO 21: from 48 to
- 90

(Ba) Polypeptide Activities: Similar to Ring-H2 Zinc Finger
Protein activities.

20

Maximum Length Sequence:

related to:

Clone IDs:

25 7337

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 22
- Ceres seq_id 1009345
- Alternative transcription start site(s) located in SEQ
- 30 ID NO 22:
- 2

(B) Polypeptide Sequence

- 35 - Pat. Appln. SEQ ID NO 23
- Ceres seq_id 1009346
- Location of start within SEQ ID NO 22: at 50 nt.
- Location of Signal Peptide Cleavage Site within SEQ
- ID NO 23: at 22 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 45 - Alignment No. 15
- gi No. 3176705
- Description:
- % Identity: 53.3
- Alignment Length: 75
- 75 - Location of Alignment in SEQ ID NO 23: from 1 to

50

(B) Polypeptide Sequence

117

- Pat. Appln. SEQ ID NO 24
 - Ceres seq_id 1009347
 - Location of start within SEQ ID NO 22: at 62 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
- 5 ID NO 24: at 18 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 16
 - gi No. 3176705
 - Description:
 - % Identity: 53.3
 - Alignment Length: 75
 - Location of Alignment in SEQ ID NO 24: from 1 to
- 10
- 15 71

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot

- 20 specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

25 Clone IDs:

6349

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 25
 - Ceres seq_id 1010140
 - Alternative transcription start site(s) located in SEQ
- 30 ID NO 25:
- 31,-29,4,5,6,10,17,34,41,749

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 26
 - Ceres seq_id 1010141
 - Location of start within SEQ ID NO 25: at 3 nt.
- 35

(C) Nomination and Annotation of Domains within
40 Predicted Polypeptide(s)

- Bacterial regulatory proteins, deoR family
- Location within SEQ ID NO 26: from 57 to 95 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 17
 - gi No. 3257798
 - Description:
 - % Identity: 40.6
 - Alignment Length: 234
 - Location of Alignment in SEQ ID NO 26: from 56 to
- 45
- 50

289

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 27
- Ceres seq_id 1010142
- Location of start within SEQ ID NO 25: at 42 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Bacterial regulatory proteins, deoR family
- Location within SEQ ID NO 27: from 44 to 82 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 18
- gi No. 3257798
- Description:
- % Identity: 40.6
- Alignment Length: 234
- Location of Alignment in SEQ ID NO 27: from 43 to 276

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 28
- Ceres seq_id 1010143
- Location of start within SEQ ID NO 25: at 231 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 19
- gi No. 3257798
- Description:
- % Identity: 40.6
- Alignment Length: 234
- Location of Alignment in SEQ ID NO 28: from 1 to 213

Maximum Length Sequence:

related to:

Clone IDs:

6261

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 29
- Ceres seq_id 1010217
- Alternative transcription start site(s) located in SEQ ID NO 29: 2,5,15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 30
- Ceres seq_id 1010218
- Location of start within SEQ ID NO 29: at 85 nt.

119

- Location of Signal Peptide Cleavage Site within SEQ ID NO 30: at 22 aa.

5 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 20

- gi No. 3341723

- Description:

10 - % Identity: 64.3

- Alignment Length: 131

- Location of Alignment in SEQ ID NO 30: from 1 to
118

15 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 31

- Ceres seq_id 1010219

- Location of start within SEQ ID NO 29: at 118 nt.

20 - Location of Signal Peptide Cleavage Site within SEQ
ID NO 31: at 13 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

25 - Alignment No. 21

- gi No. 3341723

- Description:

- % Identity: 64.3

- Alignment Length: 131

30 - Location of Alignment in SEQ ID NO 31: from 1 to
107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 32

35 - Ceres seq_id 1010220

- Location of start within SEQ ID NO 29: at 121 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

40 (Dp) Related Amino Acid Sequences

- Alignment No. 22

- gi No. 3341723

- Description:

- % Identity: 64.3

45 - Alignment Length: 131

- Location of Alignment in SEQ ID NO 32: from 1 to
106

50 (Ba) Polypeptide Activities: Similar to Constans like
Protein activities and Zinc Finger Protein Activities.

120

Maximum Length Sequence:

related to:

Clone IDs:

5 6145

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 33

- Ceres seq_id 1010302

10 ID NO 33:

-5,-3,-2,-1,2,3,4,5,6,7,8,10,11,12,13,15,19,23,45,349

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 34

15 - Ceres seq_id 1010303

- Location of start within SEQ ID NO 33: at 59 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

20 - Pathogenesis-related protein Bet v I family

- Location within SEQ ID NO 34: from 5 to 155 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 23

25 - gi No. 1321731

- Description:

- % Identity: 35.7

- Alignment Length: 159

30 155 - Location of Alignment in SEQ ID NO 34: from 5 to

Maximum Length Sequence:

related to:

Clone IDs:

35 5180

Public Genomic DNA:

gi No: 4757410

Predicted Exons:

40 INTR 37202 ... 37397 OCKHAMG-CDNA
INTR 37493 ... 37825 OCKHAMG-CDNA

INIT 37271 ... 37397 OCKHAMG-CDS

TERM 37493 ... 37704 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

45 - Pat. Appln. SEQ ID NO 35

- Ceres seq_id 1010815

ID NO 35:

15,16,17,18,19,29,31,34

50

(B) Polypeptide Sequence

121

- Pat. Appln. SEQ ID NO 36
- Ceres seq_id 1010816
- Location of start within SEQ ID NO 35: at 70 nt.

5 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 24
- gi No. 2879811
- Description:
- % Identity: 88.4
- Alignment Length: 112
- Location of Alignment in SEQ ID NO 36: from 1 to

112

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 37
- Ceres seq_id 1010817
- Location of start within SEQ ID NO 35: at 133 nt.

20

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 25
- gi No. 2879811
- Description:
- % Identity: 88.4
- Alignment Length: 112
- Location of Alignment in SEQ ID NO 37: from 1 to

30 91

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 38
- Ceres seq_id 1010818
- Location of start within SEQ ID NO 35: at 257 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 38: at 26 aa.

35

(Ba) Polypeptide Activities: Similar to ribosomal protein
activities.

40

Maximum Length Sequence:

related to:

Clone IDs:

45

42842

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 39
- Ceres seq_id 1011437
- Alternative transcription start site(s) located in SEQ

50

ID NO 39:

-28

122

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 40
- Ceres seq_id 1011438
5 - Location of start within SEQ ID NO 39: at 2 nt.
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 41
- Ceres seq_id 1011439
10 - Location of start within SEQ ID NO 39: at 1 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 41: at 29 aa.
- (C) Nomination and Annotation of Domains within
15 Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- Alignment No. 26
- gi No. 3334271
- Description:
20 - % Identity: 29.6
- Alignment Length: 54
- Location of Alignment in SEQ ID NO 41: from 13 to
65
- (B) Polypeptide Sequence
25 - Pat. Appln. SEQ ID NO 42
- Ceres seq_id 1011440
- Location of start within SEQ ID NO 39: at 28 nt.
- Location of Signal Peptide Cleavage Site within SEQ
30 ID NO 42: at 20 aa.
- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
35 - Alignment No. 27
- gi No. 3334271
- Description:
- % Identity: 29.6
- Alignment Length: 54
40 - Location of Alignment in SEQ ID NO 42: from 4 to
56
- (Ba) Polypeptide Activities: Similar to NADH Oxidoreductase
MWFE Subunit Protein Activities.
45
- Maximum Length Sequence:
related to:
Clone IDs:
50 42475
(Ac) cDNA Polynucleotide Sequence

123

- Pat. Appln. SEQ ID NO 43
- Ceres seq_id 1011616
- Alternative transcription start site(s) located in SEQ ID NO 43:

5 3,5,476

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 44
- Ceres seq_id 1011617
- Location of start within SEQ ID NO 43: at 115 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 28
- gi No. 3859560
- Description:
- % Identity: 36.2
- Alignment Length: 225
- Location of Alignment in SEQ ID NO 44: from 31 to 248

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 45
- Ceres seq_id 1011618
- Location of start within SEQ ID NO 43: at 406 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 29
- gi No. 3859560
- Description:
- % Identity: 36.2
- Alignment Length: 225
- Location of Alignment in SEQ ID NO 45: from 1 to 151

40 (Ba) Polypeptide Activities: Similar to acycl-protein thioosterases protein activities, calcium independent phospholipase A2 activities, and carboxylesterase activities.

45 Maximum Length Sequence:

related to:

Clone IDs:

42405

(Ac) cDNA Polynucleotide Sequence

- 50 - Pat. Appln. SEQ ID NO 46
- Ceres seq_id 1011631

124

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 47
5 - Ceres seq_id 1011632
- Location of start within SEQ ID NO 46: at 3 nt.
- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
10 (Dp) Related Amino Acid Sequences
- Alignment No. 30
- gi No. 3618318
- Description:
15 - % Identity: 72.7
- Alignment Length: 44
- Location of Alignment in SEQ ID NO 47: from 91 to
134
- (B) Polypeptide Sequence
20 - Pat. Appln. SEQ ID NO 48
- Ceres seq_id 1011633
- Location of start within SEQ ID NO 46: at 9 nt.
- (C) Nomination and Annotation of Domains within
25 Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- Alignment No. 31
- gi No. 3618318
- Description:
30 - % Identity: 72.7
- Alignment Length: 44
- Location of Alignment in SEQ ID NO 48: from 89 to
132
- (B) Polypeptide Sequence
35 - Pat. Appln. SEQ ID NO 49
- Ceres seq_id 1011634
- Location of start within SEQ ID NO 46: at 15 nt.
- (C) Nomination and Annotation of Domains within
40 Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- Alignment No. 32
- gi No. 3618318
45 - Description:
- % Identity: 72.7
- Alignment Length: 44
- Location of Alignment in SEQ ID NO 49: from 87 to
130
50

125

(Ba) Polypeptide Activities: Similar to Constans protein activities, and zinc finger protein activities.

Maximum Length Sequence:

5 related to:

Clone IDs:

42240

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 50

10 - Ceres seq_id 1011714

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 51

15 - Ceres seq_id 1011715

- Location of start within SEQ ID NO 50: at 2 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

20 - Bacterial mutT protein

- Location within SEQ ID NO 51: from 26 to 67 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 33

25 - gi No. 2129134

- Description:

- % Identity: 40.8

- Alignment Length: 121

30 131 - Location of Alignment in SEQ ID NO 51: from 12 to

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 52

- Ceres seq_id 1011716

35 - Location of start within SEQ ID NO 50: at 14 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

40 - Bacterial mutT protein

- Location within SEQ ID NO 52: from 22 to 63 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 34

- gi No. 2129134

45 - Description:

- % Identity: 40.8

- Alignment Length: 121

127 - Location of Alignment in SEQ ID NO 52: from 8 to

50

(B) Polypeptide Sequence

126

- Pat. Appln. SEQ ID NO 53
- Ceres seq_id 1011717
- Location of start within SEQ ID NO 50: at 185 nt.

5 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 35
- gi No. 2129134
- 10 - Description:
- % Identity: 40.8
- Alignment Length: 121
- Location of Alignment in SEQ ID NO 53: from 1 to

70

15

Maximum Length Sequence:

related to:

Clone IDs:

42169

20 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 54
 - Ceres seq_id 1011784
 - Alternative transcription start site(s) located in SEQ
- ID NO 54:
- 25 -15,-4,7,402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 55
 - Ceres seq_id 1011785
 - 30 - Location of start within SEQ ID NO 54: at 1 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
- ID NO 55: at 42 aa.

35 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Plant lipid transfer protein family
- Location within SEQ ID NO 55: from 45 to 108 aa.

(Dp) Related Amino Acid Sequences

- 40 - Alignment No. 36
 - gi No. 543565
 - Description:
 - % Identity: 56.5
 - Alignment Length: 85
 - 45 - Location of Alignment in SEQ ID NO 55: from 29 to
- 110

(B) Polypeptide Sequence

- 50 - Pat. Appln. SEQ ID NO 56
- Ceres seq_id 1011786
- Location of start within SEQ ID NO 54: at 49 nt.

127

- Location of Signal Peptide Cleavage Site within SEQ ID NO 56: at 26 aa.

- (C) Nomination and Annotation of Domains within
5 Predicted Polypeptide(s)
- Plant lipid transfer protein family
- Location within SEQ ID NO 56: from 29 to 92 aa.

- (Dp) Related Amino Acid Sequences
10 - Alignment No. 37
- gi No. 543565
- Description:
- % Identity: 56.5
- Alignment Length: 85
15 - Location of Alignment in SEQ ID NO 56: from 13 to
94

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 57
20 - Ceres seq_id 1011787
- Location of start within SEQ ID NO 54: at 3 nt.

- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
25 (Dp) Related Amino Acid Sequences

Maximum Length Sequence:

related to:

Clone IDs:

- 30 41992

- (Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 58
- Ceres seq_id 1011820
- Alternative transcription start site(s) located in SEQ
35 ID NO 58:
-40,37

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 59
40 - Ceres seq_id 1011821
- Location of start within SEQ ID NO 58: at 1 nt.

- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
45 (Dp) Related Amino Acid Sequences
- Alignment No. 38
- gi No. 3417418
- Description:
- % Identity: 23.6
50 - Alignment Length: 207

128

226 - Location of Alignment in SEQ ID NO 59: from 24 to

(B) Polypeptide Sequence

- 5 - Pat. Appln. SEQ ID NO 60
- Ceres seq_id 1011822
- Location of start within SEQ ID NO 58: at 13 nt.

10 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 15 - Alignment No. 39
- gi No. 3417418
- Description:
- % Identity: 23.6
- Alignment Length: 207
- Location of Alignment in SEQ ID NO 60: from 20 to
222

20 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 61
- Ceres seq_id 1011823
- Location of start within SEQ ID NO 58: at 151 nt.

25 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 30 - Alignment No. 40
- gi No. 3417418
- Description:
- % Identity: 23.6
- Alignment Length: 207
- Location of Alignment in SEQ ID NO 61: from 1 to
176

35 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

40 Maximum Length Sequence:
related to:

Clone IDs:

41851

45 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 62
- Ceres seq_id 1011874

50 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 63

129

- Ceres seq_id 1011875
- Location of start within SEQ ID NO 62: at 1 nt.

5 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 41
- gi No. 2911044
- Description:
- 10 - % Identity: 78.7
- Alignment Length: 95
- Location of Alignment in SEQ ID NO 63: from 28 to 121

15 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

20 41682

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 64
- Ceres seq_id 1011981

25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 65
- Ceres seq_id 1011982
- Location of start within SEQ ID NO 64: at 68 nt.

30

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 42
- 35 - gi No. 4115355
- Description:
- % Identity: 100
- Alignment Length: 52
- Location of Alignment in SEQ ID NO 65: from 1 to

40 52

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 66
- Ceres seq_id 1011983
- 45 - Location of start within SEQ ID NO 64: at 3 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

50

(B) Polypeptide Sequence

130

- Pat. Appln. SEQ ID NO 67
 - Ceres seq_id 1011984
 - Location of start within SEQ ID NO 64: at 483 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
- 5 ID NO 67: at 19 aa.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.

10

Maximum Length Sequence:

related to:

Clone IDs:

15

38470

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 68
 - Ceres seq_id 1014547
 - Alternative transcription start site(s) located in SEQ
- 20 ID NO 68:
-39,-2,-1,2,3,7,8,9,10

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 69
 - Ceres seq_id 1014548
 - Location of start within SEQ ID NO 68: at 1 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
- ID NO 69: at 32 aa.

30

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Plant lipid transfer protein family
- Location within SEQ ID NO 69: from 44 to 110 aa.

35

(Dp) Related Amino Acid Sequences

- Alignment No. 43
 - gi No. 3062791
 - Description:
 - % Identity: 72.2
 - Alignment Length: 90
 - Location of Alignment in SEQ ID NO 69: from 21 to
- 110

(B) Polypeptide Sequence

45

- Pat. Appln. SEQ ID NO 70
 - Ceres seq_id 1014549
 - Location of start within SEQ ID NO 68: at 25 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
- ID NO 70: at 24 aa.

50

131

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Plant lipid transfer protein family
- Location within SEQ ID NO 70: from 36 to 102 aa.

5

(Dp) Related Amino Acid Sequences

- Alignment No. 44
- gi No. 3062791
- Description:
- % Identity: 72.2
- Alignment Length: 90
- Location of Alignment in SEQ ID NO 70: from 13 to

102

15 Maximum Length Sequence:

related to:

Clone IDs:

38004

(Ac) cDNA Polynucleotide Sequence

20

- Pat. Appln. SEQ ID NO 71
- Ceres seq_id 1014995
- Alternative transcription start site(s) located in SEQ
ID NO 71:
2,3,4

25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 72
- Ceres seq_id 1014996
- Location of start within SEQ ID NO 71: at 2 nt.

30

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Aminotransferase class IV
- Location within SEQ ID NO 72: from 71 to 334 aa.

35

(Dp) Related Amino Acid Sequences

- Alignment No. 45
- gi No. 3540183
- Description:
- % Identity: 54.7
- Alignment Length: 287
- Location of Alignment in SEQ ID NO 72: from 56 to

341

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 73
- Ceres seq_id 1014997
- Location of start within SEQ ID NO 71: at 65 nt.

50

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

132

- Aminotransferase class IV
- Location within SEQ ID NO 73: from 50 to 313 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 46
- gi No. 3540183
- Description:
- % Identity: 54.7
- Alignment Length: 287
- Location of Alignment in SEQ ID NO 73: from 35 to 320

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 74
- Ceres seq_id 1014998
- Location of start within SEQ ID NO 71: at 167 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Aminotransferase class IV
- Location within SEQ ID NO 74: from 16 to 279 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 47
- gi No. 3540183
- Description:
- % Identity: 54.7
- Alignment Length: 287
- Location of Alignment in SEQ ID NO 74: from 1 to 286

Maximum Length Sequence:

related to:

Clone IDs:

35 37701

Public Genomic DNA:

gi No: 4699904

Predicted Exons:

SINGLE 38530 ... 37988 OCKHAMG-CDS

40 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 75
- Ceres seq_id 1015323
- Alternative transcription start site(s) located in SEQ ID NO 75:
- 1,5,6,12

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 76
- Ceres seq_id 1015324
- Location of start within SEQ ID NO 75: at 59 nt.

133

- Location of Signal Peptide Cleavage Site within SEQ ID NO 76: at 25 aa.

5 (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

10 - Alignment No. 48
- gi No. 3860308
- Description:
- % Identity: 44.5
- Alignment Length: 140
- Location of Alignment in SEQ ID NO 76: from 56 to 175

15 (Ba) Polypeptide Activities: Arabidopsis specific gene, dicot
specific gene, plant specific gene.

20 Maximum Length Sequence:
related to:
Clone IDs:

364

(Ac) cDNA Polynucleotide Sequence

25 - Pat. Appln. SEQ ID NO 77
- Ceres seq_id 1016486
- Alternative transcription start site(s) located in SEQ ID NO 77:
17,19,20,21,22,23,29,35,38

30

(B) Polypeptide Sequence

35 - Pat. Appln. SEQ ID NO 78
- Ceres seq_id 1016487
- Location of start within SEQ ID NO 77: at 1 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 78: at 46 aa.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

40 - Gamma-thionins family
- Location within SEQ ID NO 78: from 55 to 101 aa.

(Dp) Related Amino Acid Sequences

45 - Alignment No. 49
- gi No. 4038039
- Description:
- % Identity: 100
- Alignment Length: 77
- Location of Alignment in SEQ ID NO 78: from 25 to 101

134

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 79
- Ceres seq_id 1016488
- Location of start within SEQ ID NO 77: at 73 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 79: at 22 aa.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Gamma-thionins family
- Location within SEQ ID NO 79: from 31 to 77 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 50
- gi No. 4038039
- Description:
- % Identity: 100
- Alignment Length: 77
- Location of Alignment in SEQ ID NO 79: from 1 to

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 80
- Ceres seq_id 1016489
- Location of start within SEQ ID NO 77: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Gamma-thionins family
- Location within SEQ ID NO 80: from 16 to 62 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 51
- gi No. 4038039
- Description:
- % Identity: 100
- Alignment Length: 77
- Location of Alignment in SEQ ID NO 80: from 1 to

62

Maximum Length Sequence:

related to:

Clone IDs:

33891

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 81
- Ceres seq_id 1018341
- Alternative transcription start site(s) located in SEQ ID NO 81:

4

135

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 82
- Ceres seq_id 1018342
- Location of start within SEQ ID NO 81: at 71 nt.

5

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 52
- gi No. 1064887
- Description:
- % Identity: 60
- Alignment Length: 65
- Location of Alignment in SEQ ID NO 82: from 2 to

10

15 66

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 83
- Ceres seq_id 1018343
- Location of start within SEQ ID NO 81: at 143 nt.

20

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 53
- gi No. 1064887
- Description:
- % Identity: 60
- Alignment Length: 65
- Location of Alignment in SEQ ID NO 83: from 1 to

25

30

42

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 84
- Ceres seq_id 1018344
- Location of start within SEQ ID NO 81: at 146 nt.

35

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 54
- gi No. 1064887
- Description:
- % Identity: 60
- Alignment Length: 65
- Location of Alignment in SEQ ID NO 84: from 1 to

40

45

41

(Ba) Polypeptide Activities: Similar to pollen coat protein activities and LEA protein activities.

50

136

Maximum Length Sequence:

related to:

Clone IDs:

33828

5 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 85

- Ceres seq_id 1018382

- Alternative transcription start site(s) located in SEQ

ID NO 85:

10 2,4,5,6,7,8,9,10,11,14

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 86

- Ceres seq_id 1018383

15 - Location of start within SEQ ID NO 85: at 22 nt.

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 86: at 24 aa.

(C) Nomination and Annotation of Domains within

20 Predicted Polypeptide(s)

- Plant lipid transfer protein family

- Location within SEQ ID NO 86: from 28 to 115 aa.

(Dp) Related Amino Acid Sequences

25 - Alignment No. 55

- gi No. 899224

- Description:

- % Identity: 78.2

- Alignment Length: 119

30 - Location of Alignment in SEQ ID NO 86: from 1 to

119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 87

35 - Ceres seq_id 1018384

- Location of start within SEQ ID NO 85: at 73 nt.

(C) Nomination and Annotation of Domains within

40 Predicted Polypeptide(s)

- Plant lipid transfer protein family

- Location within SEQ ID NO 87: from 11 to 98 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 56

45 - gi No. 899224

- Description:

- % Identity: 78.2

- Alignment Length: 119

- Location of Alignment in SEQ ID NO 87: from 1 to

50 102

137

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 88
- Ceres seq_id 1018385
- Location of start within SEQ ID NO 85: at 3 nt.

5

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

10 Maximum Length Sequence:

related to:

Clone IDs:

30349

(Ac) cDNA Polynucleotide Sequence

15

- Pat. Appln. SEQ ID NO 89
- Ceres seq_id 1020666
- Alternative transcription start site(s) located in SEQ ID NO 89:
33,35,39,40,42,43,44,45,64,173

20

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 90
- Ceres seq_id 1020667
- Location of start within SEQ ID NO 89: at 118 nt.

25

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S7e
- Location within SEQ ID NO 90: from 7 to 187 aa.

30

(Dp) Related Amino Acid Sequences

- Alignment No. 57
- gi No. 3851636
- Description:
- % Identity: 77.4
- Alignment Length: 190
- Location of Alignment in SEQ ID NO 90: from 1 to

190

40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 91
- Ceres seq_id 1020668
- Location of start within SEQ ID NO 89: at 271 nt.

45

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S7e
- Location within SEQ ID NO 91: from 1 to 136 aa.

50

(Dp) Related Amino Acid Sequences

- Alignment No. 58

138

- gi No. 3851636
- Description:
- % Identity: 77.4
- Alignment Length: 190
- Location of Alignment in SEQ ID NO 91: from 1 to

5

139

Maximum Length Sequence:
related to:

10

Clone IDs:

30113

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 92
- Ceres seq_id 1020784

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 93
- Ceres seq_id 1020785

20

- Location of start within SEQ ID NO 92: at 60 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 93: at 25 aa.

(C) Nomination and Annotation of Domains within

25

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 59
- gi No. 3860308

- Description:

30

- % Identity: 44.5

- Alignment Length: 140

- Location of Alignment in SEQ ID NO 93: from 56 to

175

35

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.

40

Maximum Length Sequence:
related to:

Clone IDs:

29120

Public Genomic DNA:

45

gi No: 5822667

Predicted Exons:

INTR 68772 ... 69532 OCKHAMG-CDNA

SINGLE 68846 ... 69325 OCKHAMG-CDS

50

gi No: 6041831

Predicted Exons:

139
INTR 63702 ... 64462 OCKHAMG-CDNA

SINGLE 63776 ... 64255 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

5 - Pat. Appln. SEQ ID NO 94
- Ceres seq_id 1021525
- Alternative transcription start site(s) located in SEQ
ID NO 94:
25,26,27,28,29,35,36,39,51,53,54,68

10 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 95
- Ceres seq_id 1021526
- Location of start within SEQ ID NO 94: at 75 nt.

15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

20 - Alignment No. 60
- gi No. 4388980
- Description:
- % Identity: 29.1
- Alignment Length: 110
- Location of Alignment in SEQ ID NO 95: from 47 to

25 156

(Ba) Polypeptide Activities: Similar to adrenodoxin precursor
protein activities and adrenal ferredoxin activities.

30

Maximum Length Sequence:
related to:
Clone IDs:

35 2891

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 96
- Ceres seq_id 1021563
- Alternative transcription start site(s) located in SEQ

40 ID NO 96:
16,28,29,30,31,35,36,43,74,77,80,88,89,90,95

(B) Polypeptide Sequence

45 - Pat. Appln. SEQ ID NO 97
- Ceres seq_id 1021564
- Location of start within SEQ ID NO 96: at 2 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

50 (Dp) Related Amino Acid Sequences
- Alignment No. 61

140

- gi No. 2493089
- Description:
- % Identity: 29.7
- Alignment Length: 77
- Location of Alignment in SEQ ID NO 97: from 52 to

5
125

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 98
- Ceres seq_id 1021565
- Location of start within SEQ ID NO 96: at 116 nt.

10

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 62
- gi No. 2493089
- Description:
- % Identity: 29.7
- Alignment Length: 77
- Location of Alignment in SEQ ID NO 98: from 14 to

15

20

87

(Ba) Polypeptide Activities: Similar to ATPK-mouse
activities, ATP synthase activities, and mitochondrial F-
Chain activities.

25

Maximum Length Sequence:

related to:

Clone IDs:

28979

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 99
- Ceres seq_id 1021576
- Alternative transcription start site(s) located in SEQ
ID NO 99:

-13,-

11,3,5,7,11,12,13,15,24,26,28,29,31,34,35,36,37,38,39

40

43,44,45,46,47,48,50,51,52,56,58,59,61,67,68,70,75,82,83,91,1
12

244,313,318

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 100
- Ceres seq_id 1021577
- Location of start within SEQ ID NO 99: at 109 nt.

45

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Photosystem I psaG / psaK

50

141

- Location within SEQ ID NO 100: from 50 to 130 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 63
- gi No. 3885511
- Description:
- % Identity: 81.1
- Alignment Length: 128
- Location of Alignment in SEQ ID NO 100: from 1 to

127

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 101
- Ceres seq_id 1021578
- Location of start within SEQ ID NO 99: at 121 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Photosystem I psaG / psaK
- Location within SEQ ID NO 101: from 46 to 126 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 64
- gi No. 3885511
- Description:
- % Identity: 81.1
- Alignment Length: 128
- Location of Alignment in SEQ ID NO 101: from 1 to

123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 102
- Ceres seq_id 1021579
- Location of start within SEQ ID NO 99: at 124 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Photosystem I psaG / psaK
- Location within SEQ ID NO 102: from 45 to 125 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 65
- gi No. 3885511
- Description:
- % Identity: 81.1
- Alignment Length: 128
- Location of Alignment in SEQ ID NO 102: from 1 to

122

Maximum Length Sequence:
related to:

142

Clone IDs:

28177

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 103
- Ceres seq_id 1021927
- Alternative transcription start site(s) located in SEQ

ID NO 103:

2,12,20,23,29,36,46,47,53

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 104
- Ceres seq_id 1021928
- Location of start within SEQ ID NO 103: at 67 nt.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 66
- gi No. 4263779
- Description:
- % Identity: 28.2
- Alignment Length: 177
- Location of Alignment in SEQ ID NO 104: from 14

to 182

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 105
- Ceres seq_id 1021929
- Location of start within SEQ ID NO 103: at 172 nt.
- Location of Signal Peptide Cleavage Site within SEQ

ID NO 105: at 23 aa.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 67
- gi No. 4263779
- Description:
- % Identity: 28.2
- Alignment Length: 177
- Location of Alignment in SEQ ID NO 105: from 1 to

147

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 106
- Ceres seq_id 1021930
- Location of start within SEQ ID NO 103: at 220 nt.

(C) Nomination and Annotation of Domains within

0 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

143

- Alignment No. 68
- gi No. 4263779
- Description:
- % Identity: 28.2
- Alignment Length: 177
- Location of Alignment in SEQ ID NO 106: from 1 to

131

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

2807

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 107
- Ceres seq_id 1021945

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 108
- Ceres seq_id 1021946
- Location of start within SEQ ID NO 107: at 1 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 69
- gi No. 3334132
- Description:
- % Identity: 27.4
- Alignment Length: 114
- Location of Alignment in SEQ ID NO 108: from 28

to 136

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 109
- Ceres seq_id 1021947
- Location of start within SEQ ID NO 107: at 163 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 70
- gi No. 3334132
- Description:
- % Identity: 27.4
- Alignment Length: 114
- Location of Alignment in SEQ ID NO 109: from 1 to

82

144

(Ba) Polypeptide Activities: Similar to C21 ORF4 - membrane protein activities

5 Maximum Length Sequence:

related to:

Clone IDs:

27792

(Ac) cDNA Polynucleotide Sequence

10 - Pat. Appln. SEQ ID NO 110

- Ceres seq_id 1022170

- Alternative transcription start site(s) located in SEQ ID NO 110:

-4,-1,32,68

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 111

- Ceres seq_id 1022171

- Location of start within SEQ ID NO 110: at 92 nt.

20

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 71

25 - gi No. 1173456

- Description:

- % Identity: 54.7

- Alignment Length: 129

- Location of Alignment in SEQ ID NO 111: from 4 to

30 131

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 112

- Ceres seq_id 1022172

35 - Location of start within SEQ ID NO 110: at 191 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 72

40

- gi No. 1173456

- Description:

- % Identity: 54.7

- Alignment Length: 129

45

- Location of Alignment in SEQ ID NO 112: from 1 to

98

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 113

50 - Ceres seq_id 1022173

- Location of start within SEQ ID NO 110: at 1 nt.

145

- Location of Signal Peptide Cleavage Site within SEQ ID NO 113: at 19 aa.

5 (Ba) Polypeptide Activities: Similar to small nuclear ribonucleoprotein activities.

Maximum Length Sequence:

related to:

Clone IDs:

10 27167

Public Genomic DNA:

gi No: 3046850

Predicted Exons:

15 INIT 45217 ... 45131 OCKHAMG-CDS

INTR 44695 ... 44629 OCKHAMG-CDS

TERM 44554 ... 44286 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 114

- Ceres seq_id 1022554

20 - Alternative transcription start site(s) located in SEQ ID NO 114:

-49,-

19,7,22,23,28,29,30,31,32,33,35,36,37,51,57,67,75,81,82

85

25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 115

- Ceres seq_id 1022555

- Location of start within SEQ ID NO 114: at 107 nt.

30

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Heme-binding domain in cytochrome b5 and oxidoreductases

35 - Location within SEQ ID NO 115: from 7 to 84 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 73

- gi No. 4240122

40 - Description:

- % Identity: 100

- Alignment Length: 140

- Location of Alignment in SEQ ID NO 115: from 1 to

140

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 116

- Ceres seq_id 1022556

- Location of start within SEQ ID NO 114: at 317 nt.

50

146

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 74
- 5 - gi No. 4240122
- Description:
- % Identity: 100
- Alignment Length: 140
- 10 - Location of Alignment in SEQ ID NO 116: from 1 to 70

Maximum Length Sequence:

related to:

Clone IDs:

15 27109

Public Genomic DNA:

gi No: 6449507

Predicted Exons:

20	INIT	94711 ... 94519	OCKHAMG-CDS
	INTR	94417 ... 94326	OCKHAMG-CDS
	INTR	94249 ... 94131	OCKHAMG-CDS
	TERM	94046 ... 93968	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 117
- 25 - Ceres seq_id 1022594
- Alternative transcription start site(s) located in SEQ ID NO 117:
 2,15,24,25,66,69,72,74

30 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 118
- Ceres seq_id 1022595
- Location of start within SEQ ID NO 117: at 1 nt.

35 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Universal stress protein family
- Location within SEQ ID NO 118: from 98 to 183 aa.

40 (Dp) Related Amino Acid Sequences

- Alignment No. 75
- gi No. 2160182
- Description:
- 45 - % Identity: 37.5
- Alignment Length: 160
- Location of Alignment in SEQ ID NO 118: from 39 to 186

(B) Polypeptide Sequence

- 50 - Pat. Appln. SEQ ID NO 119
- Ceres seq_id 1022596

147

- Location of start within SEQ ID NO 117: at 82 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Universal stress protein family
- Location within SEQ ID NO 119: from 71 to 156 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 76
- gi No. 2160182
- Description:
- % Identity: 37.5
- Alignment Length: 160
- Location of Alignment in SEQ ID NO 119: from 12
to 159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 120
- Ceres seq_id 1022597
- Location of start within SEQ ID NO 117: at 106 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Universal stress protein family
- Location within SEQ ID NO 120: from 63 to 148 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 77
- gi No. 2160182
- Description:
- % Identity: 37.5
- Alignment Length: 160
- Location of Alignment in SEQ ID NO 120: from 4 to
151

35

(Ba) Polypeptide Activities: Similar to protein in
methanobacterium thermoautotrophicum activities.

Maximum Length Sequence:

related to:

Clone IDs:

26994

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 121
- Ceres seq_id 1022621
- Alternative transcription start site(s) located in SEQ
ID NO 121:
2, 7, 9, 13, 35, 38, 45, 57

50

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 122

148

- Ceres seq_id 1022622
- Location of start within SEQ ID NO 121: at 86 nt.

5 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 78
- gi No. 3256599
- Description:
- 10 - % Identity: 32
- Alignment Length: 128
- Location of Alignment in SEQ ID NO 122: from 7 to
128

15 (Ba) Polypeptide Activities: Similar to structural cell wall
protein activities, and larval gene protein in the Fruit fly
activities.

20 Maximum Length Sequence:

related to:

Clone IDs:

23518

(Ac) cDNA Polynucleotide Sequence

- 25 - Pat. Appln. SEQ ID NO 123
- Ceres seq_id 1024375
- Alternative transcription start site(s) located in SEQ
ID NO 123:
7,8,10,17,18,24,35,41,42,43,44,46,48,52,54,59

30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 124
- Ceres seq_id 1024376
- Location of start within SEQ ID NO 123: at 130 nt.

35

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S7e
- Location within SEQ ID NO 124: from 7 to 187 aa.

40

(Dp) Related Amino Acid Sequences

- Alignment No. 79
- gi No. 3851636
- Description:
- 45 - % Identity: 76.6
- Alignment Length: 188
- Location of Alignment in SEQ ID NO 124: from 1 to
188

50 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 125

149

- Ceres seq_id 1024377
- Location of start within SEQ ID NO 123: at 283 nt.

5 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S7e
- Location within SEQ ID NO 125: from 1 to 136 aa.

10 (Dp) Related Amino Acid Sequences

- Alignment No. 80
- gi No. 3851636
- Description:
- % Identity: 76.6
- Alignment Length: 188

15 - Location of Alignment in SEQ ID NO 125: from 1 to
137

Maximum Length Sequence:
related to:

20 Clone IDs:
23170

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 126
- Ceres seq_id 1024535
- 25 - Alternative transcription start site(s) located in SEQ
ID NO 126:
2,8,11,31,46,47,48

30 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 127
- Ceres seq_id 1024536
- Location of start within SEQ ID NO 126: at 115 nt.

35 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 81
- gi No. 2621731
- Description:
- 40 - % Identity: 35.2
- Alignment Length: 88
- Location of Alignment in SEQ ID NO 127: from 5 to

92

45 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 128
- Ceres seq_id 1024537
- Location of start within SEQ ID NO 126: at 3 nt.

50 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

150

(Dp) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 129
- Ceres seq_id 1024538
- Location of start within SEQ ID NO 126: at 253 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 82
- gi No. 2621731
- Description:
- % Identity: 35.2
- Alignment Length: 88
- Location of Alignment in SEQ ID NO 129: from 1 to 46

(Ba) Polypeptide Activities: Similar to small nuclear
ribonucleoprotein activities.

Maximum Length Sequence:

related to:

Clone IDs:

21228

Public Genomic DNA:

gi No: 4539402

Predicted Exons:

INIT	36726	...	36352	GENBANK
INTR	36257	...	36135	GENBANK
TERM	35555	...	35469	GENBANK
INTR	36791	...	36352	OCKHAMG-CDNA
INTR	36257	...	36135	OCKHAMG-CDNA
INTR	35555	...	35325	OCKHAMG-CDNA
INIT	36726	...	36352	OCKHAMG-CDS
INTR	36257	...	36135	OCKHAMG-CDS
TERM	35555	...	35469	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 130
- Ceres seq_id 1025683
- Alternative transcription start site(s) located in SEQ ID NO 130: 2,8,22

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 131
- Ceres seq_id 1025684
- Location of start within SEQ ID NO 130: at 3 nt.

151

- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
- Ribosomal protein L6
- Location within SEQ ID NO 131: from 34 to 216 aa.
- (Dp) Related Amino Acid Sequences
- Alignment No. 83
- gi No. 266945
- Description:
- % Identity: 84
- Alignment Length: 194
- Location of Alignment in SEQ ID NO 131: from 23
to 216
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 132
- Ceres seq_id 1025685
- Location of start within SEQ ID NO 130: at 69 nt.
- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
- Ribosomal protein L6
- Location within SEQ ID NO 132: from 12 to 194 aa.
- (Dp) Related Amino Acid Sequences
- Alignment No. 84
- gi No. 266945
- Description:
- % Identity: 84
- Alignment Length: 194
- Location of Alignment in SEQ ID NO 132: from 1 to
194
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 133
- Ceres seq_id 1025686
- Location of start within SEQ ID NO 130: at 96 nt.
- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
- Ribosomal protein L6
- Location within SEQ ID NO 133: from 3 to 185 aa.
- (Dp) Related Amino Acid Sequences
- Alignment No. 85
- gi No. 266945
- Description:
- % Identity: 84
- Alignment Length: 194

152

- Location of Alignment in SEQ ID NO 133: from 1 to
185

Maximum Length Sequence:

5 related to:

Clone IDs:

19274

(Ac) cDNA Polynucleotide Sequence

- 10 - Pat. Appln. SEQ ID NO 134
- Ceres seq_id 1027152
- Alternative transcription start site(s) located in SEQ
ID NO 134:
-350,3,4,10,11,13,222

15 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 135
- Ceres seq_id 1027153
- Location of start within SEQ ID NO 134: at 3 nt.

20 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 25 - Alignment No. 86
- gi No. 2879811
- Description:
- % Identity: 86.6
- Alignment Length: 112
- Location of Alignment in SEQ ID NO 135: from 26
to 137

30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 136
- Ceres seq_id 1027154
- Location of start within SEQ ID NO 134: at 78 nt.

35

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 40 - Alignment No. 87
- gi No. 2879811
- Description:
- % Identity: 86.6
- Alignment Length: 112
- Location of Alignment in SEQ ID NO 136: from 1 to
45 112

(B) Polypeptide Sequence

- 50 - Pat. Appln. SEQ ID NO 137
- Ceres seq_id 1027155
- Location of start within SEQ ID NO 134: at 141 nt.

153

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 88
- 5 - gi No. 2879811
- Description:
- % Identity: 86.6
- Alignment Length: 112
- 10 - Location of Alignment in SEQ ID NO 137: from 1 to 91

(Ba) Polypeptide Activities: Similar to ribosomal L30
protein activities.

15

Maximum Length Sequence:

related to:

Clone IDs:

17835

20 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 138
- Ceres seq_id 1028095
- Alternative transcription start site(s) located in SEQ
- ID NO 138:
- 25 -2,2,3,4,5,6,12,14,18,22,26,40,42,44,45,46,47

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 139
- Ceres seq_id 1028096
- 30 - Location of start within SEQ ID NO 138: at 55 nt.
- Location of Signal Peptide Cleavage Site within SEQ
- ID NO 139: at 29 aa.

35 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 89
- gi No. 4336325
- Description:
- 40 - % Identity: 31.7
- Alignment Length: 126
- Location of Alignment in SEQ ID NO 139: from 15
- to 135

45 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 140
- Ceres seq_id 1028097
- Location of start within SEQ ID NO 138: at 214 nt.

50 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

154

(Dp) Related Amino Acid Sequences

- Alignment No. 90
- gi No. 4336325
- Description:
- 5 - % Identity: 31.7
- Alignment Length: 126
- Location of Alignment in SEQ ID NO 140: from 1 to

82

10 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 141
- Ceres seq_id 1028098
- Location of start within SEQ ID NO 138: at 3 nt.
- Location of Signal Peptide Cleavage Site within SEQ
- 15 ID NO 141: at 16 aa.

(Ba) Polypeptide Activities: Similar to human C214 membrane protein activities.

20

Maximum Length Sequence:

related to:

Clone IDs:

17075

25 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 142
- Ceres seq_id 1028608
- Alternative transcription start site(s) located in SEQ
- ID NO 142:
- 30 -4,2,28,31,36,49,59

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 143
- Ceres seq_id 1028609
- 35 - Location of start within SEQ ID NO 142: at 95 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 40 - Alignment No. 91
- gi No. 2735528
- Description:
- % Identity: 33.9
- Alignment Length: 118
- 45 - Location of Alignment in SEQ ID NO 143: from 64
- to 178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 144
- 50 - Ceres seq_id 1028610
- Location of start within SEQ ID NO 142: at 176 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 5 - Alignment No. 92
 - gi No. 2735528
 - Description:
 - % Identity: 33.9
 - Alignment Length: 118
10 - Location of Alignment in SEQ ID NO 144: from 37
to 151

(B) Polypeptide Sequence

- 15 - Pat. Appln. SEQ ID NO 145
 - Ceres seq_id 1028611
 - Location of start within SEQ ID NO 142: at 381 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
ID NO 145: at 41 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

Maximum Length Sequence:

25 related to:

Clone IDs:

1505

(Ac) cDNA Polynucleotide Sequence

- 30 - Pat. Appln. SEQ ID NO 146
 - Ceres seq_id 1030069

(B) Polypeptide Sequence

- 35 - Pat. Appln. SEQ ID NO 147
 - Ceres seq_id 1030070
 - Location of start within SEQ ID NO 146: at 2 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 40 - Alignment No. 93
 - gi No. 4335755
 - Description:
 - % Identity: 63.6
45 - Alignment Length: 143
 - Location of Alignment in SEQ ID NO 147: from 34
to 171

(B) Polypeptide Sequence

- 50 - Pat. Appln. SEQ ID NO 148
 - Ceres seq_id 1030071

156

- Location of start within SEQ ID NO 146: at 50 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

5 (Dp) Related Amino Acid Sequences

- Alignment No. 94

- gi No. 4335755

- Description:

- % Identity: 63.6

10 - Alignment Length: 143

- Location of Alignment in SEQ ID NO 148: from 18
to 155

(B) Polypeptide Sequence

15 - Pat. Appln. SEQ ID NO 149

- Ceres seq_id 1030072

- Location of start within SEQ ID NO 146: at 170 nt.

(C) Nomination and Annotation of Domains within
20 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 95

- gi No. 4335755

- Description:

25 - % Identity: 63.6

- Alignment Length: 143

- Location of Alignment in SEQ ID NO 149: from 1 to
115

30 (Ba) Polypeptide Activities: Similar to hydroxyproline-rich
protein activities.

Maximum Length Sequence:

35 related to:

Clone IDs:

12487

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 150

40 - Ceres seq_id 1032069

- Alternative transcription start site(s) located in SEQ
ID NO 150:

4,17

45 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 151

- Ceres seq_id 1032070

- Location of start within SEQ ID NO 150: at 74 nt.

50 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 157
(Dp) Related Amino Acid Sequences
- Alignment No. 96
- gi No. 3386621
- Description:
5 - % Identity: 97.4
- Alignment Length: 234
- Location of Alignment in SEQ ID NO 151: from 1 to
231
- 10 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 152
- Ceres seq_id 1032071
- Location of start within SEQ ID NO 150: at 122 nt.
- 15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- Alignment No. 97
20 - gi No. 3386621
- Description:
- % Identity: 97.4
- Alignment Length: 234
- Location of Alignment in SEQ ID NO 152: from 1 to
215
- 25 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.
- Maximum Length Sequence:
30 related to:
Clone IDs:
11466
(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 153
35 - Ceres seq_id 1033557
- Alternative transcription start site(s) located in SEQ
ID NO 153:
62,64,65,67,72,73,74,75,166
- 40 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 154
- Ceres seq_id 1033558
- Location of start within SEQ ID NO 153: at 94 nt.
- 45 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
- Ribosomal protein L34
- Location within SEQ ID NO 154: from 105 to 145
aa.
- 50 (Dp) Related Amino Acid Sequences

158
- Alignment No. 98
- gi No. 132909
- Description:
- % Identity: 70
5 - Alignment Length: 30
- Location of Alignment in SEQ ID NO 154: from 116
to 145

(Ba) Polypeptide Activities: Similar to 50S ribosomal
10 protein L34 activities.

Maximum Length Sequence:
related to:
Clone IDs:
15 21589
106951

(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 155
- Ceres seq_id 1034688
20 - Alternative transcription start site(s) located in SEQ
ID NO 155:
2
- Clone 21589 starts at 2 and ends at in cDNA.

25 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 156
- Ceres seq_id 1034689
- Location of start within SEQ ID NO 155: at 2 nt.

30 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- Alignment No. 99
- gi No. 4335755
35 - Description:
- % Identity: 65
- Alignment Length: 143
- Location of Alignment in SEQ ID NO 156: from 33
to 170

40 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 157
- Ceres seq_id 1034690
- Location of start within SEQ ID NO 155: at 47 nt.

45 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- Alignment No. 100
50 - gi No. 4335755
- Description:

159

- % Identity: 65
- Alignment Length: 143
- Location of Alignment in SEQ ID NO 157: from 18

to 155

5

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 158
- Ceres seq_id 1034691
- Location of start within SEQ ID NO 155: at 167 nt.

10

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 101
- gi No. 4335755
- Description:
- % Identity: 65
- Alignment Length: 143
- Location of Alignment in SEQ ID NO 158: from 1 to

15

20 115

(Ba) Polypeptide Activities: Similar to hydroxy proline rich glycoprotein activities.

25

Maximum Length Sequence:

related to:

Clone IDs:

10433

30 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 159
- Ceres seq_id 1035033
- Alternative transcription start site(s) located in SEQ ID NO 159:

35

32

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 160
- Ceres seq_id 1035034
- Location of start within SEQ ID NO 159: at 3 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 160: at 47 aa.

40

(C) Nomination and Annotation of Domains within
45 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 102
- gi No. 3062795
- Description:
- % Identity: 39.8
- Alignment Length: 83

50

160

- Location of Alignment in SEQ ID NO 160: from 24
to 99

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 161
- Ceres seq_id 1035035
- Location of start within SEQ ID NO 159: at 69 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 161: at 25 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 103
- gi No. 3062795
- Description:
- % Identity: 39.8
- Alignment Length: 83
- Location of Alignment in SEQ ID NO 161: from 2 to
77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 162
- Ceres seq_id 1035036
- Location of start within SEQ ID NO 159: at 72 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 162: at 24 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 104
- gi No. 3062795
- Description:
- % Identity: 39.8
- Alignment Length: 83
- Location of Alignment in SEQ ID NO 162: from 1 to
76

- (Ba) Polypeptide Activities: Similar to Pollen coat protein
activities.

Maximum Length Sequence:

related to:

Clone IDs:

10394

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 163
- Ceres seq_id 1035071

161

- Alternative transcription start site(s) located in SEQ ID NO 163:

-2,-1,2,3,18,19,21,24,25,56,66

5 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 164

- Ceres seq_id 1035072

- Location of start within SEQ ID NO 163: at 66 nt.

10 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- KH domain

- Location within SEQ ID NO 164: from 47 to 95 aa.

15 (Dp) Related Amino Acid Sequences

- Alignment No. 105

- gi No. 133940

- Description:

- % Identity: 76

20 - Alignment Length: 246

- Location of Alignment in SEQ ID NO 164: from 1 to

148

(B) Polypeptide Sequence

25 - Pat. Appln. SEQ ID NO 165

- Ceres seq_id 1035073

- Location of start within SEQ ID NO 163: at 195 nt.

30 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- KH domain

- Location within SEQ ID NO 165: from 4 to 52 aa.

(Dp) Related Amino Acid Sequences

35 - Alignment No. 106

- gi No. 133940

- Description:

- % Identity: 76

- Alignment Length: 246

40 - Location of Alignment in SEQ ID NO 165: from 1 to

105

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 166

45 - Ceres seq_id 1035074

- Location of start within SEQ ID NO 163: at 513 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

50 (Dp) Related Amino Acid Sequences

- Alignment No. 107

162

- gi No. 133940
- Description:
- % Identity: 76
- Alignment Length: 246
- Location of Alignment in SEQ ID NO 166: from 1 to

5

97

Maximum Length Sequence:

related to:

10

Clone IDs:

10511

Public Genomic DNA:

gi No: 4539290

Predicted Exons:

15

INTR 5588 ... 5314 OCKHAMG-CDNA

INTR 5517 ... 5314 OCKHAMG-CDNA

gi No: 4914454

Predicted Exons:

20

INTR 38937 ... 38663 OCKHAMG-CDNA

INTR 38866 ... 38663 OCKHAMG-CDNA

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 167

25

- Ceres seq_id 1376587

- Alternative transcription start site(s) located in SEQ

ID NO 167:

8,9,10,12,13,14,15,16,17,30,34,39,41

30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 168

- Ceres seq_id 1376588

- Location of start within SEQ ID NO 167: at 2 nt.

35

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 108

- gi No. 4539292

40

- Description:

- % Identity: 99.4

- Alignment Length: 177

- Location of Alignment in SEQ ID NO 168: from 26

to 202

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 169

- Ceres seq_id 1376589

- Location of start within SEQ ID NO 167: at 77 nt.

50

163

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

5 - Alignment No. 109
 - gi No. 4539292
 - Description:
 - % Identity: 99.4
 - Alignment Length: 177
10 - Location of Alignment in SEQ ID NO 169: from 1 to
 177

(B) Polypeptide Sequence

 - Pat. Appln. SEQ ID NO 170
 - Ceres seq_id 1376590
15 - Location of start within SEQ ID NO 167: at 212 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

20 - Alignment No. 110
 - gi No. 4539292
 - Description:
 - % Identity: 99.4
 - Alignment Length: 177
25 - Location of Alignment in SEQ ID NO 170: from 1 to
 132

(Ba) Polypeptide Activities: Similar 40S ribosomal protein
activities.

30 Maximum Length Sequence:
 related to:

Clone IDs:

112110

35 Public Genomic DNA:

gi No: 4263774

Predicted Exons:

40	INIT	1816	...	1814	OCKHAMG-CDS
	INTR	1290	...	1112	OCKHAMG-CDS
	TERM	959	...	803	OCKHAMG-CDS

gi No: 4510360

Predicted Exons:

45	INIT	114707...	114705	OCKHAMG-CDS
	INTR	114181...	114003	OCKHAMG-CDS
	TERM	113850...	113694	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

 - Pat. Appln. SEQ ID NO 171
 - Ceres seq_id 1378581
 - Alternative transcription start site(s) located in SEQ
50 ID NO 171:
 -35,-4,-3,18,20

164

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 172
- Ceres seq_id 1378582
- 5 - Location of start within SEQ ID NO 171: at 112 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 172: at 17 aa.

(C) Nomination and Annotation of Domains within

10 Predicted Polypeptide(s)

- DnaJ domain
- Location within SEQ ID NO 172: from 57 to 101 aa.

(Dp) Related Amino Acid Sequences

- 15 - Alignment No. 111
- gi No. 4263775
- Description:
- % Identity: 100
- Alignment Length: 112
- 20 - Location of Alignment in SEQ ID NO 172: from 1 to 112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 173
- 25 - Ceres seq_id 1378583
- Location of start within SEQ ID NO 171: at 256 nt.

(C) Nomination and Annotation of Domains within

30 Predicted Polypeptide(s)

- DnaJ domain
- Location within SEQ ID NO 173: from 9 to 53 aa.

(Dp) Related Amino Acid Sequences

- 35 - Alignment No. 112
- gi No. 4263775
- Description:
- % Identity: 100
- Alignment Length: 112
- 40 - Location of Alignment in SEQ ID NO 173: from 1 to 64

Maximum Length Sequence:

related to:

Clone IDs:

45 13599

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 174
- Ceres seq_id 1383462
- Alternative transcription start site(s) located in SEQ ID NO 174:
- 50 -2,2,3,4,5,6,8,14,18,24

165

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 175
- Ceres seq_id 1383463
- 5 - Location of start within SEQ ID NO 174: at 3 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Plant lipid transfer protein family
- 10 - Location within SEQ ID NO 175: from 46 to 119 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 113
- gi No. 3128176
- 15 - Description:
- % Identity: 37
- Alignment Length: 194
- Location of Alignment in SEQ ID NO 175: from 23
- to 197

20

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 176
- Ceres seq_id 1383464
- Location of start within SEQ ID NO 174: at 42 nt.
- 25 - Location of Signal Peptide Cleavage Site within SEQ
- ID NO 176: at 24 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 30 - Plant lipid transfer protein family
- Location within SEQ ID NO 176: from 33 to 106 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 114
- 35 - gi No. 3128176
- Description:
- % Identity: 37
- Alignment Length: 194
- Location of Alignment in SEQ ID NO 176: from 10
- 40 to 184

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 177
- Ceres seq_id 1383465
- 45 - Location of start within SEQ ID NO 174: at 90 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Plant lipid transfer protein family
- 50 - Location within SEQ ID NO 177: from 17 to 90 aa.

- 166
- (Dp) Related Amino Acid Sequences
- Alignment No. 115
 - gi No. 3128176
 - Description:
 - 5 - % Identity: 37
 - Alignment Length: 194
 - Location of Alignment in SEQ ID NO 177: from 1 to 168
- 10 Maximum Length Sequence:
 related to:
 Clone IDs:
 156375
- (Ac) cDNA Polynucleotide Sequence
- 15 - Pat. Appln. SEQ ID NO 178
- Ceres seq_id 1386215
 - Alternative transcription start site(s) located in SEQ ID NO 178:
 -38,12,17,18,19,20,26
- 20 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 179
 - Ceres seq_id 1386216
 - Location of start within SEQ ID NO 178: at 2 nt.
- 25 (C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)
- Photosystem I psaG / psaK
 - Location within SEQ ID NO 179: from 77 to 138 aa.
- 30 (Dp) Related Amino Acid Sequences
- Alignment No. 116
 - gi No. 3885511
 - Description:

35 - % Identity: 79.3

 - Alignment Length: 112
 - Location of Alignment in SEQ ID NO 179: from 28
to 138
- 40 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 180
 - Ceres seq_id 1386217
 - Location of start within SEQ ID NO 178: at 83 nt.
- 45 (C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)
- Photosystem I psaG / psaK
 - Location within SEQ ID NO 180: from 50 to 111 aa.
- 50 (Dp) Related Amino Acid Sequences
- Alignment No. 117

167

- gi No. 3885511
- Description:
- % Identity: 79.3
- Alignment Length: 112
- Location of Alignment in SEQ ID NO 180: from 1 to

5
111

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 181
- Ceres seq_id 1386218
- Location of start within SEQ ID NO 178: at 95 nt.

10

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Photosystem I psaG / psaK
- Location within SEQ ID NO 181: from 46 to 107 aa.

15

(Dp) Related Amino Acid Sequences

- Alignment No. 118
- gi No. 3885511
- Description:
- % Identity: 79.3
- Alignment Length: 112
- Location of Alignment in SEQ ID NO 181: from 1 to

20

25 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 182
- Ceres seq_id 2025156
- Location of start within SEQ ID NO 178: at 502 nt.

30

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

35

Maximum Length Sequence:

related to:

Clone IDs:

21233

40

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 183
- Ceres seq_id 1388499
- Alternative transcription start site(s) located in SEQ
ID NO 183:

45

2,5,6,10,16,30,89,346,349

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 184
- Ceres seq_id 1388500
- Location of start within SEQ ID NO 183: at 62 nt.

50

168

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

5 - Alignment No. 119
 - gi No. 2829899
 - Description:
 - % Identity: 49.3
 - Alignment Length: 150
10 - Location of Alignment in SEQ ID NO 184: from 2 to
 150

(B) Polypeptide Sequence

 - Pat. Appln. SEQ ID NO 185
 - Ceres seq_id 1388501
15 - Location of start within SEQ ID NO 183: at 122 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

20 - Alignment No. 120
 - gi No. 2829899
 - Description:
 - % Identity: 49.3
 - Alignment Length: 150
25 - Location of Alignment in SEQ ID NO 185: from 1 to
 130

(B) Polypeptide Sequence

 - Pat. Appln. SEQ ID NO 186
30 - Ceres seq_id 1388502
 - Location of start within SEQ ID NO 183: at 266 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

35 - Alignment No. 121
 - gi No. 2829899
 - Description:
 - % Identity: 49.3
40 - Alignment Length: 150
 - Location of Alignment in SEQ ID NO 186: from 1 to
82

45 (Ba) Polypeptide Activities: Similar to major latex protein
 activities.

Maximum Length Sequence:
50 related to:
Clone IDs:

169

21304

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 187
- Ceres seq_id 1388519

5

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 188
- Ceres seq_id 1388520

10

- Location of start within SEQ ID NO 187: at 1 nt.

- Location of Signal Peptide Cleavage Site within SEQ ID NO 188: at 38 aa.

(C) Nomination and Annotation of Domains within

15

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 122

- gi No. 4584110

- Description:

20

- % Identity: 48.5

- Alignment Length: 163

- Location of Alignment in SEQ ID NO 188: from 20 to 182

25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 189

- Ceres seq_id 1388521

- Location of start within SEQ ID NO 187: at 58 nt.

- Location of Signal Peptide Cleavage Site within SEQ

30

ID NO 189: at 19 aa.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 123

- gi No. 4584110

- Description:

- % Identity: 48.5

- Alignment Length: 163

40

- Location of Alignment in SEQ ID NO 189: from 1 to

163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 190

45

- Ceres seq_id 1388522

- Location of start within SEQ ID NO 187: at 73 nt.

- Location of Signal Peptide Cleavage Site within SEQ ID NO 190: at 14 aa.

50

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

170

(Dp) Related Amino Acid Sequences

- Alignment No. 124

- gi No. 4584110

- Description:

5 - % Identity: 48.5

- Alignment Length: 163

- Location of Alignment in SEQ ID NO 190: from 1 to

158

10 (Ba) Polypeptide Activities: Similar to pollen specific protein activities.

Maximum Length Sequence:

related to:

15 Clone IDs:

2153

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 191

- Ceres seq_id 1388563

20 - Alternative transcription start site(s) located in SEQ ID NO 191:

-3,-2,-1,13,15,146

(B) Polypeptide Sequence

25 - Pat. Appln. SEQ ID NO 192

- Ceres seq_id 1388564

- Location of start within SEQ ID NO 191: at 2 nt.

(C) Nomination and Annotation of Domains within

30 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 193

35 - Ceres seq_id 1388565

- Location of start within SEQ ID NO 191: at 306 nt.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

40 (Dp) Related Amino Acid Sequences

- Alignment No. 125

- gi No. 3927834

- Description:

45 - % Identity: 31.5

- Alignment Length: 108

- Location of Alignment in SEQ ID NO 193: from 1 to

43

(B) Polypeptide Sequence

50 - Pat. Appln. SEQ ID NO 194

- Ceres seq_id 1388566

171

- Location of start within SEQ ID NO 191: at 455 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 194: at 36 aa.

5 (Ba) Polypeptide Activities: Similar to hydroxproline-rich
glycoprotein activities.

Maximum Length Sequence:

10 related to:

Clone IDs:

22488

Public Genomic DNA:

gi No: 5708384

15 Predicted Exons:

INIT 82228 ... 82063 OCKHAMG-CDS

TERM 81730 ... 81381 OCKHAMG-CDS

gi No: 5732090

Predicted Exons:

20 INIT 21301 ... 21136 OCKHAMG-CDS

TERM 20803 ... 20454 OCKHAMG-CDS

gi No: 5870169

Predicted Exons:

25 INIT 89258 ... 89423 OCKHAMG-CDS

TERM 89756 ... 90105 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 195

- Ceres seq_id 1388793

- Alternative transcription start site(s) located in SEQ

30 ID NO 195:

7,14,15,20,24,30,33,42,44,58,63,64,66,76,94,97,98,99,101,102
103,104,105,106,108,109,110,115,116,117

35 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 196

- Ceres seq_id 1388794

- Location of start within SEQ ID NO 195: at 154 nt.

- Location of Signal Peptide Cleavage Site within SEQ

40 ID NO 196: at 19 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

45 - Alignment No. 126

- gi No. 4584110

- Description:

- % Identity: 48.5

- Alignment Length: 163

50 - Location of Alignment in SEQ ID NO 196: from 1 to

163

172

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 197
- Ceres seq_id 1388795
- 5 - Location of start within SEQ ID NO 195: at 169 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 197: at 14 aa.

(C) Nomination and Annotation of Domains within

10 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 127
- gi No. 4584110
- Description:
- 15 - % Identity: 48.5
- Alignment Length: 163
- Location of Alignment in SEQ ID NO 197: from 1 to 158

20 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 198
- Ceres seq_id 1388796
- Location of start within SEQ ID NO 195: at 205 nt.

25 (C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 128
- gi No. 4584110
- 30 - Description:
- % Identity: 48.5
- Alignment Length: 163
- Location of Alignment in SEQ ID NO 198: from 1 to 146

35 (Ba) Polypeptide Activities: Similar to pollen specific protein activities.

Maximum Length Sequence:

40 related to:

Clone IDs:

26569

Public Genomic DNA:

gi No: 6143856

45 Predicted Exons:

INTR 78628 ... 78255 OCKHAMG-CDNA

INTR 78160 ... 78004 OCKHAMG-CDNA

INTR 78624 ... 78255 OCKHAMG-CDNA

50 INTR 78160 ... 78004 OCKHAMG-CDNA

173

	INTR	78624 ...	78255	OCKHAMG-CDNA
	INTR	78160 ...	78006	OCKHAMG-CDNA
	INTR	78624 ...	78283	OCKHAMG-CDNA

5 gi No: 6223633
 Predicted Exons:

	INTR	78629 ...	78256	OCKHAMG-CDNA
	INTR	78161 ...	78005	OCKHAMG-CDNA

10 INTR 78625 ... 78256 OCKHAMG-CDNA
 INTR 78161 ... 78005 OCKHAMG-CDNA

15 INTR 78625 ... 78256 OCKHAMG-CDNA
 INTR 78161 ... 78007 OCKHAMG-CDNA

20 INTR 78625 ... 78256 OCKHAMG-CDNA
 INTR 78161 ... 78007 OCKHAMG-CDNA

20 INIT 78587 ... 78256 OCKHAMG-CDS
 TERM 78161 ... 78152 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 199
 - Ceres seq_id 1392041
 - Alternative transcription start site(s) located in SEQ
 ID NO 199:
 25 3,4,5,6,7,12

(B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 200
 - Ceres seq_id 1392042
 30 - Location of start within SEQ ID NO 199: at 45 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
 ID NO 200: at 19 aa.

(C) Nomination and Annotation of Domains within
 35 Predicted Polypeptide(s)
 - Plant lipid transfer protein family
 - Location within SEQ ID NO 200: from 23 to 112 aa.

(Dp) Related Amino Acid Sequences
 40 - Alignment No. 129
 - gi No. 2497753
 - Description:
 - % Identity: 47
 - Alignment Length: 117
 45 - Location of Alignment in SEQ ID NO 200: from 4 to
 113

Maximum Length Sequence:
 related to:
 50 Clone IDs:
 28475

174

Public Genomic DNA:

gi No: 5731404

Predicted Exons:

	INTR	70440	...	70346	OCKHAMG-CDNA
5	INTR	70076	...	69865	OCKHAMG-CDNA
	INTR	69508	...	69434	OCKHAMG-CDNA
	INTR	69358	...	69284	OCKHAMG-CDNA
	INTR	69195	...	69115	OCKHAMG-CDNA
	INTR	69033	...	68959	OCKHAMG-CDNA
10	INTR	68868	...	68695	OCKHAMG-CDNA
	INTR	68581	...	68344	OCKHAMG-CDNA

	INIT	70056	...	69865	OCKHAMG-CDS
	INTR	69508	...	69434	OCKHAMG-CDS
15	INTR	69358	...	69284	OCKHAMG-CDS
	INTR	69195	...	69115	OCKHAMG-CDS
	INTR	69033	...	68959	OCKHAMG-CDS
	INTR	68868	...	68695	OCKHAMG-CDS
	TERM	68581	...	68546	OCKHAMG-CDS

20 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 201

- Ceres seq_id 1393342

- Alternative transcription start site(s) located in SEQ ID NO 201:

25 16,48

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 202

- Ceres seq_id 1393343

30 - Location of start within SEQ ID NO 201: at 118 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

35 - Alignment No. 130

- gi No. 3386621

- Description:

- % Identity: 83

- Alignment Length: 224

40 - Location of Alignment in SEQ ID NO 202: from 2 to 225

(Ba) Polypeptide Activities: Arabidopsis specific gene, dicot specific gene, plant specific gene.

45

Maximum Length Sequence:

related to:

Clone IDs:

29453

50 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 203

175

- Ceres seq_id 1393556
- Alternative transcription start site(s) located in SEQ
ID NO 203:

7,11,14,23,37,41,42,57,61

5

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 204
- Ceres seq_id 1393557
- Location of start within SEQ ID NO 203: at 3 nt.

10

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 131
- gi No. 1082054
- Description:
- % Identity: 36.1
- Alignment Length: 61
- Location of Alignment in SEQ ID NO 204: from 23

15

20 to 82

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 205
- Ceres seq_id 1393558
- Location of start within SEQ ID NO 203: at 69 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 205: at 41 aa.

25

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 132
- gi No. 1082054
- Description:
- % Identity: 36.1
- Alignment Length: 61
- Location of Alignment in SEQ ID NO 205: from 1 to

35

60

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 206
- Ceres seq_id 1393559
- Location of start within SEQ ID NO 203: at 72 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 206: at 40 aa.

40

45

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 133
- gi No. 1082054

50

176

- Description:
- % Identity: 36.1
- Alignment Length: 61
- Location of Alignment in SEQ ID NO 206: from 1 to

5 59

(Ba) Polypeptide Activities: Similar to transmembrane copper transporter protein activities.

10

Maximum Length Sequence:

related to:

Clone IDs:

42384

15 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 207

- Ceres seq_id 1396782

- Alternative transcription start site(s) located in SEQ ID NO 207:

20 -1,29

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 208

- Ceres seq_id 1396783

25 - Location of start within SEQ ID NO 207: at 3 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

30 - Alignment No. 134

- gi No. 4512613

- Description:

- % Identity: 99.2

- Alignment Length: 122

35 - Location of Alignment in SEQ ID NO 208: from 11 to 132

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 209

40 - Ceres seq_id 1396784

- Location of start within SEQ ID NO 207: at 33 nt.

- Location of Signal Peptide Cleavage Site within SEQ ID NO 209: at 19 aa.

45 (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 135

- gi No. 4512613

50 - Description:

- % Identity: 99.2

177

- Alignment Length: 122
- Location of Alignment in SEQ ID NO 209: from 1 to 122

5 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 210
- Ceres seq_id 1396785
- Location of start within SEQ ID NO 207: at 45 nt.

10 (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 136
- gi No. 4512613
- 15 - Description:
- % Identity: 99.2
- Alignment Length: 122
- Location of Alignment in SEQ ID NO 210: from 1 to 118

20

(Ba) Polypeptide Activities: Similar to intergenic region of cyt2-MDH1 of yeast activities.

Maximum Length Sequence:

25 related to:

Clone IDs:

42402

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 211
- 30 - Ceres seq_id 1396802
- Alternative transcription start site(s) located in SEQ ID NO 211:
-145,-56

35 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 212
- Ceres seq_id 1396803
- Location of start within SEQ ID NO 211: at 1 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 212: at 19 aa.

45 (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 45 - Alignment No. 137
- gi No. 2463339
- Description:
- % Identity: 38.6
- Alignment Length: 70
- 50 - Location of Alignment in SEQ ID NO 212: from 136 to 205

178

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 213
- Ceres seq_id 1396804
- 5 - Location of start within SEQ ID NO 211: at 136 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 10 - Alignment No. 138
- gi No. 2463339
- Description:
- % Identity: 38.6
- Alignment Length: 70
- 15 - Location of Alignment in SEQ ID NO 213: from 91
to 160

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 214
- 20 - Ceres seq_id 1396805
- Location of start within SEQ ID NO 211: at 172 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 25 - Alignment No. 139
- gi No. 2463339
- Description:
- % Identity: 38.6
- 30 - Alignment Length: 70
- Location of Alignment in SEQ ID NO 214: from 79
to 148

- (Ba) Polypeptide Activities: Similar to rbcX protein
35 activities.

Maximum Length Sequence:

related to:

Clone IDs:

- 40 5105

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 215
- Ceres seq_id 1397130
- Alternative transcription start site(s) located in SEQ
45 ID NO 215:
-1

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 216
- 50 - Ceres seq_id 1397131
- Location of start within SEQ ID NO 215: at 1 nt.

179

- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- 5 - Alignment No. 140
 - gi No. 2827551
 - Description:
 - % Identity: 63.1
 - Alignment Length: 179
10 - Location of Alignment in SEQ ID NO 216: from 2 to
 176
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 217
15 - Ceres seq_id 1397132
 - Location of start within SEQ ID NO 215: at 52 nt.
- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- 20 - Alignment No. 141
 - gi No. 2827551
 - Description:
 - % Identity: 63.1
25 - Alignment Length: 179
 - Location of Alignment in SEQ ID NO 217: from 1 to
 159
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 218
30 - Ceres seq_id 1397133
 - Location of start within SEQ ID NO 215: at 211 nt.
- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- 35 - Alignment No. 142
 - gi No. 2827551
 - Description:
40 - % Identity: 63.1
 - Alignment Length: 179
 - Location of Alignment in SEQ ID NO 218: from 1 to
 106
- 45 (Ba) Polypeptide Activities: Similar to meth CpG binding
 protein activities.
- Maximum Length Sequence:
50 related to:
 Clone IDs:

180

92204

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 219
- Ceres seq_id 1398004
- 5 - Alternative transcription start site(s) located in SEQ ID NO 219:
2,3,5,8,28

(B) Polypeptide Sequence

- 10 - Pat. Appln. SEQ ID NO 220
- Ceres seq_id 1398005
- Location of start within SEQ ID NO 219: at 68 nt.

15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 143
- gi No. 4454037
- Description:
- 20 - % Identity: 99.3
- Alignment Length: 151
- Location of Alignment in SEQ ID NO 220: from 1 to 151

25 (Ba) Polypeptide Activities: Similar to major latex protein
activities.

Maximum Length Sequence:

related to:

Clone IDs:

30 98584

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 221
- Ceres seq_id 1399370

35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 222
- Ceres seq_id 1399371
- 40 - Location of start within SEQ ID NO 221: at 3 nt.

45 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 144
- 45 - gi No. 4886285
- Description:
- % Identity: 28.8
- Alignment Length: 59
- Location of Alignment in SEQ ID NO 222: from 25
- 50 to 83

181

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 223
- Ceres seq_id 1399372
- Location of start within SEQ ID NO 221: at 45 nt.

5

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 145
- 10 - gi No. 4886285
- Description:
- % Identity: 28.8
- Alignment Length: 59
- 15 - Location of Alignment in SEQ ID NO 223: from 11
to 69

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 224
- Ceres seq_id 1399373
- 20 - Location of start within SEQ ID NO 221: at 60 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 224: at 25 aa.

(C) Nomination and Annotation of Domains within
25 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 140
- gi No. 4886285
- Description:
- 30 - % Identity: 28.8
- Alignment Length: 59
- Location of Alignment in SEQ ID NO 224: from 6 to
64

- 35 (Ba) Polypeptide Activities: Similar to outer envelope
membrane protein in chloroplast in pea activities.

Maximum Length Sequence:

40 related to:

Clone IDs:

107400

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 225
- 45 - Ceres seq_id 1425147
- Alternative transcription start site(s) located in SEQ
ID NO 225:
20,31,49,58,80

50 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 226

182

- Ceres seq_id 1425148
- Location of start within SEQ ID NO 225: at 85 nt.

5 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 147
- gi No. 3510256
- Description:
- 10 - % Identity: 37.8
- Alignment Length: 158
- Location of Alignment in SEQ ID NO 226: from 1 to
155

15 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 227
- Ceres seq_id 1425149
- Location of start within SEQ ID NO 225: at 241 nt.

20 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 148
- gi No. 3510256
- 25 - Description:
- % Identity: 37.8
- Alignment Length: 158
- Location of Alignment in SEQ ID NO 227: from 1 to
103

30 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.

Maximum Length Sequence:

35 related to:

Clone IDs:

11073

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 228
- 40 - Ceres seq_id 1441102
- Alternative transcription start site(s) located in SEQ
ID NO 228:
2,3,4,5,8,10,16,22,51,69,388

45 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 229
- Ceres seq_id 1441103
- Location of start within SEQ ID NO 228: at 1 nt.

50 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 183
- (Dp) Related Amino Acid Sequences
- Alignment No. 149
 - gi No. 4337175
 - Description:
 - % Identity: 100
 - Alignment Length: 179
 - Location of Alignment in SEQ ID NO 229: from 19 to 197
- 10 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 230
 - Ceres seq_id 1441104
 - Location of start within SEQ ID NO 228: at 55 nt.
- 15 (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (Dp) Related Amino Acid Sequences
- Alignment No. 150
 - gi No. 4337175
 - Description:
 - % Identity: 100
 - Alignment Length: 179
 - Location of Alignment in SEQ ID NO 230: from 1 to 179
- 25 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 231
 - Ceres seq_id 1441105
 - Location of start within SEQ ID NO 228: at 94 nt.
- 30 (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)
- (Dp) Related Amino Acid Sequences
- Alignment No. 151
 - gi No. 4337175
 - Description:
 - % Identity: 100
 - Alignment Length: 179
 - Location of Alignment in SEQ ID NO 231: from 1 to 166
- 40 (Ba) Polypeptide Activities: Arabidopsis specific gene, dicot specific gene, plant specific gene.
- 45 Maximum Length Sequence:
related to:
Clone IDs:
267227
- (Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 232
 - Ceres seq_id 1447480
- 50

184

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 233
5 - Ceres seq_id 1447481
- Location of start within SEQ ID NO 232: at 52 nt.
- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
10 (Dp) Related Amino Acid Sequences
- Alignment No. 152
- gi No. 3510256
- Description:
- % Identity: 54
15 - Alignment Length: 50
- Location of Alignment in SEQ ID NO 233: from 77
to 126
- (B) Polypeptide Sequence
20 - Pat. Appln. SEQ ID NO 234
- Ceres seq_id 1447482
- Location of start within SEQ ID NO 232: at 208 nt.
- (C) Nomination and Annotation of Domains within
25 Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- Alignment No. 153
- gi No. 3510256
- Description:
30 - % Identity: 54
- Alignment Length: 50
- Location of Alignment in SEQ ID NO 234: from 25
to 74
- 35 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.
- Maximum Length Sequence:
related to:
40 Clone IDs:
268712
- (Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 235
45 - Ceres seq_id 1447577
- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 236
- Ceres seq_id 1447578
50 - Location of start within SEQ ID NO 235: at 2 nt.

185

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 154
- 5 - gi No. 5080769
- Description:
- % Identity: 100
- Alignment Length: 17
- 10 to 32 - Location of Alignment in SEQ ID NO 236: from 16

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 237
- Ceres seq_id 1447579
- 15 - Location of start within SEQ ID NO 235: at 165 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 20 - Alignment No. 155
- gi No. 5080769
- Description:
- % Identity: 91.5
- Alignment Length: 153
- 25 - Location of Alignment in SEQ ID NO 237: from 1 to
- 115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 238
- 30 - Ceres seq_id 1447580
- Location of start within SEQ ID NO 235: at 298 nt.

(Ba) Polypeptide Activities: Similar to
hydroxyproline-rich glycoprotein activities.

35

Maximum Length Sequence:

related to:

Clone IDs:

- 40 94821

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 239
- Ceres seq_id 1447922
- Alternative transcription start site(s) located in SEQ
- 45 ID NO 239:
- 12,16

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 240
- 50 - Ceres seq_id 1447923
- Location of start within SEQ ID NO 239: at 81 nt.

186

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 5 - Alignment No. 156
- gi No. 3510256
- Description:
- % Identity: 37.8
- Alignment Length: 158
- 10 - Location of Alignment in SEQ ID NO 240: from 1 to
- 155

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 241
- 15 - Ceres seq_id 1447924
- Location of start within SEQ ID NO 239: at 237 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 20 - Alignment No. 157
- gi No. 3510256
- Description:
- % Identity: 37.8
- 25 - Alignment Length: 158
- Location of Alignment in SEQ ID NO 241: from 1 to
- 103

(Ba) Polypeptide Activities: Arabidopsis specific gene,
30 dicot specific gene, plant specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

35 20539

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 242
- Ceres seq_id 1448012
- Alternative transcription start site(s) located in SEQ
- 40 ID NO 242:
- 30,-6

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 243
- 45 - Ceres seq_id 1448013
- Location of start within SEQ ID NO 242: at 79 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 50 - Ribosomal protein S16
- Location within SEQ ID NO 243: from 9 to 70 aa.

187

(Dp) Related Amino Acid Sequences

- Alignment No. 158
- gi No. 3096931
- Description:
- % Identity: 57.5
- Alignment Length: 113
- Location of Alignment in SEQ ID NO 243: from 1 to

112

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 244
- Ceres seq_id 1448014
- Location of start within SEQ ID NO 242: at 139 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S16
- Location within SEQ ID NO 244: from 1 to 50 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 159
- gi No. 3096931
- Description:
- % Identity: 57.5
- Alignment Length: 113
- Location of Alignment in SEQ ID NO 244: from 1 to

92

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 245
- Ceres seq_id 1448015
- Location of start within SEQ ID NO 242: at 232 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 160
- gi No. 3096931
- Description:
- % Identity: 57.5
- Alignment Length: 113
- Location of Alignment in SEQ ID NO 245: from 1 to

61

Maximum Length Sequence:

related to:

Clone IDs:

34091

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 246

188

- Ceres seq_id 1448135
- Alternative transcription start site(s) located in SEQ
ID NO 246:
-1

5

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 247
- Ceres seq_id 1448136
- Location of start within SEQ ID NO 246: at 3 nt.

10

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 248
- Ceres seq_id 1448137
- Location of start within SEQ ID NO 246: at 68 nt.

20

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S14p/S29e
- Location within SEQ ID NO 248: from 3 to 54 aa.

25

(Dp) Related Amino Acid Sequences

- Alignment No. 161
- gi No. 4506717
- Description:
- % Identity: 72.2
- Alignment Length: 54
- Location of Alignment in SEQ ID NO 248: from 1 to

54

(B) Polypeptide Sequence

35

- Pat. Appln. SEQ ID NO 249
- Ceres seq_id 1448138
- Location of start within SEQ ID NO 246: at 85 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

40

(Dp) Related Amino Acid Sequences

Maximum Length Sequence:

related to:

45

Clone IDs:

39285

Public Genomic DNA:

gi No: 4406776

Predicted Exons:

50

SINGLE 61584 ... 61895 GENBANK

- 189
SINGLE 61584 ... 61895 OCKHAMG-CDS
- (Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 250
 - Ceres seq_id 1448185
- 5 - Alternative transcription start site(s) located in SEQ ID NO 250:
-36,-18,-17,16,19
- (B) Polypeptide Sequence
- 10 - Pat. Appln. SEQ ID NO 251
- Ceres seq_id 1448186
 - Location of start within SEQ ID NO 250: at 41 nt.
- (C) Nomination and Annotation of Domains within
- 15 Predicted Polypeptide(s)
- (Dp) Related Amino Acid Sequences
- Alignment No. 162
 - gi No. 4406787
 - Description:
- 20 - % Identity: 100
- Alignment Length: 103
 - Location of Alignment in SEQ ID NO 251: from 1 to 103
- (B) Polypeptide Sequence
- 25 - Pat. Appln. SEQ ID NO 252
- Ceres seq_id 1448187
 - Location of start within SEQ ID NO 250: at 68 nt.
- (C) Nomination and Annotation of Domains within
- 30 Predicted Polypeptide(s)
- (Dp) Related Amino Acid Sequences
- Alignment No. 163
 - gi No. 4406787
 - Description:
- 35 - % Identity: 100
- Alignment Length: 103
 - Location of Alignment in SEQ ID NO 252: from 1 to 94
- (B) Polypeptide Sequence
- 40 - Pat. Appln. SEQ ID NO 253
- Ceres seq_id 1448188
 - Location of start within SEQ ID NO 250: at 89 nt.
- (C) Nomination and Annotation of Domains within
- 45 Predicted Polypeptide(s)
- (Dp) Related Amino Acid Sequences
- Alignment No. 164
 - gi No. 4406787
 - Description:
- 50

190

- % Identity: 100
- Alignment Length: 103
- Location of Alignment in SEQ ID NO 253: from 1 to 87

5 (Ba) Polypeptide Activities: Similar to NADH dehydrogenase protein activities

10 Maximum Length Sequence:

related to:

Clone IDs:

99119

(Ac) cDNA Polynucleotide Sequence

- 15
- Pat. Appln. SEQ ID NO 254
 - Ceres seq_id 1450875

(B) Polypeptide Sequence

- 20
- Pat. Appln. SEQ ID NO 255
 - Ceres seq_id 1450876
 - Location of start within SEQ ID NO 254: at 2 nt.
 - Location of Signal Peptide Cleavage Site within SEQ ID NO 255: at 26 aa.

25

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- ATPases associated with various cellular activities (AAA)

- 30
- Location within SEQ ID NO 255: from 391 to 598 aa.

(Dp) Related Amino Acid Sequences

- 35
- Alignment No. 165
 - gi No. 4309734
 - Description:
 - % Identity: 86
 - Alignment Length: 633
 - Location of Alignment in SEQ ID NO 255: from 9 to

40 634

(B) Polypeptide Sequence

- 45
- Pat. Appln. SEQ ID NO 256
 - Ceres seq_id 1450877
 - Location of start within SEQ ID NO 254: at 14 nt.
 - Location of Signal Peptide Cleavage Site within SEQ ID NO 256: at 22 aa.

50 (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

191

- ATPases associated with various cellular activities (AAA)
- Location within SEQ ID NO 256: from 387 to 594
aa.

5

(Dp) Related Amino Acid Sequences

- Alignment No. 166
- gi No. 4309734
- Description:
10 - % Identity: 86
- Alignment Length: 633
- Location of Alignment in SEQ ID NO 256: from 5 to
630

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 257
- Ceres seq_id 1450878
- Location of start within SEQ ID NO 254: at 68 nt.

20

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- ATPases associated with various cellular activities (AAA)
- Location within SEQ ID NO 257: from 369 to 576
25 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 167
- gi No. 4309734
30 - Description:
- % Identity: 86
- Alignment Length: 633
- Location of Alignment in SEQ ID NO 257: from 1 to
612

35

Maximum Length Sequence:

related to:

Clone IDs:

269321

40

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 258
- Ceres seq_id 1459191

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 259
- Ceres seq_id 1459192
- Location of start within SEQ ID NO 258: at 1 nt.

50

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- 192
- (Dp) Related Amino Acid Sequences
- Alignment No. 168
 - gi No. 4490728
 - Description:
 - 5 - % Identity: 100
 - Alignment Length: 17
 - Location of Alignment in SEQ ID NO 259: from 21
 - to 37
- 10 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 260
 - Ceres seq_id 1459193
 - Location of start within SEQ ID NO 258: at 3 nt.
- 15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
- (Dp) Related Amino Acid Sequences
- Alignment No. 169
 - gi No. 4490728
 - 20 - Description:
 - % Identity: 85.9
 - Alignment Length: 85
 - Location of Alignment in SEQ ID NO 260: from 37
 - to 110
- 25 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.
- Maximum Length Sequence:
- 30 related to:
- Clone IDs:
- 8446
- (Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 261
 - 35 - Ceres seq_id 1461848
 - Alternative transcription start site(s) located in SEQ
 - ID NO 261:
 - 3,6,7,11,31,32,34,62,63,69,70,71,97
- 40 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 262
 - Ceres seq_id 1461849
 - Location of start within SEQ ID NO 261: at 113 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
 - 45 ID NO 262: at 36 aa.
- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
- MAPEG family
 - 50 - Location within SEQ ID NO 262: from 59 to 136 aa.

193

(Dp) Related Amino Acid Sequences

- Alignment No. 170
- gi No. 4758714
- Description:
- % Identity: 41.9
- Alignment Length: 131
- Location of Alignment in SEQ ID NO 262: from 8 to

136

10 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 263
- Ceres seq_id 1461850
- Location of start within SEQ ID NO 261: at 197 nt.

15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- MAPEG family
- Location within SEQ ID NO 263: from 31 to 108 aa.

20 (Dp) Related Amino Acid Sequences

- Alignment No. 171
- gi No. 4758714
- Description:
- % Identity: 41.9
- Alignment Length: 131
- Location of Alignment in SEQ ID NO 263: from 1 to

108

30 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 264
 - Ceres seq_id 1461851
 - Location of start within SEQ ID NO 261: at 329 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
- ID NO 264: at 22 aa.

35

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- MAPEG family
- Location within SEQ ID NO 264: from 1 to 64 aa.

40

40 (Dp) Related Amino Acid Sequences

- Alignment No. 172
- gi No. 4758714
- Description:
- % Identity: 41.9
- Alignment Length: 131
- Location of Alignment in SEQ ID NO 264: from 1 to

64

50 Maximum Length Sequence:
related to:

194

Clone IDs:

25093

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 265
- 5 - Ceres seq_id 1472772
- Alternative transcription start site(s) located in SEQ ID NO 265:
 - 1,3

10 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 266
- Ceres seq_id 1472773
- Location of start within SEQ ID NO 265: at 3 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 266: at 32 aa.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Plant lipid transfer protein family
- 20 - Location within SEQ ID NO 266: from 45 to 108 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 173
- gi No. 3062791
- 25 - Description:
- % Identity: 72.2
- Alignment Length: 90
- Location of Alignment in SEQ ID NO 266: from 21 to 110

30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 267
- Ceres seq_id 1472774
- Location of start within SEQ ID NO 265: at 27 nt.
- 35 - Location of Signal Peptide Cleavage Site within SEQ ID NO 267: at 24 aa.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Plant lipid transfer protein family
- 40 - Location within SEQ ID NO 267: from 37 to 100 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 174
- 45 - gi No. 3062791
- Description:
- % Identity: 72.2
- Alignment Length: 90
- Location of Alignment in SEQ ID NO 267: from 13

50 to 102

195

Maximum Length Sequence:

related to:

Clone IDs:

42300

5 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 268

- Ceres seq_id 1533352

- Alternative transcription start site(s) located in SEQ

ID NO 268:

10 17

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 269

- Ceres seq_id 1533353

15 - Location of start within SEQ ID NO 268: at 1 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- haloacid dehalogenase-like hydrolase

20 - Location within SEQ ID NO 269: from 82 to 266 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 175

- gi No. 3913203

25 - Description:

- % Identity: 32.8

- Alignment Length: 196

- Location of Alignment in SEQ ID NO 269: from 81
to 266

30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 270

- Ceres seq_id 1533354

35 - Location of start within SEQ ID NO 268: at 25 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- haloacid dehalogenase-like hydrolase

40 - Location within SEQ ID NO 270: from 74 to 258 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 176

- gi No. 3913203

- Description:

45 - % Identity: 32.8

- Alignment Length: 196

- Location of Alignment in SEQ ID NO 270: from 73
to 258

50 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 271

196

- Ceres seq_id 1533355
- Location of start within SEQ ID NO 268: at 265 nt.

- 5 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
- haloacid dehalogenase-like hydrolase
 - Location within SEQ ID NO 271: from 1 to 178 aa.

- 10 (Dp) Related Amino Acid Sequences
- Alignment No. 177
 - gi No. 3913203
 - Description:
 - % Identity: 32.8
 - Alignment Length: 196
 - 15 - Location of Alignment in SEQ ID NO 271: from 1 to
178

Maximum Length Sequence:

- related to:
- 20 Clone IDs:
- 158412
- (Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 272
 - Ceres seq_id 1534544

25

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 273
 - Ceres seq_id 1534545
 - 30 - Location of start within SEQ ID NO 272: at 2 nt.

- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
- 35 (Dp) Related Amino Acid Sequences
- Alignment No. 178
 - gi No. 2317676
 - Description:
 - % Identity: 37.2
 - Alignment Length: 115
 - 40 - Location of Alignment in SEQ ID NO 273: from 22
to 134

- (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 274
 - 45 - Ceres seq_id 1534546
 - Location of start within SEQ ID NO 272: at 524 nt.

- (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
- 50 (Dp) Related Amino Acid Sequences
- Alignment No. 179

197

- gi No. 4836939
- Description:
- % Identity: 47.3
- Alignment Length: 150
- Location of Alignment in SEQ ID NO 274: from 19
5 to 166

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 275
- Ceres seq_id 1534547
- Location of start within SEQ ID NO 272: at 815 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

15 (Dp) Related Amino Acid Sequences

- Alignment No. 180
- gi No. 4836939
- Description:
- % Identity: 47.3
- Alignment Length: 150
- Location of Alignment in SEQ ID NO 275: from 1 to
20 69

25 (Ba) Polypeptide Activities: Similar to calcium independent
phrophospholipase A2 protein activities, and acy-protein
thioesterase activities.

Maximum Length Sequence:

30 related to:

Clone IDs:

108109

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 276
- Ceres seq_id 1567172
- Alternative transcription start site(s) located in SEQ
ID NO 276:
22

40 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 277
- Ceres seq_id 1567173
- Location of start within SEQ ID NO 276: at 152 nt.

45 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 181
- gi No. 1076301

198

- Description: CONSTANS protein - Arabidopsis
thaliana >gi|1161514|emb|CAA64407| (X94937) CONSTANS protein
[Arabidopsis thaliana]

5 - % Identity: 49.2
- Alignment Length: 63
- Location of Alignment in SEQ ID NO 277: from 12
to 74

(B) Polypeptide Sequence

10 - Pat. Appln. SEQ ID NO 278
- Ceres seq_id 1567174
- Location of start within SEQ ID NO 276: at 155 nt.

(C) Nomination and Annotation of Domains within
15 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

20 - Alignment No. 182
- gi No. 1076301
- Description: CONSTANS protein - Arabidopsis
thaliana >gi|1161514|emb|CAA64407| (X94937) CONSTANS protein
[Arabidopsis thaliana]
- % Identity: 49.2
- Alignment Length: 63
- Location of Alignment in SEQ ID NO 278: from 11
25 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 279
- Ceres seq_id 1567175
30 - Location of start within SEQ ID NO 276: at 443 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

35 - Alignment No. 183
- gi No. 1076301
- Description: CONSTANS protein - Arabidopsis
thaliana >gi|1161514|emb|CAA64407| (X94937) CONSTANS protein
[Arabidopsis thaliana]
40 - % Identity: 67.4
- Alignment Length: 43
- Location of Alignment in SEQ ID NO 279: from 261
to 303

45 Maximum Length Sequence:
related to:

Clone IDs:

168

Public Genomic DNA:

50 gi No: 4895213

Predicted Exons:

199
INIT 22484 ... 22368 OCKHAMG-CDS
TERM 21760 ... 21704 OCKHAMG-CDS
(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 280
5 - Ceres seq_id 1567535
- Alternative transcription start site(s) located in SEQ
ID NO 280:
12,22,23,25,28,36,68

10 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 281
- Ceres seq_id 1567536
- Location of start within SEQ ID NO 280: at 104 nt.

15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences
- Alignment No. 184
- gi No. 1351365
20 - Description: UBIQUINOL-CYTOCHROME C REDUCTASE
COMPLEX 6.7 KD PROTEIN (CR6) >gi|2130002|pir||S68969
ubiquinol--cytochrome-c reductase (EC 1.10.2.2) - potato
>gi|633683|emb|CAA57768| (X82325) cytochrome c reductase
subunit [Solanum tuberosum]
25 - % Identity: 52.6
- Alignment Length: 58
- Location of Alignment in SEQ ID NO 281: from 2 to
57

30 Maximum Length Sequence:
related to:
Clone IDs:
21305
(Ac) cDNA Polynucleotide Sequence
35 - Pat. Appln. SEQ ID NO 282
- Ceres seq_id 1569689
- Alternative transcription start site(s) located in SEQ
ID NO 282:
28,29,49

40 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 283
- Ceres seq_id 1569690
- Location of start within SEQ ID NO 282: at 1 nt.
45 - Location of Signal Peptide Cleavage Site within SEQ
ID NO 283: at 32 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
50 (Dp) Related Amino Acid Sequences

200

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 284
- Ceres seq_id 1569691
- Location of start within SEQ ID NO 282: at 92 nt.

5

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 185
- gi No. 2191138
- Description: (AF007269) A_IG002N01.18 gene
product [Arabidopsis thaliana]
- % Identity: 19.5
- Alignment Length: 87
- Location of Alignment in SEQ ID NO 284: from 3 to

10

15

83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 285
- Ceres seq_id 1569692
- Location of start within SEQ ID NO 282: at 248 nt.

20

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 186
- gi No. 2191138
- Description: (AF007269) A_IG002N01.18 gene
product [Arabidopsis thaliana]
- % Identity: 19.5
- Alignment Length: 87
- Location of Alignment in SEQ ID NO 285: from 1 to

25

30

31

35 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.

Maximum Length Sequence:

related to:

40

Clone IDs:

41988

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 286
- Ceres seq_id 1571042
- Alternative transcription start site(s) located in SEQ
ID NO 286:
-1,2,3,4,7

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 287
- Ceres seq_id 1571043

50

201

- Location of start within SEQ ID NO 286: at 63 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

5 (Dp) Related Amino Acid Sequences

- Alignment No. 187

- gi No. 2129641

10 - Description: major latex protein type 1 -
Arabidopsis thaliana >gi|1107493|emb|CAA63026| (X91960) major
latex protein type1 [Arabidopsis thaliana]

- % Identity: 71.3

- Alignment Length: 150

- Location of Alignment in SEQ ID NO 287: from 1 to
150

15

Maximum Length Sequence:

related to:

Clone IDs:

16143

20 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 288

- Ceres seq_id 1571079

- Alternative transcription start site(s) located in SEQ
ID NO 288:

25 -5,37,86,341,350

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 289

- Ceres seq_id 1571080

30 - Location of start within SEQ ID NO 288: at 51 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

35 - Pathogenesis-related protein Bet v I family

- Location within SEQ ID NO 289: from 5 to 155 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 188

- gi No. 1321731

40 - Description: (Z72439) major allergen Cor a 1
[Corylus avellana]

- % Identity: 35.7

- Alignment Length: 159

45 - Location of Alignment in SEQ ID NO 289: from 5 to
155

Maximum Length Sequence:

related to:

Clone IDs:

50 42101

(Ac) cDNA Polynucleotide Sequence

202

- Pat. Appln. SEQ ID NO 290
- Ceres seq_id 1572097

5 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 291
- Ceres seq_id 1572098
- Location of start within SEQ ID NO 290: at 63 nt.

10 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Adhesion lipoprotein
- Location within SEQ ID NO 291: from 118 to 191

aa.

15

(Dp) Related Amino Acid Sequences

- Alignment No. 189
- gi No. 2129641
- Description: major latex protein type 1 -

20 Arabidopsis thaliana >gi|1107493|emb|CAA63026| (X91960) major
latex protein type1 [Arabidopsis thaliana]

- % Identity: 69.5
- Alignment Length: 154
- Location of Alignment in SEQ ID NO 291: from 1 to

25 154

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 292
- Ceres seq_id 1572099
- Location of start within SEQ ID NO 290: at 336 nt.

30

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Adhesion lipoprotein
- Location within SEQ ID NO 292: from 27 to 100 aa.

35

(Dp) Related Amino Acid Sequences

- Alignment No. 190
- gi No. 2129641
- Description: major latex protein type 1 -

40 Arabidopsis thaliana >gi|1107493|emb|CAA63026| (X91960) major
latex protein type1 [Arabidopsis thaliana]

- % Identity: 69.5
- Alignment Length: 154
- Location of Alignment in SEQ ID NO 292: from 1 to

45

63

Maximum Length Sequence:

related to:

50 Clone IDs:
27643

203

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 293
- Ceres seq_id 1572890
- Alternative transcription start site(s) located in SEQ

5 ID NO 293:

-10

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 294
- Ceres seq_id 1572891
- Location of start within SEQ ID NO 293: at 1 nt.

10

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Photosystem I psaG / psaK
- Location within SEQ ID NO 294: from 71 to 151 aa.

15

(Dp) Related Amino Acid Sequences

- Alignment No. 191
- gi No. 3885511
- Description: (AF084200) similar to PSI-K subunit
of photosystem I from barley [Medicago sativa]

20

- % Identity: 80.3

- Alignment Length: 128

- Location of Alignment in SEQ ID NO 294: from 22
to 148

25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 295
- Ceres seq_id 1572892
- Location of start within SEQ ID NO 293: at 64 nt.

30

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Photosystem I psaG / psaK
- Location within SEQ ID NO 295: from 50 to 130 aa.

35

(Dp) Related Amino Acid Sequences

- Alignment No. 192
- gi No. 3885511
- Description: (AF084200) similar to PSI-K subunit
of photosystem I from barley [Medicago sativa]
- % Identity: 80.3
- Alignment Length: 128
- Location of Alignment in SEQ ID NO 295: from 1 to
127

40

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 296
- Ceres seq_id 1572893
- Location of start within SEQ ID NO 293: at 76 nt.

50

204

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Photosystem I psaG / psaK
- Location within SEQ ID NO 296: from 46 to 126 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 193
- gi No. 3885511
- Description: (AF084200) similar to PSI-K subunit
of photosystem I from barley [Medicago sativa]
- % Identity: 80.3
- Alignment Length: 128
- Location of Alignment in SEQ ID NO 296: from 1 to
123

Maximum Length Sequence:

related to:

Clone IDs:

33027

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 297
- Ceres seq_id 1573606
- Alternative transcription start site(s) located in SEQ
ID NO 297:
7,8,13

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 298
- Ceres seq_id 1573607
- Location of start within SEQ ID NO 297: at 56 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 298: at 19 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Pollen proteins Ole e I family
- Location within SEQ ID NO 298: from 32 to 131 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 194
- gi No. 4584110
- Description: (AJ133639) SAH7 protein [Arabidopsis
thaliana]
- % Identity: 48.5
- Alignment Length: 163
- Location of Alignment in SEQ ID NO 298: from 1 to
163

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 299

205

- Ceres seq_id 1573608
- Location of start within SEQ ID NO 297: at 71 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 299: at 14 aa.

5

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Pollen proteins Ole e I family
- Location within SEQ ID NO 299: from 27 to 126 aa.

10

(Dp) Related Amino Acid Sequences

- Alignment No. 195
- gi No. 4584110
- Description: (AJ133639) SAH7 protein [Arabidopsis

15 thaliana]

- % Identity: 48.5
- Alignment Length: 163
- Location of Alignment in SEQ ID NO 299: from 1 to

158

20

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 300
- Ceres seq_id 1573609
- Location of start within SEQ ID NO 297: at 107 nt.

25

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Pollen proteins Ole e I family
- Location within SEQ ID NO 300: from 15 to 114 aa.

30

(Dp) Related Amino Acid Sequences

- Alignment No. 196
- gi No. 4584110
- Description: (AJ133639) SAH7 protein [Arabidopsis

35 thaliana]

- % Identity: 48.5
- Alignment Length: 163
- Location of Alignment in SEQ ID NO 300: from 1 to

146

40

Maximum Length Sequence:

related to:

Clone IDs:

31422

45

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 301
- Ceres seq_id 1573861

50

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 302

206

- Ceres seq_id 1573862
- Location of start within SEQ ID NO 301: at 67 nt.

(C) Nomination and Annotation of Domains within
5 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 197
- gi No. 2191138
- Description: (AF007269) A_IG002N01.18 gene

10 product [Arabidopsis thaliana]

- % Identity: 28.1
- Alignment Length: 160
- Location of Alignment in SEQ ID NO 302: from 3 to

156

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 303
- Ceres seq_id 1573863
- Location of start within SEQ ID NO 301: at 223 nt.

20

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 198
- gi No. 2191138
- Description: (AF007269) A_IG002N01.18 gene

25

product [Arabidopsis thaliana]

- % Identity: 28.1
- Alignment Length: 160
- Location of Alignment in SEQ ID NO 303: from 1 to

30

104

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.

35

Maximum Length Sequence:

related to:

Clone IDs:

40916

40 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 304
- Ceres seq_id 1574093

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 305
- Ceres seq_id 1574094
- Location of start within SEQ ID NO 304: at 47 nt.

50

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

207

- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 305: from 152 to 192

aa.

5 (Dp) Related Amino Acid Sequences

- Alignment No. 199
- gi No. 3790593
- Description: (AF079185) RING-H2 finger protein

RHY1a [Arabidopsis thaliana]

- % Identity: 55.1
- Alignment Length: 49
- Location of Alignment in SEQ ID NO 305: from 148 to 196

15 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 306
- Ceres seq_id 1574095
- Location of start within SEQ ID NO 304: at 56 nt.

20 (C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 306: from 149 to 189

aa.

25 (Dp) Related Amino Acid Sequences

- Alignment No. 200
- gi No. 3790593
- Description: (AF079185) RING-H2 finger protein

30 RHY1a [Arabidopsis thaliana]

- % Identity: 55.1
- Alignment Length: 49
- Location of Alignment in SEQ ID NO 306: from 145 to 193

35 Maximum Length Sequence:
related to:

Clone IDs:

35447

40 Public Genomic DNA:

gi No: 4263694

Predicted Exons:

INIT	79640 ...	79806	GENBANK
TERM	79888 ...	80164	GENBANK

45	INTR	79508 ...	79806	OCKHAMG-CDNA
	INTR	79888 ...	80309	OCKHAMG-CDNA

50	INIT	79640 ...	79806	OCKHAMG-CDS
	TERM	79888 ...	80164	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

208

- Pat. Appln. SEQ ID NO 307
- Ceres seq_id 1580388
- Alternative transcription start site(s) located in SEQ
ID NO 307:

5 2,3,4,5,6,7,63,94

(B) Polypeptide Sequence

10 - Pat. Appln. SEQ ID NO 308
- Ceres seq_id 1580389
- Location of start within SEQ ID NO 307: at 133 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 308: at 27 aa.

15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Cystatin domain
- Location within SEQ ID NO 308: from 87 to 141 aa.

20 (Dp) Related Amino Acid Sequences

- Alignment No. 201
- gi No. 2204077
- Description: (D85623) extracellular insoluble
cystatin [Daucus carota]
25 - % Identity: 44.9
- Alignment Length: 136
- Location of Alignment in SEQ ID NO 308: from 6 to
141

30 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 309
- Ceres seq_id 1580390
- Location of start within SEQ ID NO 307: at 142 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 309: at 24 aa.

35 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Cystatin domain
- Location within SEQ ID NO 309: from 84 to 138 aa.

40 (Dp) Related Amino Acid Sequences

- Alignment No. 202
- gi No. 2204077
- Description: (D85623) extracellular insoluble
45 cystatin [Daucus carota]
- % Identity: 44.9
- Alignment Length: 136
- Location of Alignment in SEQ ID NO 309: from 3 to
138

50 Maximum Length Sequence:

209

related to:

Clone IDs:

22677

Public Genomic DNA:

gi No: 4972043

Predicted Exons:

SINGLE 18935 ... 19282 GENBANK

INTR 18856 ... 19527 OCKHAMG-CDNA

SINGLE 18935 ... 19282 OCKHAMG-CDS

gi No: 4972077

Predicted Exons:

INTR 60360 ... 61031 OCKHAMG-CDNA

SINGLE 60439 ... 60786 OCKHAMG-CDS

gi No: 5748495

Predicted Exons:

INTR 60360 ... 61031 OCKHAMG-CDNA

SINGLE 60439 ... 60786 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 310

- Ceres seq_id 1582959

- Alternative transcription start site(s) located in SEQ

ID NO 310:

2,5,6,7,58,61

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 311

- Ceres seq_id 1582960

- Location of start within SEQ ID NO 310: at 80 nt.

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 311: at 19 aa.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

- Dehydrins

- Location within SEQ ID NO 311: from 37 to 113 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 203

- gi No. 4972049

- Description: (AL078470) glycine-rich protein like

[Arabidopsis thaliana]

- % Identity: 100

- Alignment Length: 115

- Location of Alignment in SEQ ID NO 311: from 1 to

115

Maximum Length Sequence:

210

related to:

Clone IDs:

15190

34118

5 Public Genomic DNA:

gi No: 4582444

Predicted Exons:

	INIT	39128	...	39157	GENBANK
	INTR	39241	...	39388	GENBANK
10	INTR	39469	...	39640	GENBANK
	INTR	39922	...	40108	GENBANK
	TERM	40198	...	40413	GENBANK
	INTR	39945	...	40108	OCKHAMG-CDNA
15	INTR	40198	...	40660	OCKHAMG-CDNA
	INTR	39054	...	39157	OCKHAMG-CDNA
	INTR	39241	...	39388	OCKHAMG-CDNA
	INTR	39469	...	39640	OCKHAMG-CDNA
20	INTR	39922	...	40108	OCKHAMG-CDNA
	INTR	40198	...	40626	OCKHAMG-CDNA
	INIT	39128	...	39157	OCKHAMG-CDS
	INTR	39241	...	39388	OCKHAMG-CDS
25	INTR	39469	...	39640	OCKHAMG-CDS
	INTR	39922	...	40108	OCKHAMG-CDS
	TERM	40198	..	40413	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

30 - Pat. Appln. SEQ ID NO 312
 - Ceres seq_id 1663221
 - Alternative transcription start site(s) located in SEQ
 ID NO 312:
 -5,2,3,4,5,12,40,448
 - Clone 15190 starts at 448 and ends at 1076 in cDNA.
 35 - Clone 34118 starts at 1 and ends at 1042 in cDNA.

(B) Polypeptide Sequence

40 - Pat. Appln. SEQ ID NO 313
 - Ceres seq_id 1663222
 - Location of start within SEQ ID NO 312: at 75 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

45 - Ribosomal protein S3, C-terminal domain.
 - Location within SEQ ID NO 313: from 104 to 188
 aa.

(Dp) Related Amino Acid Sequences

50 - Alignment No. 204
 - gi No. 133940

211

- Description: 40S RIBOSOMAL PROTEIN S3A (S1A)
>gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed
frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a
[Xenopus laevis]

5 - % Identity: 80.1
 - Alignment Length: 231
 - Location of Alignment in SEQ ID NO 313: from 1 to
228

10 (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 314
 - Ceres seq_id 1663223
 - Location of start within SEQ ID NO 312: at 204 nt.

15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
 - Ribosomal protein S3, C-terminal domain.
 - Location within SEQ ID NO 314: from 61 to 145 aa.

20 (Dp) Related Amino Acid Sequences
 - Alignment No. 205
 - gi No. 133940
 - Description: 40S RIBOSOMAL PROTEIN S3A (S1A)
>gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed
25 frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a
[Xenopus laevis]
 - % Identity: 80.1
 - Alignment Length: 231
 - Location of Alignment in SEQ ID NO 314: from 1 to

30 185

Maximum Length Sequence:
related to:

Clone IDs:

35 3996
 2749

(Ac) cDNA Polynucleotide Sequence

 - Pat. Appln. SEQ ID NO 315
 - Ceres seq_id 1663275
40 - Alternative transcription start site(s) located in SEQ
ID NO 315:
 3,4,5,6,7,8,9,15
 - Clone 3996 starts at 1 and ends at 484 in cDNA.
 - Clone 2749 starts at 7 and ends at 488 in cDNA.

45 (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 316
 - Ceres seq_id 1663276
 - Location of start within SEQ ID NO 315: at 75 nt.

50

212

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S14p/S29e
- Location within SEQ ID NO 316: from 3 to 54 aa.

5

(Dp) Related Amino Acid Sequences

- Alignment No. 206
- gi No. 4506717
- Description: ref|NP_001023.1|pRPS29| ribosomal

10 protein S29 >gi|266972|sp|P30054|RS29_HUMAN 40S RIBOSOMAL
PROTEIN S29 >gi|631884|pir||S30298 ribosomal protein S29 -
rat >gi|1362934|pir||S55919 ribosomal protein S29 - human
protein S29 [Homo sapiens]

- % Identity: 72.2

15 - Alignment Length: 54

- Location of Alignment in SEQ ID NO 316: from 1 to

54

(B) Polypeptide Sequence

- 20 - Pat. Appln. SEQ ID NO 317
- Ceres seq_id 1663277
 - Location of start within SEQ ID NO 315: at 92 nt.

(C) Nomination and Annotation of Domains within
25 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

Maximum Length Sequence:

related to:

30 Clone IDs:

114940

25068

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NC 318

35 - Ceres seq_id 1665304

- Alternative transcription start site(s) located in SEQ
ID NO 318:

-8,-3,-1,2,3,4,8,17,251

- Clone 114940 starts at 1 and ends at 743 in cDNA.

40 - Clone 25068 starts at 4 and ends at 760 in cDNA.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 319

- Ceres seq_id 1665305

45 - Location of start within SEQ ID NO 318: at 63 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 207

50 - gi No. 2129641

213

- Description: major latex protein type 1 -
Arabidopsis thaliana >gi|1107493|emb|CAA63026| (X91960) major
latex protein type1 [Arabidopsis thaliana]

- % Identity: 71.3

5 - Alignment Length: 150

- Location of Alignment in SEQ ID NO 319: from 1 to
150

Maximum Length Sequence:

10 related to:

Clone IDs:

94673

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 320

15 - Ceres seq_id 1709970

- Alternative transcription start site(s) located in SEQ
ID NO 320:

-2,-1,11,41,42,43,44,45,46,47,48,51

20 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 321

- Ceres seq_id 1709971

- Location of start within SEQ ID NO 320: at 276 nt.

25 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 208

- gi No. 2961300

30 - Description: (AJ225027) ribosomal protein L24
[Cicer arietinum]

- % Identity: 86.2

- Alignment Length: 160

35 - Location of Alignment in SEQ ID NO 321: from 1 to
107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 322

- Ceres seq_id 1709972

40 - Location of start within SEQ ID NO 320: at 424 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

45 Maximum Length Sequence:
related to:

Clone IDs:

112835

50 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 323

214

- Ceres seq_id 1711273
- Alternative transcription start site(s) located in SEQ
ID NO 323:
2,28,30,33,56,62,235

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 324
- Ceres seq_id 1711274
- Location of start within SEQ ID NO 323: at 92 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Helix-turn-helix
- Location within SEQ ID NO 324: from 87 to 141 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 209
- gi No. 1632831
- Description: (Z49698) orf [Ricinus communis]
- % Identity: 81
- Alignment Length: 142
- Location of Alignment in SEQ ID NO 324: from 1 to

142

Maximum Length Sequence:
related to:

Clone IDs:

17878

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 325
- Ceres seq_id 1715423
- Alternative transcription start site(s) located in SEQ
ID NO 325:
2,4,7,66

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 326
- Ceres seq_id 1715424
- Location of start within SEQ ID NO 325: at 25 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 210
- gi No. 4337175
- Description: (AC006416) ESTs gb|T20589,
gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428,
gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457,
gb|T20921, gb|AA042762 and gb|AA720210 come from this gene.
[Arabidopsis thaliana]
- % Identity: 44.8

215

- Alignment Length: 67
- Location of Alignment in SEQ ID NO 326: from 15

to 81

- 5 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 327
 - Ceres seq_id 1715425
 - Location of start within SEQ ID NO 325: at 40 nt.

- 10 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 15 - Alignment No. 211
- gi No. 4337175
- Description: (AC006416) ESTs gb|T20589,
gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428,
gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457,
gb|T20921, gb|AA042762 and gb|AA720210 come from this gene.
[Arabidopsis thaliana]

- 20 - % Identity: 44.8
- Alignment Length: 67
- Location of Alignment in SEQ ID NO 327: from 10
- to 76

- 25 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 328
 - Ceres seq_id 1715426
 - Location of start within SEQ ID NO 325: at 260 nt.

- 30 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 35 - Alignment No. 212
- gi No. 4337175
- Description: (AC006416) ESTs gb|T20589,
gb|T04648, gb|AA597906, gb|T04111, gb|R84180, gb|R65428,
gb|T44439, gb|T76570, gb|R90004, gb|T45020, gb|T42457,
gb|T20921, gb|AA042762 and gb|AA720210 come from this gene.
[Arabidopsis thaliana]

- 40 - % Identity: 56.1
- Alignment Length: 57
- Location of Alignment in SEQ ID NO 328: from 5 to
- 61

- 45 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.

Maximum Length Sequence:

related to:

- 50 Clone IDs:
- 26744

216

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 329
- Ceres seq_id 1715962
- Alternative transcription start site(s) located in SEQ

5 ID NO 329:

2,7,9,10,26,28,30,31,32,38,39,42,43,47,48,194,247

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 330
- Ceres seq_id 1715963
- Location of start within SEQ ID NO 329: at 87 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein L6
- Location within SEQ ID NO 330: from 12 to 194 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 213
 - gi No. 1710581
 - Description: 60S RIBOSOMAL PROTEIN L9
- >gi|2129720|pir||S71255 ribosomal protein L9 - Arabidopsis
thaliana >gi|1107489|emb|CAA63024| (X91958) 60S ribosomal
protein L9 [Arabidopsis thaliana]
- % Identity: 93.3
 - Alignment Length: 195
 - Location of Alignment in SEQ ID NO 330: from 1 to
194

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 331
- Ceres seq_id 1715964
- Location of start within SEQ ID NO 329: at 114 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein L6
- Location within SEQ ID NO 331: from 3 to 185 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 214
 - gi No. 1710581
 - Description: 60S RIBOSOMAL PROTEIN L9
- >gi|2129720|pir||S71255 ribosomal protein L9 - Arabidopsis
thaliana >gi|1107489|emb|CAA63024| (X91958) 60S ribosomal
protein L9 [Arabidopsis thaliana]
- % Identity: 93.3
 - Alignment Length: 195
 - Location of Alignment in SEQ ID NO 331: from 1 to
185

217

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 332
- Ceres seq_id 1715965
- Location of start within SEQ ID NO 329: at 369 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein L6
- Location within SEQ ID NO 332: from 1 to 100 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 215
- gi No. 1710581
- Description: 60S RIBOSOMAL PROTEIN L9

>gi|2129720|pir||S71255 ribosomal protein L9 - Arabidopsis
thaliana >gi|1107489|emb|CAA63024| (X91958) 60S ribosomal
protein L9 [Arabidopsis thaliana]

- % Identity: 93.3
- Alignment Length: 195
- Location of Alignment in SEQ ID NO 332: from 1 to

100

Maximum Length Sequence:

related to:

Clone IDs:

41712

Public Genomic DNA:

gi No: 4512656

Predicted Exons:

INIT	106774...	106633	GENBANK
INTR	106277...	106194	GENBANK
INTR	105920...	105838	GENBANK
TERM	105749...	105630	GENBANK
INTR	106841...	106633	OCKHAMG-CDNA
INTR	106277...	106194	OCKHAMG-CDNA
INTR	105920...	105838	OCKHAMG-CDNA
INTR	105749...	105453	OCKHAMG-CDNA
INIT	106774...	106633	OCKHAMG-CDS
INTR	106277...	106194	OCKHAMG-CDS
INTR	105920...	105838	OCKHAMG-CDS
TERM	105749...	105630	OCKHAMG-CDS

gi No: 4559319

Predicted Exons:

INIT	10855 ...	10714	GENBANK
INTR	10358 ...	10275	GENBANK
INTR	10001 ...	9919	GENBANK
TERM	9830 ...	9711	GENBANK

INTR	10922 ...	10714	OCKHAMG-CDNA
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218

	INTR	10358	...	10275	OCKHAMG-CDNA
	INTR	10001	...	9919	OCKHAMG-CDNA
	INTR	9830	...	9534	OCKHAMG-CDNA

5

	INIT	10855	...	10714	OCKHAMG-CDS
	INTR	10358	...	10275	OCKHAMG-CDS
	INTR	10001	...	9919	OCKHAMG-CDS
	TERM	9830	...	9711	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

10

- Pat. Appln. SEQ ID NO 333
- Ceres seq_id 1808584
- Alternative transcription start site(s) located in SEQ ID NO 333:

34

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 334
- Ceres seq_id 1808585
- Location of start within SEQ ID NO 333: at 1 nt.

20

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Helix-turn-helix
- Location within SEQ ID NO 334: from 110 to 164

25 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 216
- gi No. 1632831
- Description: (Z49698) orf [Ricinus communis]
- % Identity: 81
- Alignment Length: 142
- Location of Alignment in SEQ ID NO 334: from 24

30 to 165

35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 335
- Ceres seq_id 1808586
- Location of start within SEQ ID NO 333: at 70 nt.

40

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Helix-turn-helix
- Location within SEQ ID NO 335: from 87 to 141 aa.

45

(Dp) Related Amino Acid Sequences

- Alignment No. 217
- gi No. 1632831
- Description: (Z49698) orf [Ricinus communis]
- % Identity: 81
- Alignment Length: 142

50

219

142 - Location of Alignment in SEQ ID NO 335: from 1 to

Maximum Length Sequence:

5 related to:

Clone IDs:

42211

Public Genomic DNA:

gi No: 4914400

10 Predicted Exons:

INTR 90159 ... 89532 OCKHAMG-CDNA

SINGLE 90124 ... 89615 OCKHAMG-CDS

gi No: 4938473

15 Predicted Exons:

SINGLE 2368 ... 1859 GENBANK

INTR 2403 ... 1776 OCKHAMG-CDNA

20 SINGLE 2368 ... 1859 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 336

- Ceres seq_id 1808591

25 ID NO 336:
7,10

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 337

30 - Ceres seq_id 1808592

- Location of start within SEQ ID NO 336: at 2 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 337: at 36 aa.

35 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 218

- gi No. 4926823

40 - Description: (AC004135) T17H7.8 [Arabidopsis
thaliana]

- % Identity: 46.1

- Alignment Length: 178

45 - Location of Alignment in SEQ ID NO 337: from 13
to 177

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 338

- Ceres seq_id 1808593

50 - Location of start within SEQ ID NO 336: at 38 nt.

220

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 338: at 24 aa.

(C) Nomination and Annotation of Domains within
5 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 219

- gi No. 4926823

10 thaliana]

- % Identity: 46.1

- Alignment Length: 178

- Location of Alignment in SEQ ID NO 338: from 1 to
165

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 339

- Ceres seq_id 1808594

- Location of start within SEQ ID NO 336: at 164 nt.

20

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 220

25 - gi No. 4926823

thaliana]

- % Identity: 46.1

- Alignment Length: 178

30 - Location of Alignment in SEQ ID NO 339: from 1 to
123

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant specific gene.

35

Maximum Length Sequence:

related to:

Clone IDs:

2217

40 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 340

- Ceres seq_id 1920563

- Alternative transcription start site(s) located in SEQ
ID NO 340:

45

6

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 341

- Ceres seq_id 1920564

50 - Location of start within SEQ ID NO 340: at 1 nt.

221

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Oxidoreductase FAD/NAD-binding domain
- Location within SEQ ID NO 341: from 45 to 167 aa.

5

(Dp) Related Amino Acid Sequences

- Alignment No. 221
- gi No. 729477
- Description: FERREDOXIN--NADP REDUCTASE PRECURSOR

10 (FNR) >gi|320548|pir||A44974 ferredoxin--NADP+ reductase (EC
1.18.1.2) precursor - common ice plant >gi|167256 (M25528)
ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
[Mesembryanthemum

- % Identity: 89.8
- Alignment Length: 197
- Location of Alignment in SEQ ID NO 341: from 1 to
197

(B) Polypeptide Sequence

- 20
- Pat. Appln. SEQ ID NO 342
 - Ceres seq_id 1920565
 - Location of start within SEQ ID NO 340: at 112 nt.

(C) Nomination and Annotation of Domains within
25 Predicted Polypeptide(s)

- Oxidoreductase FAD/NAD-binding domain
- Location within SEQ ID NO 342: from 8 to 130 aa.

(Dp) Related Amino Acid Sequences

30

- Alignment No. 222
- gi No. 729477
- Description: FERREDOXIN--NADP REDUCTASE PRECURSOR

(FNR) >gi|320548|pir||A44974 ferredoxin--NADP+ reductase (EC
1.18.1.2) precursor - common ice plant >gi|167256 (M25528)
35 ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
[Mesembryanthemum

- % Identity: 89.8
- Alignment Length: 197
- Location of Alignment in SEQ ID NO 342: from 1 to

40 160

(B) Polypeptide Sequence

- 45
- Pat. Appln. SEQ ID NO 343
 - Ceres seq_id 1920566
 - Location of start within SEQ ID NO 340: at 118 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 50
- Oxidoreductase FAD/NAD-binding domain
 - Location within SEQ ID NO 343: from 6 to 128 aa.

222

(Dp) Related Amino Acid Sequences

- Alignment No. 223

- gi No. 729477

- Description: FERREDOXIN--NADP REDUCTASE PRECURSOR

5 (FNR) >gi|320548|pir||A44974 ferredoxin--NADP+ reductase (EC
1.18.1.2) precursor - common ice plant >gi|167256 (M25528)
ferredoxin-NADP+ reductase precursor (fnrA; EC 1.6.7.1)
[Mesembryanthemum

- % Identity: 89.8

10 - Alignment Length: 197

- Location of Alignment in SEQ ID NO 343: from 1 to
158

Maximum Length Sequence:

15 related to:

Clone IDs:

13864

Public Genomic DNA:

gi No: 4309719

20 Predicted Exons:

INIT 50987 ... 50773 GENBANK

INTR 49622 ... 49352 GENBANK

INTR 49257 ... 49162 GENBANK

INTR 48896 ... 48786 GENBANK

25 INTR 48686 ... 48377 GENBANK

INTR 48133 ... 48043 GENBANK

INTR 47924 ... 47591 GENBANK

INTR 47475 ... 47327 GENBANK

TERM 47084 ... 46550 GENBANK

30 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 344

- Ceres seq_id 1974419

- Alternative transcription start site(s) located in SEQ
ID NO 344:

35 -5

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 345

- Ceres seq_id 1974420

40 - Location of start within SEQ ID NO 344: at 81 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

45 - ATPases associated with various cellular
activities (AAA)

- Location within SEQ ID NO 345: from 454 to 664
aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 224

- gi No. 4006905

50

223

- Description: (Z99708) ATPase-like protein
[Arabidopsis thaliana]
- % Identity: 84.3
- Alignment Length: 633
- Location of Alignment in SEQ ID NO 345: from 72
to 700

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 346
- Ceres seq_id 1974421
- Location of start within SEQ ID NO 344: at 96 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- ATPases associated with various cellular
activities (AAA)
- Location within SEQ ID NO 346: from 449 to 659
aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 225
- gi No. 4006905
- Description: (Z99708) ATPase-like protein
[Arabidopsis thaliana]
- % Identity: 84.3
- Alignment Length: 633
- Location of Alignment in SEQ ID NO 346: from 67
to 695

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 347
- Ceres seq_id 1974422
- Location of start within SEQ ID NO 344: at 141 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- ATPases associated with various cellular
activities (AAA)
- Location within SEQ ID NO 347: from 434 to 644
aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 226
- gi No. 4006905
- Description: (Z99708) ATPase-like protein
[Arabidopsis thaliana]
- % Identity: 84.3
- Alignment Length: 633
- Location of Alignment in SEQ ID NO 347: from 52
to 680

224

Maximum Length Sequence:

related to:

Clone IDs:

36333

5 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 348

- Ceres seq_id 1975983

10 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 349

- Ceres seq_id 1975984

- Location of start within SEQ ID NO 348: at 90 nt.

15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 227

- gi No. 3688432

20 - Description: (AJ011705) 40S ribosomal protein S10
[Lumbricus rubellus]

- % Identity: 55.3

- Alignment Length: 164

- Location of Alignment in SEQ ID NO 349: from 32

25 to 192

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 350

- Ceres seq_id 1975985

30 - Location of start within SEQ ID NO 348: at 135 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

35 - Alignment No. 228

- gi No. 3688432

- Description: (AJ011705) 40S ribosomal protein S10
[Lumbricus rubellus]

- % Identity: 55.3

40 - Alignment Length: 164

- Location of Alignment in SEQ ID NO 350: from 17

to 177

(B) Polypeptide Sequence

45 - Pat. Appln. SEQ ID NO 351

- Ceres seq_id 1975986

- Location of start within SEQ ID NO 348: at 183 nt.

50 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

225

- Alignment No. 229
- gi No. 3688432
- Description: (AJ011705) 40S ribosomal protein S10

[Lumbricus rubellus]

- % Identity: 55.3
- Alignment Length: 164

- Location of Alignment in SEQ ID NO 351: from 1 to 161

(Ba) Polypeptide Activities: Similar to glycine-rich RNA binding ABA inducible protein activities.

Maximum Length Sequence:
related to:

Clone IDs:

24587
41072

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 352
- Ceres seq_id 1976019
- Alternative transcription start site(s) located in SEQ ID NO 352:
13
- Clone 24587 starts at 13 and ends at in cDNA.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 353
- Ceres seq_id 1976020
- Location of start within SEQ ID NO 352: at 101 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 230
 - gi No. 3688432
 - Description: (AJ011705) 40S ribosomal protein S10
- [Lumbricus rubellus]
- % Identity: 55.3
 - Alignment Length: 164
 - Location of Alignment in SEQ ID NO 353: from 1 to

161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 354
- Ceres seq_id 1976021
- Location of start within SEQ ID NO 352: at 239 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 231
- gi No. 3688432

226

- Description: (AJ011705) 40S ribosomal protein S10
[Lumbricus rubellus]

- % Identity: 55.3

- Alignment Length: 164

- Location of Alignment in SEQ ID NO 354: from 1 to
115

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 355

- Ceres seq_id 1976022

- Location of start within SEQ ID NO 352: at 287 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 232

- gi No. 3688432

- Description: (AJ011705) 40S ribosomal protein S10
[Lumbricus rubellus]

- % Identity: 55.3

- Alignment Length: 164

- Location of Alignment in SEQ ID NO 355: from 1 to
99

(Ba) Polypeptide Activities: Extensin like protein
activities and glycine rich protein activities.

Maximum Length Sequence:

related to:

Clone IDs:

117263

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 356

- Ceres seq_id 1976673

- Alternative transcription start site(s) located in SEQ
ID NO 356:

-46,2,3,6,7

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 357

- Ceres seq_id 1976674

- Location of start within SEQ ID NO 356: at 3 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 357: at 34 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S21

- Location within SEQ ID NO 357: from 106 to 155
aa.

227

(Dp) Related Amino Acid Sequences

- Alignment No. 233

- gi No. 1710750

- Description: 30S RIBOSOMAL PROTEIN S21 (BS-B)

5 >gi|1303814|dbj|BAA12470| (D84432) YqeX [Bacillus subtilis]

>gi|1890063|dbj|BAA12082| (D83717) YqeX [Bacillus subtilis]

>gi|2634987|emb|CAB14483| (Z99117) ribosomal protein S21
[Bacillus subtilis]

- % Identity: 38.5

10 - Alignment Length: 52

- Location of Alignment in SEQ ID NO 357: from 106
to 157

(B) Polypeptide Sequence

15 - Pat. Appln. SEQ ID NO 358

- Ceres seq_id 1976675

- Location of start within SEQ ID NO 356: at 48 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 358: at 19 aa.

20

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S21

- Location within SEQ ID NO 358: from 91 to 140 aa.

25

(Dp) Related Amino Acid Sequences

- Alignment No. 234

- gi No. 1710750

- Description: 30S RIBOSOMAL PROTEIN S21 (BS-B)

30 >gi|1303814|dbj|BAA12470| (D84432) YqeX [Bacillus subtilis]

>gi|1890063|dbj|BAA12082| (D83717) YqeX [Bacillus subtilis]

>gi|2634987|emb|CAB14483| (Z99117) ribosomal protein S21
[Bacillus subtilis]

- % Identity: 38.5

35 - Alignment Length: 52

- Location of Alignment in SEQ ID NO 358: from 91
to 142

(B) Polypeptide Sequence

40 - Pat. Appln. SEQ ID NO 359

- Ceres seq_id 1976676

- Location of start within SEQ ID NO 356: at 192 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

45

- Ribosomal protein S21

- Location within SEQ ID NO 359: from 43 to 92 aa.

(Dp) Related Amino Acid Sequences

50 - Alignment No. 235

- gi No. 1710750

228

- Description: 30S RIBOSOMAL PROTEIN S21 (BS-B)

>gi|1303814|dbj|BAA12470| (D84432) YqeX [Bacillus subtilis]

>gi|1890063|dbj|BAA12082| (D83717) YqeX [Bacillus subtilis]

>gi|2634987|emb|CAB14483| (Z99117) ribosomal protein S21

5 [Bacillus subtilis]

- % Identity: 38.5

- Alignment Length: 52

- Location of Alignment in SEQ ID NO 359: from 43

to 94

10

Maximum Length Sequence:

related to:

Clone IDs:

42333

15 Public Genomic DNA:

gi No: 6041810

Predicted Exons:

INTR 93582 ... 94052 OCKHAMG-CDNA

INTR 94169 ... 94771 OCKHAMG-CDNA

20

INIT 93630 ... 94052 OCKHAMG-CDS

TERM 94169 ... 94687 OCKHAMG-CDS

gi No: 6091711

Predicted Exons:

25

INTR 60479 ... 60949 OCKHAMG-CDNA

INTR 61066 ... 61668 OCKHAMG-CDNA

INIT 60527 ... 60949 OCKHAMG-CDS

TERM 61066 ... 61584 OCKHAMG-CDS

30

gi No: 6102641

Predicted Exons:

INTR 52165 ... 52635 OCKHAMG-CDNA

INTR 52752 ... 53354 OCKHAMG-CDNA

35

INIT 52213 ... 52635 OCKHAMG-CDS

TERM 52752 ... 53270 OCKHAMG-CDS

gi No: 6453849

Predicted Exons:

40

INTR 59432 ... 58964 OCKHAMG-CDNA

INTR 58847 ... 58243 OCKHAMG-CDNA

INIT 59386 ... 58964 OCKHAMG-CDS

TERM 58847 ... 58329 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

45

- Pat. Appln. SEQ ID NO 360

- Ceres seq_id 2025186

(B) Polypeptide Sequence

50

- Pat. Appln. SEQ ID NO 361

- Ceres seq_id 2025187

229

- Location of start within SEQ ID NO 360: at 1 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- D-isomer specific 2-hydroxyacid dehydrogenases
- Location within SEQ ID NO 361: from 93 to 295 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 236
- gi No. 5458864
- Description: (AJ248287) GLYCERATE DEHYDROGENASE
[Pyrococcus abyssi]
- % Identity: 42.8
- Alignment Length: 299
- Location of Alignment in SEQ ID NO 361: from 36

to 322

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 362
- Ceres seq_id 2025188
- Location of start within SEQ ID NO 360: at 49 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- D-isomer specific 2-hydroxyacid dehydrogenases
- Location within SEQ ID NO 362: from 77 to 279 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 237
- gi No. 5458864
- Description: (AJ248287) GLYCERATE DEHYDROGENASE
[Pyrococcus abyssi]
- % Identity: 42.8
- Alignment Length: 299
- Location of Alignment in SEQ ID NO 362: from 20

to 306

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 363
- Ceres seq_id 2025189
- Location of start within SEQ ID NO 360: at 70 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- D-isomer specific 2-hydroxyacid dehydrogenases
- Location within SEQ ID NO 363: from 70 to 272 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 238
- gi No. 5458864

230

- Description: (AJ248287) GLYCERATE DEHYDROGENASE
[Pyrococcus abyssi]

- % Identity: 42.8

- Alignment Length: 299

5 - Location of Alignment in SEQ ID NO 363: from 13
to 299

Maximum Length Sequence:

related to:

10 Clone IDs:

267004

Public Genomic DNA:

gi No: 2924730

Predicted Exons:

15 INTR 8331 ... 8882 OCKHAMG-CDNA

SINGLE 8366 ... 8686 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 364

20 - Ceres seq_id 2025372

- Alternative transcription start site(s) located in SEQ
ID NO 364:

21

25 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 365

- Ceres seq_id 2025373

- Location of start within SEQ ID NO 364: at 1 nt.

30 (C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 239

- gi No. 132825

35 - Description: 50S RIBOSOMAL PROTEIN CL25,
CHLOROPLAST PRECURSOR >gi|71308|pir||R5PM25 ribosomal protein
PsCL25 precursor, chloroplast - garden pea
>gi|20877|emb|CAA32187| (X14022) PsCL25 ribosomal preprotein
(AA -30 to 74) [Pisum sativum]

40 - % Identity: 56.1

- Alignment Length: 82

- Location of Alignment in SEQ ID NO 365: from 14
to 95

45 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 366

- Ceres seq_id 2025374

- Location of start within SEQ ID NO 364: at 37 nt.

50 - Location of Signal Peptide Cleavage Site within SEQ
ID NO 366: at 16 aa.

231

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 240

- gi No. 132825

- Description: 50S RIBOSOMAL PROTEIN CL25,
CHLOROPLAST PRECURSOR >gi|71308|pir||R5PM25 ribosomal protein
PsCL25 precursor, chloroplast - garden pea

>gi|20877|emb|CAA32187| (X14022) PsCL25 ribosomal preprotein
(AA -30 to 74) [Pisum sativum]

- % Identity: 56.1

- Alignment Length: 82

- Location of Alignment in SEQ ID NO 366: from 2 to

83

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 367

- Ceres seq_id 2025375

- Location of start within SEQ ID NO 364: at 142 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 241

- gi No. 132825

- Description: 50S RIBOSOMAL PROTEIN CL25,
CHLOROPLAST PRECURSOR >gi|71308|pir||R5PM25 ribosomal protein
PsCL25 precursor, chloroplast - garden pea

>gi|20877|emb|CAA32187| (X14022) PsCL25 ribosomal preprotein
(AA -30 to 74) [Pisum sativum]

- % Identity: 56.1

- Alignment Length: 82

- Location of Alignment in SEQ ID NO 367: from 1 to

48

Maximum Length Sequence:

related to:

Clone IDs:

26930

Public Genomic DNA:

gi No: 5225383

Predicted Exons:

SINGLE 64539 ... 64276 GENBANK

INIT 64787 ... 64692 OCKHAMG-CDS

TERM 64620 ... 64276 OCKHAMG-CDS

gi No: 6136349

Predicted Exons:

INIT 126797... 126892 OCKHAMG-CDS

TERM 126964... 127308 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

232

- Pat. Appln. SEQ ID NO 368
- Ceres seq_id 2025471
- Alternative transcription start site(s) located in SEQ ID NO 368:

5 95,96,97,98,100,101,102,105,106,110

- Clone 26930 starts at 97 and ends at 631 in cDNA.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 369
- Ceres seq_id 2025472
- Location of start within SEQ ID NO 368: at 1 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

15 (Dp) Related Amino Acid Sequences

- Alignment No. 242
- gi No. 5732082
- Description: (AF162444) contains similarity to Solanum lycopersicum (tomato) wound induced protein (GB:X59882) [Arabidopsis thaliana]
- % Identity: 100
- Alignment Length: 87
- Location of Alignment in SEQ ID NO 369: from 60 to 146

25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 370
- Ceres seq_id 2025473
- Location of start within SEQ ID NO 368: at 178 nt.

30

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 243
- gi No. 5732082
- Description: (AF162444) contains similarity to Solanum lycopersicum (tomato) wound induced protein (GB:X59882) [Arabidopsis thaliana]
- % Identity: 100
- Alignment Length: 87
- Location of Alignment in SEQ ID NO 370: from 1 to 87

40

87

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 371
- Ceres seq_id 2025474
- Location of start within SEQ ID NO 368: at 214 nt.

45

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

50

(Dp) Related Amino Acid Sequences

233

- Alignment No. 244
- gi No. 5732082
- Description: (AF162444) contains similarity to
Solanum lycopersicum (tomato) wound induced protein
5 (GB:X59882) [Arabidopsis thaliana]
- % Identity: 100
- Alignment Length: 87
- Location of Alignment in SEQ ID NO 371: from 1 to

75

10

Maximum Length Sequence:

related to:

Clone IDs:

27681

15

Public Genomic DNA:

gi No: 6434227

Predicted Exons:

INTR 51354 ... 51417 OCKHAMG-CDNA

INTR 51529 ... 51786 OCKHAMG-CDNA

20

INIT 47952 ... 48020 OCKHAMG-CDS

INTR 48144 ... 48440 OCKHAMG-CDS

INTR 48542 ... 48757 OCKHAMG-CDS

INTR 48908 ... 49027 OCKHAMG-CDS

25

INTR 49117 ... 49654 OCKHAMG-CDS

TERM 50075 ... 50184 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 372

- Ceres seq_id 2025475

30

- Alternative transcription start site(s) located in SEQ
ID NO 372:

1242,1251,1270,1271,1275,1276,1280,1287,1288,1290,1292,1293,1
301,1302,1305,1307,1314,1318,1321,1325

35

1326,1330

- Clone 27681 starts at 1242 and ends at 2029 in cDNA.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 373

40

- Ceres seq_id 2025476

- Location of start within SEQ ID NO 372: at 1 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

45

(Dp) Related Amino Acid Sequences

- Alignment No. 245

- gi No. 2739366

- Description: (AC002505) SF16 like protein
[Arabidopsis thaliana]

50

- % Identity: 45

- Alignment Length: 373

234

- Location of Alignment in SEQ ID NO 373: from 61
to 418

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 374
- Ceres seq_id 2025477
- Location of start within SEQ ID NO 372: at 316 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 246
- gi No. 2739366
- Description: (AC002505) SF16 like protein

[Arabidopsis thaliana]

- % Identity: 45
- Alignment Length: 373
- Location of Alignment in SEQ ID NO 374: from 1 to

313

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 375
- Ceres seq_id 2025478
- Location of start within SEQ ID NO 372: at 364 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 375: at 21 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 247
- gi No. 2739366
- Description: (AC002505) SF16 like protein

[Arabidopsis thaliana]

- % Identity: 45
- Alignment Length: 373
- Location of Alignment in SEQ ID NO 375: from 1 to

297

Maximum Length Sequence:

related to:

Clone IDs:

14564

Public Genomic DNA:

gi No: 4415905

Predicted Exons:

INTR	3235	...	3181	OCKHAMG-CDNA
INTR	2694	...	2619	OCKHAMG-CDNA
INTR	2509	...	2408	OCKHAMG-CDNA
INTR	2319	...	2171	OCKHAMG-CDNA
INTR	2076	...	1784	OCKHAMG-CDNA

235

5 INIT 3191 ... 3181 OCKHAMG-CDS
 INTR 2694 ... 2619 OCKHAMG-CDS
 INTR 2509 ... 2408 OCKHAMG-CDS
 INTR 2319 ... 2171 OCKHAMG-CDS
 TERM 2076 ... 1920 OCKHAMG-CDS
 gi No: 4581138
 Predicted Exons:
 10 INTR 100911... 100857 OCKHAMG-CDNA
 INTR 100370... 100295 OCKHAMG-CDNA
 INTR 100185... 100084 OCKHAMG-CDNA
 INTR 99995 ... 99847 OCKHAMG-CDNA
 INTR 99752 ... 99460 OCKHAMG-CDNA
 15 INIT 100867... 100857 OCKHAMG-CDS
 INTR 100370... 100295 OCKHAMG-CDS
 INTR 100185... 100084 OCKHAMG-CDS
 INTR 99995 ... 99847 OCKHAMG-CDS
 TERM 99752 ... 99596 OCKHAMG-CDS
 20 (Ac) cDNA Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 376
 - Ceres seq_id 2025524
 - Alternative transcription start site(s) located in SEQ
 ID NO 376:
 25 -35,-26,-25,-2,2,3,4,5,6,7,8,9,15,16,17,32

 (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 377
 - Ceres seq_id 2025525
 30 - Location of start within SEQ ID NO 376: at 47 nt.

 (C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)
 - Ribosomal protein L24e
 35 - Location within SEQ ID NO 377: from 3 to 73 aa.

 (Dp) Related Amino Acid Sequences
 - Alignment No. 248
 - gi No. 6094040
 40 - Description: 60S RIBOSOMAL PROTEIN L24
 >gi|2961300|emb|CAA12358| (AJ225027) ribosomal protein L24
 [Cicer arietinum]
 - % Identity: 88.3
 - Alignment Length: 163
 45 - Location of Alignment in SEQ ID NO 377: from 1 to
 163

 (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 378
 50 - Ceres seq_id 2025526
 - Location of start within SEQ ID NO 376: at 212 nt.

236

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

5 - Alignment No. 249

- gi No. 6094040

- Description: 60S RIBOSOMAL PROTEIN L24

>gi|2961300|emb|CAA12358| (AJ225027) ribosomal protein L24
[Cicer arietinum]

10 - % Identity: 88.3

- Alignment Length: 163

- Location of Alignment in SEQ ID NO 378: from 1 to
108

15 Maximum Length Sequence:

related to:

Clone IDs:

20767

Public Genomic DNA:

20 gi No: 4519195

Predicted Exons:

INIT 50757 ... 50625 OCKHAMG-CDS

INTR 50001 ... 49847 OCKHAMG-CDS

INTR 49644 ... 49561 OCKHAMG-CDS

25 INTR 49391 ... 49236 OCKHAMG-CDS

INTR 49128 ... 49023 OCKHAMG-CDS

TERM 48810 ... 48662 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 379

30 - Ceres seq_id 2025544

- Alternative transcription start site(s) located in SEQ
ID NO 379:

656,672,680,685,701,703,706,709,713,717,728,736,741,743

35 - Clone 20767 starts at 656 and ends at 1623 in cDNA.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 380

- Ceres seq_id 2025545

40 - Location of start within SEQ ID NO 379: at 599 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Domain of unknown function

45 - Location within SEQ ID NO 380: from 134 to 247
aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 250

50 - gi No. 1708292

237

- Description: HEAT-RESPONSIVE PROTEIN 12
>gi|1255116 (U50631) heat-responsive protein [Mus musculus]
- % Identity: 54.3
- Alignment Length: 129
5 - Location of Alignment in SEQ ID NO 380: from 119
to 247

(B) Polypeptide Sequence

10 - Pat. Appln. SEQ ID NO 381
- Ceres seq_id 2025546
- Location of start within SEQ ID NO 379: at 1 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 381: at 50 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

15 - Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 381: from 171 to 211
aa.

(Dp) Related Amino Acid Sequences

20 - Alignment No. 251
- gi No. 2435518
- Description: (AF024504) contains similarity to
25 C3HC4-type zinc fingers [Arabidopsis thaliana]
- % Identity: 31.4
- Alignment Length: 221
- Location of Alignment in SEQ ID NO 381: from 35
to 211

(B) Polypeptide Sequence

30 - Pat. Appln. SEQ ID NO 382
- Ceres seq_id 2025547
- Location of start within SEQ ID NO 379: at 16 nt.
35 - Location of Signal Peptide Cleavage Site within SEQ
ID NO 382: at 45 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

40 - Zinc finger, C3HC4 type (RING finger)
- Location within SEQ ID NO 382: from 166 to 206
aa.

(Dp) Related Amino Acid Sequences

45 - Alignment No. 252
- gi No. 2435518
- Description: (AF024504) contains similarity to
C3HC4-type zinc fingers [Arabidopsis thaliana]
- % Identity: 31.4
50 - Alignment Length: 221

238

- Location of Alignment in SEQ ID NO 382: from 30
to 206

Maximum Length Sequence:

5 related to:

Clone IDs:

7802

Public Genomic DNA:

gi No: 441592C

10 Predicted Exons:

INTR 60672 ... 61210 OCKHAMG-CDNA

SINGLE 60712 ... 61119 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

15 - Pat. Appln. SEQ ID NO 383

- Ceres seq_id 2026207

- Alternative transcription start site(s) located in SEQ
ID NO 383:

2,3,4,5

20

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 384

- Ceres seq_id 2026208

- Location of start within SEQ ID NO 383: at 2 nt.

25

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 253

30 - gi No. 4757974

- Description: ref|NP_004057.1|pCETN1| centrin, EF-
hand protein, 1 >gi|2493440|sp|Q12798|CAT2_HUMAN CALTRACTIN,
ISOFORM 2 (CENTRIN) >gi|414993 (U03270) centrin [Homo
sapiens]

35

- % Identity: 34.3

- Alignment Length: 102

- Location of Alignment in SEQ ID NO 384: from 19
to 120

40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 385

- Ceres seq_id 2026209

- Location of start within SEQ ID NO 383: at 41 nt.

45

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 254

- gi No. 4757974

50

- Description: ref|NP_004057.1|pCETN1| centrin, EF-
hand protein, 1 >gi|2493440|sp|Q12798|CAT2_HUMAN CALTRACTIN,

239

ISOFORM 2 (CENTRIN) >gi|414993 (U03270) centrin [Homo sapiens]

- % Identity: 34.3

- Alignment Length: 102

- Location of Alignment in SEQ ID NO 385: from 6 to 107

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 386

- Ceres seq_id 2026210

- Location of start within SEQ ID NO 383: at 62 nt.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 255

- gi No. 4757974

- Description: ref|NP_004057.1|pCETN1| centrin, EF-hand protein, 1 >gi|2493440|sp|Q12798|CAT2_HUMAN CALTRACTIN, ISOFORM 2 (CENTRIN) >gi|414993 (U03270) centrin [Homo sapiens]

- % Identity: 34.3

- Alignment Length: 102

- Location of Alignment in SEQ ID NO 386: from 1 to 100

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4038029

Predicted Exons:

INIT	46188	...	46125	GENBANK
------	-------	-----	-------	---------

TERM	46021	...	45852	GENBANK
------	-------	-----	-------	---------

INTR	46258	...	46125	OCKHAMG-CDNA
------	-------	-----	-------	--------------

INTR	46021	...	45663	OCKHAMG-CDNA
------	-------	-----	-------	--------------

INIT	47157	...	47119	OCKHAMG-CDS
------	-------	-----	-------	-------------

INTR	46278	...	46125	OCKHAMG-CDS
------	-------	-----	-------	-------------

TERM	46021	...	45852	OCKHAMG-CDS
------	-------	-----	-------	-------------

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 387

- Ceres seq_id 2026982

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 388

- Ceres seq_id 2026983

- Location of start within SEQ ID NO 387: at 1 nt.

- Location of Signal Peptide Cleavage Site within SEQ ID NO 388: at 73 aa.

240

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Gamma-thionins family
- 5 - Location within SEQ ID NO 388: from 74 to 120 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 256
- gi No. 1209258
- 10 - Description: (L31937) protease inhibitor II
- [Brassica rapa]
- % Identity: 87
- Alignment Length: 77
- Location of Alignment in SEQ ID NO 388: from 44
- 15 to 120

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 389
- Ceres seq_id 2026984
- 20 - Location of start within SEQ ID NO 387: at 34 nt.
- Location of Signal Peptide Cleavage Site within SEQ
- ID NO 389: at 54 aa.

(C) Nomination and Annotation of Domains within
25 Predicted Polypeptide(s)

- Gamma-thionins family
- Location within SEQ ID NO 389: from 63 to 109 aa.

(Dp) Related Amino Acid Sequences

- 30 - Alignment No. 257
- gi No. 1209258
- Description: (L31937) protease inhibitor II
- [Brassica rapa]
- % Identity: 87
- 35 - Alignment Length: 77
- Location of Alignment in SEQ ID NO 389: from 33
- to 109

(B) Polypeptide Sequence

- 40 - Pat. Appln. SEQ ID NO 390
- Ceres seq_id 2026985
- Location of start within SEQ ID NO 387: at 130 nt.
- Location of Signal Peptide Cleavage Site within SEQ
- ID NO 390: at 22 aa.

(C) Nomination and Annotation of Domains within
45 Predicted Polypeptide(s)

- Gamma-thionins family
- Location within SEQ ID NO 390: from 31 to 77 aa.

50

(Dp) Related Amino Acid Sequences

241

- Alignment No. 258
- gi No. 1209258
- Description: (L31937) protease inhibitor II

[Brassica rapa]

- % Identity: 87
- Alignment Length: 77
- Location of Alignment in SEQ ID NO 390: from 1 to

77

10 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 391
- Ceres seq_id 2026986
- Location of start within SEQ ID NO 387: at 30 nt.

15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
(Dp) Related Amino Acid Sequences

Maximum Length Sequence:

20 related to:

Clone IDs:

251127

Public Genomic DNA:

gi No: 4220640

25 Predicted Exons:

INIT	67833	...	68135	OCKHAMG-CDS
INTR	68253	...	68366	OCKHAMG-CDS
INTR	68457	...	68552	OCKHAMG-CDS
INTR	68720	...	68794	OCKHAMG-CDS
INTR	68898	...	68965	OCKHAMG-CDS
INTR	69056	...	69066	OCKHAMG-CDS
INTR	69422	...	69624	OCKHAMG-CDS
INTR	69858	...	70202	OCKHAMG-CDS
INTR	70315	...	70428	OCKHAMG-CDS
INTR	70516	...	70611	OCKHAMG-CDS
INTR	70923	...	70997	OCKHAMG-CDS
INTR	71103	...	71173	OCKHAMG-CDS
TERM	71737	...	71749	OCKHAMG-CDS

40 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 392
- Ceres seq_id 2027300
- Alternative transcription start site(s) located in SEQ ID NO 392:
38, 53, 55, 63, 82, 84, 85, 103, 160

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 393
- Ceres seq_id 2027301
- Location of start within SEQ ID NO 392: at 177 nt.

50

242

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 259

- gi No. 5020103

- Description: (AF148219) fibrillin [Nostoc

PCC8009]

- % Identity: 30.3

- Alignment Length: 122

- Location of Alignment in SEQ ID NO 393: from 75
to 189

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 394

- Ceres seq_id 2027302

- Location of start within SEQ ID NO 392: at 213 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 260

- gi No. 5020103

- Description: (AF148219) fibrillin [Nostoc

PCC8009]

- % Identity: 30.3

- Alignment Length: 122

- Location of Alignment in SEQ ID NO 394: from 63
to 177

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 395

- Ceres seq_id 2027303

- Location of start within SEQ ID NO 392: at 252 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 261

- gi No. 5020103

- Description: (AF148219) fibrillin [Nostoc

PCC8009]

- % Identity: 30.3

- Alignment Length: 122

- Location of Alignment in SEQ ID NO 395: from 50
to 164

Maximum Length Sequence:

related to:

Clone IDs:

271260

Public Genomic DNA:

243

gi No: 6056186

Predicted Exons:

INIT 66600 ... 66465 OCKHAMG-CDS

TERM 66390 ... 66083 OCKHAMG-CDS

gi No: 6087919

Predicted Exons:

INIT 31657 ... 31522 OCKHAMG-CDS

TERM 31447 ... 31140 OCKHAMG-CDS

gi No: 6119514

Predicted Exons:

INIT 32265 ... 32130 OCKHAMG-CDS

TERM 32055 ... 31748 OCKHAMG-CDS

gi No: 6143857

Predicted Exons:

INIT 34633 ... 34768 OCKHAMG-CDS

TERM 34843 ... 35150 OCKHAMG-CDS

gi No: 6175136

Predicted Exons:

INIT 34136 ... 34271 OCKHAMG-CDS

TERM 34346 ... 34653 OCKHAMG-CDS

gi No: 6223634

Predicted Exons:

INIT 34137 ... 34272 OCKHAMG-CDS

TERM 34347 ... 34654 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 396

- Ceres seq_id 2027375

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 397

- Ceres seq_id 2027376

- Location of start within SEQ ID NO 396: at 2 nt.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

- Bacterial mutT protein

- Location within SEQ ID NO 397: from 27 to 68 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 262

- gi No. 2622420

- Description: (AE000895) mutator MutT protein

[Methanobacterium thermoautotrophicum]

- % Identity: 42.3

- Alignment Length: 98

- Location of Alignment in SEQ ID NO 397: from 13

to 109

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 398

244

- Ceres seq_id 2027377
- Location of start within SEQ ID NO 396: at 17 nt.

- (C) Nomination and Annotation of Domains within
 5 Predicted Polypeptide(s)
 - Bacterial mutT protein
 - Location within SEQ ID NO 398: from 22 to 63 aa.

- (Dp) Related Amino Acid Sequences
 10 - Alignment No. 263
 - gi No. 2622420
 - Description: (AE000895) mutator MutT protein
 [Methanobacterium thermoautotrophicum]
 - % Identity: 42.3
 15 - Alignment Length: 98
 - Location of Alignment in SEQ ID NO 398: from 8 to
 104

- (B) Polypeptide Sequence
 20 - Pat. Appln. SEQ ID NO 399
 - Ceres seq_id 2027378
 - Location of start within SEQ ID NO 396: at 188 nt.

- (C) Nomination and Annotation of Domains within
 25 Predicted Polypeptide(s)
 (Dp) Related Amino Acid Sequences
 - Alignment No. 264
 - gi No. 2622420
 - Description: (AE000895) mutator MutT protein
 30 [Methanobacterium thermoautotrophicum]
 - % Identity: 42.3
 - Alignment Length: 98
 - Location of Alignment in SEQ ID NO 399: from 1 to
 47

- 35 Maximum Length Sequence:
 Public Genomic DNA:
 gi No: 5868932
 Predicted Exons:
 40 INIT 99857 ... 96712 GENBANK
 INTR 96123 ... 95883 GENBANK
 TERM 95642 ... 95199 GENBANK

 INTR 96097 ... 95883 OCKHAMG-CDNA
 45 INTR 95642 ... 95047 OCKHAMG-CDNA

 INIT 96035 ... 95883 OCKHAMG-CDS
 TERM 95642 ... 95199 OCKHAMG-CDS

- 50 (Ac) cDNA Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 400

245

- Ceres seq_id 2028729

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 401
- Ceres seq_id 2028730
- Location of start within SEQ ID NO 400: at 1 nt.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

- C2 domain
- Location within SEQ ID NO 401: from 671 to 762

aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 265
- gi No. 3142295
- Description: (AC002411) Strong similarity to phosphoribosylanthranilate transferase gb|D86180 from *Pisum sativum*. [*Arabidopsis thaliana*]
- % Identity: 45.6
- Alignment Length: 865
- Location of Alignment in SEQ ID NO 401: from 211 to 1050

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 402
- Ceres seq_id 2028731
- Location of start within SEQ ID NO 400: at 199 nt.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

- C2 domain
- Location within SEQ ID NO 402: from 605 to 696

aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 266
- gi No. 3142295
- Description: (AC002411) Strong similarity to phosphoribosylanthranilate transferase gb|D86180 from *Pisum sativum*. [*Arabidopsis thaliana*]
- % Identity: 45.6
- Alignment Length: 865
- Location of Alignment in SEQ ID NO 402: from 145 to 984

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 403
- Ceres seq_id 2028732
- Location of start within SEQ ID NO 400: at 232 nt.

246

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- C2 domain

5 - Location within SEQ ID NO 403: from 594 to 685
aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 267

10 - gi No. 3142295

- Description: (AC002411) Strong similarity to
phosphoribosylanthranilate transferase gb|D86180 from *Pisum*
sativum. [*Arabidopsis thaliana*]

- % Identity: 45.6

15 - Alignment Length: 865

- Location of Alignment in SEQ ID NO 403: from 134
to 973

Maximum Length Sequence:

20 related to:

Clone IDs:

9214

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 404

25 - Ceres seq_id 2029079

- Alternative transcription start site(s) located in SEQ
ID NO 404:

-4,-1,2,3,4,8,9,10,11,14,15,16,17,18,20,23,24

30 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 405

- Ceres seq_id 2029080

- Location of start within SEQ ID NO 404: at 3 nt.

35 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 268

- gi No. 132825

40 - Description: 50S RIBOSOMAL PROTEIN CL25,
CHLOROPLAST PRECURSOR >gi|71308|pir||R5PM25 ribosomal protein
PsCL25 precursor, chloroplast - garden pea
>gi|20877|emb|CAA32187| (X14022) PsCL25 ribosomal preprotein
(AA -30 to 74) [*Pisum sativum*]

45 - % Identity: 56.1

- Alignment Length: 82

- Location of Alignment in SEQ ID NO 405: from 14
to 95

50 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 406

247

- Ceres seq_id 2029081
- Location of start within SEQ ID NO 404: at 39 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 406: at 16 aa.

5 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 269
- 10 - gi No. 132825
- Description: 50S RIBOSOMAL PROTEIN CL25,
CHLOROPLAST PRECURSOR >gi|71308|pir||R5PM25 ribosomal protein
PsCL25 precursor, chloroplast - garden pea
>gi|20877|emb|CAA32187| (X14022) PsCL25 ribosomal preprotein
- 15 (AA -30 to 74) [Pisum sativum]
- % Identity: 56.1
- Alignment Length: 82
- Location of Alignment in SEQ ID NO 406: from 2 to

83

20 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 407
- Ceres seq_id 2029082
- Location of start within SEQ ID NO 404: at 144 nt.

25 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 270
- 30 - gi No. 132825
- Description: 50S RIBOSOMAL PROTEIN CL25,
CHLOROPLAST PRECURSOR >gi|71308|pir||R5PM25 ribosomal protein
PsCL25 precursor, chloroplast - garden pea
>gi|20877|emb|CAA32187| (X14022) PsCL25 ribosomal preprotein
- 35 (AA -30 to 74) [Pisum sativum]
- % Identity: 56.1
- Alignment Length: 82
- Location of Alignment in SEQ ID NO 407: from 1 to

48

40 Maximum Length Sequence:
Public Genomic DNA:

gi No: 6434227

Predicted Exons:

45	INTR	50076 ... 50370	OCKHAMG-CDNA
	INTR	50793 ... 50874	OCKHAMG-CDNA
	INTR	51163 ... 51227	OCKHAMG-CDNA
	INTR	51331 ... 51417	OCKHAMG-CDNA
	INTR	51529 ... 51786	OCKHAMG-CDNA
50	INIT	50200 ... 50370	OCKHAMG-CDS

248

INTR	50793	...	50874	OCKHAMG-CDS
INTR	51163	...	51227	OCKHAMG-CDS
INTR	51331	...	51417	OCKHAMG-CDS
TERM	51529	...	51630	OCKHAMG-CDS

5

(Ac) cDNA Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 408
 - Ceres seq_id 2029225

10

(B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 409
 - Ceres seq_id 2029226
 - Location of start within SEQ ID NO 408: at 125 nt.

15

(C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

20

- Alignment No. 271

- gi No. 1352051

- Description: ATP SYNTHASE D CHAIN, MITOCHONDRIAL

>gi|484646|pir||JS0739 H⁺-transporting ATP synthase (EC
 3.6.1.34) chain d precursor - rat >gi|286204|dbj|BAA02422|
 (D13120) ATP synthase subunit d precursor [Rattus norvegicus]

25

- % Identity: 28.6

- Alignment Length: 145

- Location of Alignment in SEQ ID NO 409: from 15

to 154

30

(B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 410
 - Ceres seq_id 2029227
 - Location of start within SEQ ID NO 408: at 194 nt.

35

(C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 272

- gi No. 1352051

40

- Description: ATP SYNTHASE D CHAIN, MITOCHONDRIAL

>gi|484646|pir||JS0739 H⁺-transporting ATP synthase (EC
 3.6.1.34) chain d precursor - rat >gi|286204|dbj|BAA02422|
 (D13120) ATP synthase subunit d precursor [Rattus norvegicus]

45

- % Identity: 28.6

- Alignment Length: 145

- Location of Alignment in SEQ ID NO 410: from 1 to

131

Maximum Length Sequence:

50

Public Genomic DNA:

gi No: 6056185

249

Predicted Exons:

INTR 21555 ... 22692 OCKHAMG-CDNA
 INTR 22891 ... 23339 OCKHAMG-CDNA

5 INTR 22502 ... 22692 OCKHAMG-CDNA
 INTR 22891 ... 23338 OCKHAMG-CDNA

INIT 21706 ... 22692 OCKHAMG-CDS
 TERM 22891 ... 23124 OCKHAMG-CDS

10 gi No: 6091703

Predicted Exons:

INTR 21555 ... 22692 OCKHAMG-CDNA
 INTR 22891 ... 23339 OCKHAMG-CDNA

15 INTR 22502 ... 22692 OCKHAMG-CDNA
 INTR 22891 ... 23338 OCKHAMG-CDNA

INIT 21706 ... 22692 OCKHAMG-CDS
 TERM 22891 ... 23124 OCKHAMG-CDS

20

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 411
- Ceres seq_id 2029422

25

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 412
- Ceres seq_id 2029423
- Location of start within SEQ ID NO 411: at 152 nt.

30

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

- CONSTANS family zinc finger
- Location within SEQ ID NO 412: from 17 to 57 aa.

35

(Dp) Related Amino Acid Sequences

- Alignment No. 273
- gi No. 1076301
- Description: CONSTANS protein - Arabidopsis

40 thaliana >gi|1161514|emb|CAA64407| (X94937) CONSTANS protein
 [Arabidopsis thaliana]

- % Identity: 49.2
- Alignment Length: 63
- Location of Alignment in SEQ ID NO 412: from 12

45 to 74

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 413
- Ceres seq_id 2029424
- Location of start within SEQ ID NO 411: at 155 nt.

50

250

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- CONSTANS family zinc finger
- Location within SEQ ID NO 413: from 16 to 56 aa.

5

(Dp) Related Amino Acid Sequences

- Alignment No. 274
- gi No. 1076301
- Description: CONSTANS protein - Arabidopsis
- 10 thaliana >gi|1161514|emb|CAA64407| (X94937) CONSTANS protein
- [Arabidopsis thaliana]
- % Identity: 49.2
- Alignment Length: 63
- Location of Alignment in SEQ ID NO 413: from 11

15 to 73

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 414
- Ceres seq_id 2029425
- 20 - Location of start within SEQ ID NO 411: at 443 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 25 - Alignment No. 275
- gi No. 1076301
- Description: CONSTANS protein - Arabidopsis
- thaliana >gi|1161514|emb|CAA64407| (X94937) CONSTANS protein
- [Arabidopsis thaliana]
- 30 - % Identity: 69.8
- Alignment Length: 43
- Location of Alignment in SEQ ID NO 414: from 260
- to 302

35 Maximum Length Sequence:

Public Genomic DNA:

gi No: 5832738

Predicted Exons:

40	INTR	56241 ... 56150	OCKHAMG-CDNA
	INTR	56041 ... 55864	OCKHAMG-CDNA
	INTR	55493 ... 55317	OCKHAMG-CDNA
	INTR	55216 ... 55085	OCKHAMG-CDNA
	INTR	54898 ... 54803	OCKHAMG-CDNA
	INTR	54725 ... 54609	OCKHAMG-CDNA
45	INTR	54510 ... 54415	OCKHAMG-CDNA
	INTR	54288 ... 54176	OCKHAMG-CDNA
	INTR	54077 ... 53779	OCKHAMG-CDNA
50	INIT	56181 ... 56150	OCKHAMG-CDS
	INTR	56041 ... 55864	OCKHAMG-CDS
	INTR	55493 ... 55317	OCKHAMG-CDS

251

INTR	55216	...	55085	OCKHAMG-CDS
INTR	54898	...	54803	OCKHAMG-CDS
INTR	54725	...	54609	OCKHAMG-CDS
INTR	54510	...	54415	OCKHAMG-CDS
INTR	54288	...	54176	OCKHAMG-CDS
TERM	54077	...	53954	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 415

- Ceres seq_id 2029806

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 416

- Ceres seq_id 2029807

- Location of start within SEQ ID NO 415: at 1 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Aminotransferase class IV

- Location within SEQ ID NO 416: from 68 to 352 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 276

- gi No. 3540183

- Description: (AC004122) Highly Similar to
branched-chain amino acid aminotransferase [Arabidopsis
thaliana]

- % Identity: 53.8

- Alignment Length: 318

- Location of Alignment in SEQ ID NO 416: from 55
to 371

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 417

- Ceres seq_id 2029808

- Location of start within SEQ ID NO 415: at 61 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Aminotransferase class IV

- Location within SEQ ID NO 417: from 48 to 332 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 277

- gi No. 3540183

- Description: (AC004122) Highly Similar to
branched-chain amino acid aminotransferase [Arabidopsis
thaliana]

- % Identity: 53.8

- Alignment Length: 318

252

- Location of Alignment in SEQ ID NO 417: from 35
to 351

(B) Polypeptide Sequence

- 5 - Pat. Appln. SEQ ID NO 418
 - Ceres seq_id 2029809
 - Location of start within SEQ ID NO 415: at 163 nt.

10 (C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)

- Aminotransferase class IV
 - Location within SEQ ID NO 418: from 14 to 298 aa.

(Dp) Related Amino Acid Sequences

- 15 - Alignment No. 278
 - gi No. 3540183
 - Description: (AC004122) Highly Similar to
brached-chain amino acid aminotransferase [Arabidopsis
thaliana]
20 - % Identity: 53.8
 - Alignment Length: 318
 - Location of Alignment in SEQ ID NO 418: from 1 to
317

25 Maximum Length Sequence:

Public Genomic DNA:

gi No: 5822667

Predicted Exons:

30 INTR 59013 ... 59999 OCKHAMG-CDNA

 SINGLE 59071 ... 59769 OCKHAMG-CDS

gi No: 6041831

Predicted Exons:

35 INTR 53943 ... 54929 OCKHAMG-CDNA

 SINGLE 54001 ... 54699 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- 40 - Pat. Appln. SEQ ID NO 419
 - Ceres seq_id 2030038

(B) Polypeptide Sequence

- 45 - Pat. Appln. SEQ ID NO 420
 - Ceres seq_id 2030039
 - Location of start within SEQ ID NO 419: at 2 nt.

50 (C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 279

253

aureus]

- gi No. 4009495
- Description: (AF068904) YlmG [Staphylococcus
- % Identity: 31.7
- Alignment Length: 63
- Location of Alignment in SEQ ID NO 420: from 177

to 239

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 421
- Ceres seq_id 2030040
- Location of start within SEQ ID NO 419: at 59 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 421: at 19 aa.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 280
- gi No. 4009495
- Description: (AF068904) YlmG [Staphylococcus
- % Identity: 31.7
- Alignment Length: 63
- Location of Alignment in SEQ ID NO 421: from 158

to 220

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4539290

Predicted Exons:

INIT	6134	...	6132	GENBANK
INTR	6021	...	5973	GENBANK
INTR	5588	...	5309	GENBANK
INTR	5226	...	5106	GENBANK
TERM	4951	...	4871	GENBANK
INTR	6208	...	6132	OCKHAMG-CDNA
INTR	6021	...	5973	OCKHAMG-CDNA
INTR	5588	...	5309	OCKHAMG-CDNA
INTR	5226	...	5106	OCKHAMG-CDNA
INTR	4951	...	4724	OCKHAMG-CDNA
INIT	6134	...	6132	OCKHAMG-CDS
INTR	6021	...	5973	OCKHAMG-CDS
INTR	5588	...	5309	OCKHAMG-CDS
INTR	5226	...	5106	OCKHAMG-CDS
TERM	4951	...	4871	OCKHAMG-CDS

gi No: 4914454

Predicted Exons:

INTR	39557	...	39481	OCKHAMG-CDNA
------	-------	-----	-------	--------------

254
INTR 39370 ... 39322 OCKHAMG-CDNA
INTR 38937 ... 38658 OCKHAMG-CDNA
INTR 38575 ... 38455 OCKHAMG-CDNA
INTR 38300 ... 38073 OCKHAMG-CDNA

5

(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 422
- Ceres seq_id 2031778

10

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 423
- Ceres seq_id 2031779
- Location of start within SEQ ID NO 422: at 3 nt.

15

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

20

- Alignment No. 281
- gi No. 3688432
- Description: (AJ011705) 40S ribosomal protein S10
[Lumbricus rubellus]

25

- % Identity: 53.1
- Alignment Length: 164
- Location of Alignment in SEQ ID NO 423: from 25
to 186

30

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 424
- Ceres seq_id 2031780
- Location of start within SEQ ID NO 422: at 75 nt.

35

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 282
- gi No. 3688432
- Description: (AJ011705) 40S ribosomal protein S10
[Lumbricus rubellus]

40

- % Identity: 53.1
- Alignment Length: 164
- Location of Alignment in SEQ ID NO 424: from 1 to

162

45

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 425
- Ceres seq_id 2031781
- Location of start within SEQ ID NO 422: at 210 nt.

50

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

255

(Dp) Related Amino Acid Sequences

- Alignment No. 283
- gi No. 3688432
- Description: (AJ011705) 40S ribosomal protein S10
- % Identity: 53.1
- Alignment Length: 164
- Location of Alignment in SEQ ID NO 425: from 1 to

117

Maximum Length Sequence:

Public Genomic DNA:

gi No: 6434226

Predicted Exons:

INTR	17873 ... 17514	OCKHAMG-CDNA
INTR	17046 ... 16869	OCKHAMG-CDNA
INIT	17854 ... 17514	OCKHAMG-CDS
TERM	17046 ... 17028	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 426
- Ceres seq_id 2032723

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 427
- Ceres seq_id 2032724
- Location of start within SEQ ID NO 426: at 20 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 427: at 24 aa.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Plant lipid transfer protein family
- Location within SEQ ID NO 427: from 28 to 115 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 284
- gi No. 899224
- Description: (X60318) E2 [Brassica napus]
- % Identity: 79
- Alignment Length: 119
- Location of Alignment in SEQ ID NO 427: from 1 to

119

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 428
- Ceres seq_id 2032725

256

- Location of start within SEQ ID NO 426: at 71 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 5 - Plant lipid transfer protein family
 - Location within SEQ ID NO 428: from 11 to 98 aa.

(Dp) Related Amino Acid Sequences

- 10 - Alignment No. 285
 - gi No. 899224
 - Description: (X60318) E2 [Brassica napus]
>gi|384340|prf||1905428A phospholipid transfer protein
[Brassica napus]
15 - % Identity: 79
 - Alignment Length: 119
 - Location of Alignment in SEQ ID NO 428: from 1 to
102

(B) Polypeptide Sequence

- 20 - Pat. Appln. SEQ ID NO 429
 - Ceres seq_id 2032726
 - Location of start within SEQ ID NO 426: at 1 nt.

(C) Nomination and Annotation of Domains within
25 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

Maximum Length Sequence:

Public Genomic DNA:

- 30 gi No: 6143856
 Predicted Exons:
 INIT 30571 ... 30464 OCKHAMG-CDS
 TERM 30327 ... 30238 OCKHAMG-CDS
 gi No: 6223633
35 Predicted Exons:
 INIT 30571 ... 30464 OCKHAMG-CDS
 TERM 30327 ... 30238 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- 40 - Pat. Appln. SEQ ID NO 430
 - Ceres seq_id 2035536

(B) Polypeptide Sequence

- 45 - Pat. Appln. SEQ ID NO 431
 - Ceres seq_id 2035537
 - Location of start within SEQ ID NO 430: at 1 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
ID NO 431: at 20 aa.

50

257

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 286

- gi No. 3024192

- Description: NADH-UBIQUINONE OXIDOREDUCTASE MWFE
SUBUNIT (COMPLEX I-MWFE) (CI-MWFE) >gi|2275037|emb|CAA68977|
(Y07708) NADH dehydrogenase [Mus musculus]

- % Identity: 31.5

- Alignment Length: 54

- Location of Alignment in SEQ ID NO 431: from 4 to

56

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 432

- Ceres seq_id 2035538

- Location of start within SEQ ID NO 430: at 2 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 433

- Ceres seq_id 2035539

- Location of start within SEQ ID NO 430: at 25 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 433: at 17 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 287

- gi No. 3024192

- Description: NADH-UBIQUINONE OXIDOREDUCTASE MWFE
SUBUNIT (COMPLEX I-MWFE) (CI-MWFE) >gi|2275037|emb|CAA68977|
(Y07708) NADH dehydrogenase [Mus musculus]

- % Identity: 31.5

- Alignment Length: 54

- Location of Alignment in SEQ ID NO 433: from 1 to

48

Maximum Length Sequence:

Public Genomic DNA:

gi No: 6136357

Predicted Exons:

INIT	51922 ...	51830	OCKHAMG-CDS
INTR	51129 ...	51055	OCKHAMG-CDS
INTR	50958 ...	50806	OCKHAMG-CDS
INTR	50706 ...	50608	OCKHAMG-CDS
TERM	50326 ...	50243	OCKHAMG-CDS

258

gi No: 6143858

Predicted Exons:

	INIT	51922	...	51830	OCKHAMG-CDS
	INTR	51129	...	51055	OCKHAMG-CDS
5	INTR	50958	...	50806	OCKHAMG-CDS
	INTR	50706	...	50608	OCKHAMG-CDS
	TERM	50326	...	50243	OCKHAMG-CDS

gi No: 6449510

Predicted Exons:

10	INTR	9035	...	9111	OCKHAMG-CDNA
	INTR	9208	...	9360	OCKHAMG-CDNA
	INTR	9460	...	9558	OCKHAMG-CDNA
	INTR	9840	...	9992	OCKHAMG-CDNA

15 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 434

- Ceres seq_id 2035575

20 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 435

- Ceres seq_id 2035576

- Location of start within SEQ ID NO 434: at 1 nt.

25 (C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 288

- gi No. 6066609

30 - Description: (AJ009987) chloroplast channel

forming outer membrane protein [Pisum sativum]

- % Identity: 54.2

- Alignment Length: 177

- Location of Alignment in SEQ ID NO 435: from 1 to

35 167

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 436

- Ceres seq_id 2035577

40 - Location of start within SEQ ID NO 434: at 13 nt.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 289

- gi No. 6066609

45 - Description: (AJ009987) chloroplast channel

forming outer membrane protein [Pisum sativum]

- % Identity: 54.2

- Alignment Length: 177

50

259

- Location of Alignment in SEQ ID NO 436: from 1 to
163

(B) Polypeptide Sequence

- 5 - Pat. Appln. SEQ ID NO 437
 - Ceres seq_id 2035578
 - Location of start within SEQ ID NO 434: at 40 nt.

(C) Nomination and Annotation of Domains within
10 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 15 - Alignment No. 290
 - gi No. 6066609
 - Description: (AJ009987) chloroplast channel
forming outer membrane protein [Pisum sativum]
 - % Identity: 54.2
 - Alignment Length: 177
 - Location of Alignment in SEQ ID NO 437: from 1 to
154

Maximum Length Sequence:

Public Genomic DNA:

gi No: 6434213

Predicted Exons:

25 INIT 54056 ... 54085 OCKHAMG-CDS
 INTR 54178 ... 54325 OCKHAMG-CDS
 INTR 54401 ... 54572 OCKHAMG-CDS
 INTR 54807 ... 54993 OCKHAMG-CDS
30 TERM 55079 ... 55291 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- 35 - Pat. Appln. SEQ ID NO 438
 - Ceres seq_id 2036457

(B) Polypeptide Sequence

- 40 - Pat. Appln. SEQ ID NO 439
 - Ceres seq_id 2036458
 - Location of start within SEQ ID NO 438: at 1 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 45 - Ribosomal protein S3, C-terminal domain.
 - Location within SEQ ID NO 439: from 104 to 188
aa.

(Dp) Related Amino Acid Sequences

- 50 - Alignment No. 291
 - gi No. 133940
 - Description: 40S RIBOSOMAL PROTEIN S3A (S1A)
>gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed

260

frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a
[Xenopus laevis]

- % Identity: 75.1

- Alignment Length: 250

- Location of Alignment in SEQ ID NO 439: from 1 to

249

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 440

- Ceres seq_id 2036459

- Location of start within SEQ ID NO 438: at 130 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S3, C-terminal domain.

- Location within SEQ ID NO 440: from 61 to 145 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 292

- gi No. 133940

- Description: 40S RIBOSOMAL PROTEIN S3A (S1A)

>gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed
frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a
[Xenopus laevis]

- % Identity: 75.1

- Alignment Length: 250

- Location of Alignment in SEQ ID NO 440: from 1 to

206

Maximum Length Sequence:

Public Genomic DNA:

gi No: 6434218

Predicted Exons:

INIT	85292	...	85282	OCKHAMG-CDS
INTR	84903	...	84828	OCKHAMG-CDS
INTR	84730	...	84629	OCKHAMG-CDS
INTR	84524	...	84376	OCKHAMG-CDS
INTR	84282	...	84156	OCKHAMG-CDS
TERM	84148	...	84065	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 441

- Ceres seq_id 2036585

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 442

- Ceres seq_id 2036586

- Location of start within SEQ ID NO 441: at 1 nt.

261

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein L24e
- Location within SEQ ID NO 442: from 3 to 73 aa.

5

(Dp) Related Amino Acid Sequences

- Alignment No. 293
- gi No. 6094040
- Description: 60S RIBOSOMAL PROTEIN L24

10 >gi|2961300|emb|CAA12358| (AJ225027) ribosomal protein L24
[Cicer arietinum]

- % Identity: 86.6
- Alignment Length: 158
- Location of Alignment in SEQ ID NO 442: from 1 to

15 156

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 443
- Ceres seq_id 2036587
- Location of start within SEQ ID NO 441: at 166 nt.

20

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 294
- gi No. 6094040
- Description: 60S RIBOSOMAL PROTEIN L24

25 >gi|2961300|emb|CAA12358| (AJ225027) ribosomal protein L24
[Cicer arietinum]

- % Identity: 86.6
- Alignment Length: 158
- Location of Alignment in SEQ ID NO 443: from 1 to

30

101

35 Maximum Length Sequence:

Public Genomic DNA:

gi No: 5668776

Predicted Exons:

INIT	19552 ...	19704	OCKHAMG-CDS
TERM	19947 ...	20279	OCKHAMG-CDS

40

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 444
- Ceres seq_id 2039554

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 445
- Ceres seq_id 2039555
- Location of start within SEQ ID NO 444: at 1 nt.

50

262

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 295

- gi No. 5882720

- Description: (AC008263) Similar to gb|D86180
phosphoribosylanthranilate transferase from Pisum sativum and
contains 2 PF|00168 C2 (phospholipid binding) domains. ESTs
gb|H76726, gb|T45544 and gb|N96377 come from this gene.

[Arab...

- % Identity: 99.3

- Alignment Length: 151

- Location of Alignment in SEQ ID NO 445: from 1 to

151

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 446

- Ceres seq_id 2039556

- Location of start within SEQ ID NO 444: at 136 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 296

- gi No. 5882720

- Description: (AC008263) Similar to gb|D86180
phosphoribosylanthranilate transferase from Pisum sativum and
contains 2 PF|00168 C2 (phospholipid binding) domains. ESTs
gb|H76726, gb|T45544 and gb|N96377 come from this gene.

[Arab...

- % Identity: 99.3

- Alignment Length: 151

- Location of Alignment in SEQ ID NO 446: from 1 to

106

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4263586

Predicted Exons:

INIT	44660	...	44729	OCKHAMG-CDS
INTR	44822	...	44985	OCKHAMG-CDS
INTR	45066	...	45099	OCKHAMG-CDS
INTR	45171	...	45264	OCKHAMG-CDS
TERM	45352	...	45367	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 447

- Ceres seq_id 2044283

(B) Polypeptide Sequence

263

- Pat. Appln. SEQ ID NO 448
- Ceres seq_id 2044284
- Location of start within SEQ ID NO 447: at 1 nt.
- Location of Signal Peptide Cleavage Site within SEQ

5 ID NO 448: at 19 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 10 - Alignment No. 297
- gi No. 4512613
- Description: (AC004793) F28K20.12 [Arabidopsis
thaliana]
- % Identity: 99.2
- 15 - Alignment Length: 122
- Location of Alignment in SEQ ID NO 448: from 1 to
122

(B) Polypeptide Sequence

- 20 - Pat. Appln. SEQ ID NO 449
- Ceres seq_id 2044285
- Location of start within SEQ ID NO 447: at 13 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 25 - Alignment No. 298
- gi No. 4512613
- Description: (AC004793) F28K20.12 [Arabidopsis
30 thaliana]
- % Identity: 99.2
- Alignment Length: 122
- Location of Alignment in SEQ ID NO 449: from 1 to
118

(B) Polypeptide Sequence

- 35 - Pat. Appln. SEQ ID NO 450
- Ceres seq_id 2044286
- Location of start within SEQ ID NO 447: at 16 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 40 - Alignment No. 299
- 45 - gi No. 4512613
- Description: (AC004793) F28K20.12 [Arabidopsis
thaliana]
- % Identity: 99.2
- Alignment Length: 122
- 50 - Location of Alignment in SEQ ID NO 450: from 1 to
117

264

Maximum Length Sequence:

related to:

Clone IDs:

5 157859

Public Genomic DNA:

gi No: 4519187

Predicted Exons:

	INIT	64212 ... 64316	OCKHAMG-CDS
10	INTR	64435 ... 64599	OCKHAMG-CDS
	INTR	64655 ... 64789	OCKHAMG-CDS
	INTR	64869 ... 64952	OCKHAMG-CDS
	INTR	65028 ... 65143	OCKHAMG-CDS
	INTR	65245 ... 65346	OCKHAMG-CDS
15	INTR	65417 ... 65530	OCKHAMG-CDS
	INTR	65621 ... 65677	OCKHAMG-CDS
	INTR	65790 ... 65856	OCKHAMG-CDS
	INTR	65929 ... 65982	OCKHAMG-CDS
	INTR	66089 ... 66163	OCKHAMG-CDS
20	INTR	66558 ... 66593	OCKHAMG-CDS
	INTR	66699 ... 66811	OCKHAMG-CDS
	TERM	68086 ... 68098	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 451

25 - Ceres seq_id 2048114

- Alternative transcription start site(s) located in SEQ

ID NO 451:

456

- Clone 157859 starts at 456 and ends at in cDNA.

30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 452

- Ceres seq_id 2048115

- Location of start within SEQ ID NO 451: at 1 nt.

35 - Location of Signal Peptide Cleavage Site within SEQ

ID NO 452: at 34 aa.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

40 (Dp) Related Amino Acid Sequences

- Alignment No. 300

- gi No. 4850384

- Description: (AC007357) F3F19.3 [Arabidopsis
thaliana]

45 - % Identity: 66.2

- Alignment Length: 201

- Location of Alignment in SEQ ID NO 452: from 95
to 295

50 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 453

265

- Ceres seq_id 2048116
 - Location of start within SEQ ID NO 451: at 19 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
 ID NO 453: at 28 aa.

5

(C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

10 - Alignment No. 301
 - gi No. 4850384
 - Description: (AC007357) F3F19.3 [Arabidopsis
 thaliana]
 - % Identity: 66.2
 - Alignment Length: 201
 15 - Location of Alignment in SEQ ID NO 453: from 89
 to 289

(B) Polypeptide Sequence

20 - Pat. Appln. SEQ ID NO 454
 - Ceres seq_id 2048117
 - Location of start within SEQ ID NO 451: at 22 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
 ID NO 454: at 27 aa.

25 (C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

30 - Alignment No. 302
 - gi No. 4850384
 - Description: (AC007357) F3F19.3 [Arabidopsis
 thaliana]
 - % Identity: 66.2
 - Alignment Length: 201
 35 - Location of Alignment in SEQ ID NO 454: from 88
 to 288

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4519194

40 Predicted Exons:

INTR	15272	...	15482	OCKHAMG-CDNA
INTR	15570	...	15615	OCKHAMG-CDNA
INTR	16443	...	16834	OCKHAMG-CDNA

45	INIT	15350	...	15482	OCKHAMG-CDS
	INTR	15570	...	15615	OCKHAMG-CDS
	TERM	16443	...	16671	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

50 - Pat. Appln. SEQ ID NO 455
 - Ceres seq_id 2048271

266

(B) Polypeptide Sequence

- 5 - Pat. Appln. SEQ ID NO 456
 - Ceres seq_id 2048272
 - Location of start within SEQ ID NO 455: at 79 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 10 - Ribosomal protein S16
 - Location within SEQ ID NO 456: from 9 to 70 aa.

(Dp) Related Amino Acid Sequences

- 15 - Alignment No. 303
 - gi No. 3861401
 - Description: (AJ235273) 30S RIBOSOMAL PROTEIN S16
(rpsP) [Rickettsia prowazekii]
 - % Identity: 43.7
 - Alignment Length: 103
20 - Location of Alignment in SEQ ID NO 456: from 1 to
102

(B) Polypeptide Sequence

- 25 - Pat. Appln. SEQ ID NO 457
 - Ceres seq_id 2048273
 - Location of start within SEQ ID NO 455: at 139 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 30 - Ribosomal protein S16
 - Location within SEQ ID NO 457: from 1 to 50 aa.

(Dp) Related Amino Acid Sequences

- 35 - Alignment No. 304
 - gi No. 3861401
 - Description: (AJ235273) 30S RIBOSOMAL PROTEIN S16
(rpsP) [Rickettsia prowazekii]
 - % Identity: 43.7
 - Alignment Length: 103
40 - Location of Alignment in SEQ ID NO 457: from 1 to
82

(B) Polypeptide Sequence

- 45 - Pat. Appln. SEQ ID NO 458
 - Ceres seq_id 2048274
 - Location of start within SEQ ID NO 455: at 232 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- 50 (Dp) Related Amino Acid Sequences
 - Alignment No. 305

267

- gi No. 3861401
 - Description: (AJ235273) 30S RIBOSOMAL PROTEIN S16
 (rpsP) [Rickettsia prowazekii]
 - % Identity: 43.7
 - Alignment Length: 103
 - Location of Alignment in SEQ ID NO 458: from 1 to

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4519195

Predicted Exons:

INIT	48116	...	48096	OCKHAMG-CDS
INTR	48033	...	47989	OCKHAMG-CDS
INTR	47604	...	47531	OCKHAMG-CDS
INTR	47435	...	47386	OCKHAMG-CDS
TERM	47286	...	47192	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 459
 - Ceres seq_id 2048331

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 460
 - Ceres seq_id 2048332
 - Location of start within SEQ ID NO 459: at 1 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Domain of unknown function
 - Location within SEQ ID NO 460: from 8 to 92 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 306
 - gi No. 5032215
 - Description: ref|NP_005827.1|pUK114|
 translational inhibitor protein p14.5
 >gi|1717975|sp|P52758|UK14_HUMAN 14.5 KD TRANSLATIONAL
 INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN HOMOLOG)
 >gi|1177435|emb|CAA64670| sapiens]
 - % Identity: 58.8
 - Alignment Length: 85
 - Location of Alignment in SEQ ID NO 460: from 8 to

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 461
 - Ceres seq_id 2048333
 - Location of start within SEQ ID NO 459: at 79 nt.

268

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Domain of unknown function
- Location within SEQ ID NO 461: from 1 to 66 aa.

5

(Dp) Related Amino Acid Sequences

- Alignment No. 307
- gi No. 5032215
- Description: ref|NP_005827.1|pUK114|

10 translational inhibitor protein p14.5
>gi|1717975|sp|P52758|UK14_HUMAN 14.5 KD TRANSLATIONAL
INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN HOMOLOG)
>gi|1177435|emb|CAA64670| sapiens]

- % Identity: 58.8
- Alignment Length: 85
- Location of Alignment in SEQ ID NO 461: from 1 to
66

(B) Polypeptide Sequence

- 20 - Pat. Appln. SEQ ID NO 462
- Ceres seq_id 2048334
- Location of start within SEQ ID NO 459: at 139 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 308
- gi No. 5032215
- Description: ref|NP_005827.1|pUK114|

30 translational inhibitor protein p14.5
>gi|1717975|sp|P52758|UK14_HUMAN 14.5 KD TRANSLATIONAL
INHIBITOR PROTEIN (P14.5) (UK114 ANTIGEN HOMOLOG)
>gi|1177435|emb|CAA64670| sapiens]

- 35 - % Identity: 58.8
- Alignment Length: 85
- Location of Alignment in SEQ ID NO 462: from 1 to
46

Maximum Length Sequence:

40 Public Genomic DNA:

gi No: 4589412

Predicted Exons:

	INIT	37105	...	37091	OCKHAMG-CDS
	INTR	36413	...	36339	OCKHAMG-CDS
45	INTR	36224	...	36176	OCKHAMG-CDS
	INTR	35977	...	35698	OCKHAMG-CDS
	INTR	35603	...	35471	OCKHAMG-CDS
	TERM	35193	...	35119	OCKHAMG-CDS

50 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 463

269

- Ceres seq_id 2048466

(B) Polypeptide Sequence

- 5 - Pat. Appln. SEQ ID NO 464
 - Ceres seq_id 2048467
 - Location of start within SEQ ID NO 463: at 1 nt.

(C) Nomination and Annotation of Domains within
10 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 309
 - gi No. 3688432
 - Description: (AJ011705) 40S ribosomal protein S10
15 [Lumbricus rubellus]
 - % Identity: 50.6
 - Alignment Length: 164
 - Location of Alignment in SEQ ID NO 464: from 30
to 193

20 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 465
 - Ceres seq_id 2048468
 - Location of start within SEQ ID NO 463: at 4 nt.

25 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 310
30 - gi No. 3688432
 - Description: (AJ011705) 40S ribosomal protein S10
[Lumbricus rubellus]
 - % Identity: 50.6
 - Alignment Length: 164
35 - Location of Alignment in SEQ ID NO 465: from 29
to 192

(B) Polypeptide Sequence

- 40 - Pat. Appln. SEQ ID NO 466
 - Ceres seq_id 2048469
 - Location of start within SEQ ID NO 463: at 88 nt.

(C) Nomination and Annotation of Domains within
45 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 311
 - gi No. 3688432
 - Description: (AJ011705) 40S ribosomal protein S10
50 [Lumbricus rubellus]
 - % Identity: 50.6
 - Alignment Length: 164

270

- Location of Alignment in SEQ ID NO 466: from 1 to 164

Maximum Length Sequence:

- 5 Public Genomic DNA:
 gi No: 4914400
 Predicted Exons:
 INTR 97410 ... 97833 OCKHAMG-CDNA
- 10 SINGLE 97525 ... 97797 OCKHAMG-CDS
 gi No: 4938473
 Predicted Exons:
 SINGLE 9769 ... 10041 GENBANK
- 15 INTR 9654 ... 10078 OCKHAMG-CDNA
 INTR 10721 ... 10880 OCKHAMG-CDNA
 SINGLE 9769 ... 10041 OCKHAMG-CDS
- 20 (Ac) cDNA Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 467
 - Ceres seq_id 2050485
- 25 (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 468
 - Ceres seq_id 2050486
 - Location of start within SEQ ID NO 467: at 2 nt.
- 30 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
 (Dp) Related Amino Acid Sequences
 - Alignment No. 312
 - gi No. 2493089
- 35 - Description: ATP SYNTHASE F CHAIN, MITOCHONDRIAL
 - % Identity: 29.7
 - Alignment Length: 77
 - Location of Alignment in SEQ ID NO 468: from 52
to 125
- 40 (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 469
 - Ceres seq_id 2050487
 - Location of start within SEQ ID NO 467: at 116 nt.
- 45 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
 (Dp) Related Amino Acid Sequences
 - Alignment No. 313
 - gi No. 2493089
- 50 - Description: ATP SYNTHASE F CHAIN, MITOCHONDRIAL

271

- % Identity: 29.7
- Alignment Length: 77
- Location of Alignment in SEQ ID NO 469: from 14

to 87

5

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4454022

Predicted Exons:

10 INIT 55210 ... 55024 GENBANK
 TERM 54477 ... 54209 GENBANK

 INTR 55270 ... 55024 OCKHAMG-CDNA
 INTR 54477 ... 54299 OCKHAMG-CDNA

15 INIT 55210 ... 55024 OCKHAMG-CDS
 TERM 54477 ... 54209 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- 20 - Pat. Appln. SEQ ID NO 470
 - Ceres seq_id 2050708

(B) Polypeptide Sequence

- 25 - Pat. Appln. SEQ ID NO 471
 - Ceres seq_id 2050709
 - Location of start within SEQ ID NO 470: at 61 nt.

(C) Nomination and Annotation of Domains within

30 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 314
 - gi No. 2129641
 - Description: major latex protein type 1 -
- 35 Arabidopsis thaliana >gi|1107493|emb|CAA63026| (X91960) major
 latex protein type1 [Arabidopsis thaliana]
 - % Identity: 71.3
 - Alignment Length: 150
 - Location of Alignment in SEQ ID NO 471: from 1 to

40 150

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4914454

Predicted Exons:

45 INTR 42446 ... 41456 OCKHAMG-CDS
 INTR 40358 ... 40280 OCKHAMG-CDS
 INTR 39551 ... 39481 OCKHAMG-CDS
 INTR 39415 ... 39322 OCKHAMG-CDS

50 INTR 39280 ... 39268 OCKHAMG-CDS
 INTR 38937 ... 38658 OCKHAMG-CDS

272

INTR	38575 ... 38455	OCKHAMG-CDS
TERM	38300 ... 38220	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- 5 - Pat. Appln. SEQ ID NO 472
 - Ceres seq_id 2050901

(B) Polypeptide Sequence

- 10 - Pat. Appln. SEQ ID NO 473
 - Ceres seq_id 2050902
 - Location of start within SEQ ID NO 472: at 3 nt.

(C) Nomination and Annotation of Domains within
 15 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 20 - Alignment No. 315
 - gi No. 3688432
 - Description: (AJ011705) 40S ribosomal protein S10
 [Lumbricus rubellus]
 - % Identity: 53.1
 - Alignment Length: 147
 - Location of Alignment in SEQ ID NO 473: from 416
 to 560

(B) Polypeptide Sequence

- 25 - Pat. Appln. SEQ ID NO 474
 - Ceres seq_id 2050903
 - Location of start within SEQ ID NO 472: at 123 nt.

(C) Nomination and Annotation of Domains within
 30 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 35 - Alignment No. 316
 - gi No. 3688432
 - Description: (AJ011705) 40S ribosomal protein S10
 [Lumbricus rubellus]
 - % Identity: 53.1
 - Alignment Length: 147
 - Location of Alignment in SEQ ID NO 474: from 376
 to 520

(B) Polypeptide Sequence

- 45 - Pat. Appln. SEQ ID NO 475
 - Ceres seq_id 2050904
 - Location of start within SEQ ID NO 472: at 678 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
 ID NO 475: at 39 aa.

50 (C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)

273

(Dp) Related Amino Acid Sequences

- Alignment No. 317
- gi No. 3688432
- Description: (AJ011705) 40S ribosomal protein S10

5 [Lumbricus rubellus]

- % Identity: 53.1
- Alignment Length: 147
- Location of Alignment in SEQ ID NO 475: from 191

to 335

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4725940

Predicted Exons:

15 SINGLE 96089 ... 95736 GENBANK

INTR 96156 ... 95622 OCKHAMG-CDNA

SINGLE 96083 ... 95736 OCKHAMG-CDS

20 gi No: 5823567

Predicted Exons:

SINGLE 96089 ... 95736 GENBANK

INTR 96156 ... 95622 OCKHAMG-CDNA

25 SINGLE 96083 ... 95736 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 476
- Ceres seq_id 2051325

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 477
- Ceres seq_id 2051326
- Location of start within SEQ ID NO 476: at 68 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 477: at 30 aa.

(C) Nomination and Annotation of Domains within Predicted Polypeptide(s)

- Plant lipid transfer protein family
- Location within SEQ ID NO 477: from 34 to 115 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 318
- gi No. 4725952
- Description: (AL049730) AIR1A-like protein

[Arabidopsis thaliana]

- % Identity: 100
- Alignment Length: 117

274

117 - Location of Alignment in SEQ ID NO 477: from 1 to

(B) Polypeptide Sequence

5 - Pat. Appln. SEQ ID NO 478
 - Ceres seq_id 2051327
 - Location of start within SEQ ID NO 476: at 74 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
 ID NO 478: at 28 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Plant lipid transfer protein family
 - Location within SEQ ID NO 478: from 32 to 113 aa.

(Dp) Related Amino Acid Sequences

20 - Alignment No. 319
 - gi No. 4725952
 - Description: (AL049730) AIR1A-like protein
 [Arabidopsis thaliana]
 - % Identity: 100
 - Alignment Length: 117
 - Location of Alignment in SEQ ID NO 478: from 1 to

(B) Polypeptide Sequence

25 - Pat. Appln. SEQ ID NO 479
 - Ceres seq_id 2051328
 - Location of start within SEQ ID NO 476: at 288 nt.
 30 - Location of Signal Peptide Cleavage Site within SEQ
 ID NO 479: at 61 aa.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4490717

Predicted Exons:

INIT	87492	...	87378	GENBANK
INTR	87034	...	86928	GENBANK
INTR	86683	...	86641	GENBANK
TERM	86445	...	86402	GENBANK
INTR	87555	...	87378	OCKHAMG-CDNA
INTR	87034	...	86928	OCKHAMG-CDNA
INTR	86683	...	86641	OCKHAMG-CDNA
INTR	86445	...	86257	OCKHAMG-CDNA
INIT	87492	...	87378	OCKHAMG-CDS

275

INTR	87034	...	86928	OCKHAMG-CDS
INTR	86683	...	86641	OCKHAMG-CDS
TERM	86445	...	86402	OCKHAMG-CDS

- 5 (Ac) cDNA Polynucleotide Sequence
 - Pat. Appln. SEQ ID NO 480
 - Ceres seq_id 2051633

- 10 (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 481
 - Ceres seq_id 2051634
 - Location of start within SEQ ID NO 480: at 1 nt.

- 15 (C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)
 (Dp) Related Amino Acid Sequences
 - Alignment No. 320
 - gi No. 1083282
 20 - Description: cytochrome-c oxidase (EC 1.9.3.1) -
 mouse >gi|567766 (L06465) cytochrome c oxidase [Mus musculus]
 >gi|1094404|prf||2106151A cytochrome c oxidase:SUBUNIT=VIa
 [Mus musculus]
 - % Identity: 41.4
 25 - Alignment Length: 106
 - Location of Alignment in SEQ ID NO 481: from 22
 to 120

- (B) Polypeptide Sequence
 30 - Pat. Appln. SEQ ID NO 482
 - Ceres seq_id 2051635
 - Location of start within SEQ ID NO 480: at 64 nt.

- (C) Nomination and Annotation of Domains within
 35 Predicted Polypeptide(s)
 (Dp) Related Amino Acid Sequences
 - Alignment No. 321
 - gi No. 1083282
 - Description: cytochrome-c oxidase (EC 1.9.3.1) -
 40 mouse >gi|567766 (L06465) cytochrome c oxidase [Mus musculus]
 >gi|1094404|prf||2106151A cytochrome c oxidase:SUBUNIT=VIa
 [Mus musculus]
 - % Identity: 41.4
 - Alignment Length: 106
 45 - Location of Alignment in SEQ ID NO 482: from 1 to
 99

Maximum Length Sequence:

Public Genomic DNA:

- 50 gi No: 4584531
 Predicted Exons:

276
INTR 56873 ... 56641 OCKHAMG-CDNA
INTR 56627 ... 56451 OCKHAMG-CDNA

SINGLE 56812 ... 56645 OCKHAMG-CDS

5

(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 483
- Ceres seq_id 2051906

10

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 484
- Ceres seq_id 2051907
- Location of start within SEQ ID NO 483: at 2 nt.

15

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

20

- Alignment No. 322
- gi No. 4850407
- Description: (AC007357) EST gb|T21221 comes from
this gene. [Arabidopsis thaliana]
- % Identity: 57.1
- Alignment Length: 35
- Location of Alignment in SEQ ID NO 484: from 37
to 70

25

(B) Polypeptide Sequence

30

- Pat. Appln. SEQ ID NO 485
- Ceres seq_id 2051908
- Location of start within SEQ ID NO 483: at 62 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

35

(Dp) Related Amino Acid Sequences

40

- Alignment No. 323
- gi No. 4850407
- Description: (AC007357) EST gb|T21221 comes from
this gene. [Arabidopsis thaliana]
- % Identity: 57.1
- Alignment Length: 35
- Location of Alignment in SEQ ID NO 485: from 17
to 50

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 486
- Ceres seq_id 2051909
- Location of start within SEQ ID NO 483: at 74 nt.

50

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

277

(Dp) Related Amino Acid Sequences

- Alignment No. 324
- gi No. 4850407
- Description: (AC007357) EST gb|T21221 comes from
5 this gene. [Arabidopsis thaliana]
- % Identity: 57.1
- Alignment Length: 35
- Location of Alignment in SEQ ID NO 486: from 13
10 to 46

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4584841

Predicted Exons:

15	INTR	75983 ... 75751	OCKHAMG-CDNA
	INTR	75412 ... 74936	OCKHAMG-CDNA
	INTR	75992 ... 75751	OCKHAMG-CDNA
	INTR	75412 ... 75090	OCKHAMG-CDNA
20	INIT	75937 ... 75751	OCKHAMG-CDS
	TERM	75412 ... 75132	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 487
- Ceres seq_id 2052403

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 488
- Ceres seq_id 2052404
- Location of start within SEQ ID NO 487: at 56 nt.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

- Pathogenesis-related protein Bet v I family
- Location within SEQ ID NO 488: from 5 to 155 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 325
- gi No. 1321731
- Description: (Z72439) major allergen Cor a 1
[Corylus avellana]
- % Identity: 36.3
- Alignment Length: 159
- Location of Alignment in SEQ ID NO 488: from 5 to
155

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4699904

278

Predicted Exons:

	INTR	82618	...	82845	OCKHAMG-CDNA
	INTR	83226	...	83301	OCKHAMG-CDNA
	INTR	83389	...	83561	OCKHAMG-CDNA
5	INTR	84124	...	84385	OCKHAMG-CDNA
	INIT	82730	...	82845	OCKHAMG-CDS
	INTR	83226	...	83301	OCKHAMG-CDS
	INTR	83389	...	83561	OCKHAMG-CDS
10	TERM	84124	...	84199	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 489
- Ceres seq_id 2053545

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 490
- Ceres seq_id 2053546
- Location of start within SEQ ID NO 489: at 113 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 490: at 36 aa.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

- MAPEG family
- Location within SEQ ID NO 490: from 59 to 136 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 326
- gi No. 4758714
- Description: ref|NP_004519.1|pMGST3| microsomal glutathione S-transferase 3 >gi|2583081 (AF026977) microsomal glutathione S-transferase 3 [Homo sapiens]

- % Identity: 41.9
- Alignment Length: 131
- Location of Alignment in SEQ ID NO 490: from 8 to 136

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 491
- Ceres seq_id 2053547
- Location of start within SEQ ID NO 489: at 197 nt.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

- MAPEG family
- Location within SEQ ID NO 491: from 31 to 108 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 327

279

- gi No. 4758714
 - Description: ref|NP_004519.1|pMGST3| microsomal
 glutathione S-transferase 3 >gi|2583081 (AF026977) microsomal
 glutathione S-transferase 3 [Homo sapiens]

5 - % Identity: 41.9
 - Alignment Length: 131
 - Location of Alignment in SEQ ID NO 491: from 1 to
 108

10 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 492
 - Ceres seq_id 2053548
 - Location of start within SEQ ID NO 489: at 329 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
 15 ID NO 492: at 22 aa.

(C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)

20 - MAPEG family
 - Location within SEQ ID NO 492: from 1 to 64 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 328
 - gi No. 4758714
 25 - Description: ref|NP_004519.1|pMGST3| microsomal
 glutathione S-transferase 3 >gi|2583081 (AF026977) microsomal
 glutathione S-transferase 3 [Homo sapiens]
 - % Identity: 41.9
 - Alignment Length: 131
 30 - Location of Alignment in SEQ ID NO 492: from 1 to
 64

Maximum Length Sequence:
 related to:

35 Clone IDs:
 2004
 31675
 266907

Public Genomic DNA:

40 gi No: 4887737

Predicted Exons:

	INTR	7907	...	8579	OCKHAMG-CDNA
	INTR	7913	...	8587	OCKHAMG-CDNA
45	INTR	7911	...	8579	OCKHAMG-CDNA
	INTR	7909	...	8579	OCKHAMG-CDNA
50	INTR	7913	...	8578	OCKHAMG-CDNA

280

INTR 7913 ... 8509 OCKHAMG-CDNA

SINGLE 7958 ... 8425 OCKHAMG-CDS

gi No: 5019264

5 Predicted Exons:

SINGLE 4143 ... 4610 GENBANK

INTR 4092 ... 4764 OCKHAMG-CDNA

10 INTR 4098 ... 4772 OCKHAMG-CDNA

INTR 4096 ... 4764 OCKHAMG-CDNA

15 INTR 4094 ... 4764 OCKHAMG-CDNA

INTR 4098 ... 4763 OCKHAMG-CDNA

INTR 4098 ... 4694 OCKHAMG-CDNA

20 SINGLE 4143 ... 4610 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 493
- Ceres seq_id 2053884
- Alternative transcription start site(s) located in SEQ

25 ID NO 493:

-47,-3,2,3,4,5,6,7,8,10,11,12,13,14,15,16,20,21,28,29

38,44,45,60,68

- Clone 2004 starts at 1 and ends at 677 in cDNA.
- Clone 31675 starts at 3 and ends at 607 in cDNA.

30 - Clone 266907 starts at 4 and ends at 677 in cDNA.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 494
- Ceres seq_id 2053885

35 - Location of start within SEQ ID NO 493: at 1 nt.

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

40 - Alignment No. 329

- gi No. 2498177

- Description: BASP1 PROTEIN

- % Identity: 28

- Alignment Length: 164

45 - Location of Alignment in SEQ ID NO 494: from 2 to

159

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 495
- Ceres seq_id 2053886

50 - Location of start within SEQ ID NO 493: at 52 nt.

281

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

5 - Alignment No. 330
 - gi No. 2498177
 - Description: BASP1 PROTEIN
 - % Identity: 28
10 - Alignment Length: 164
 - Location of Alignment in SEQ ID NO 495: from 1 to
142

(B) Polypeptide Sequence

15 - Pat. Appln. SEQ ID NO 496
 - Ceres seq_id 2053887
 - Location of start within SEQ ID NO 493: at 172 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

20 (Dp) Related Amino Acid Sequences

 - Alignment No. 331
 - gi No. 2498177
 - Description: BASP1 PROTEIN
25 - % Identity: 28
 - Alignment Length: 164
 - Location of Alignment in SEQ ID NO 496: from 1 to
102

Maximum Length Sequence:

30 Public Genomic DNA:

 gi No: 4887738

 Predicted Exons:

 INTR 45004 ... 44725 OCKHAMG-CDNA
 INTR 44038 ... 43918 OCKHAMG-CDNA
35 INTR 43839 ... 43444 OCKHAMG-CDNA

 INIT 44942 ... 44725 OCKHAMG-CDS

 INTR 44038 ... 43918 OCKHAMG-CDS

 TERM 43839 ... 43564 OCKHAMG-CDS

40 gi No: 5103850

 Predicted Exons:

 INIT 44944 ... 44727 GENBANK

 INTR 44040 ... 43920 GENBANK

45 TERM 43841 ... 43566 GENBANK

 INTR 45006 ... 44727 OCKHAMG-CDNA

 INTR 44040 ... 43920 OCKHAMG-CDNA

 INTR 43841 ... 43446 OCKHAMG-CDNA

50 INIT 44944 ... 44727 OCKHAMG-CDS

 INTR 44040 ... 43920 OCKHAMG-CDS

282

TERM 43841 ... 43566 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 497

5 - Ceres seq_id 2053908

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 498

10 - Ceres seq_id 2053909

- Location of start within SEQ ID NO 497: at 63 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

15 (Dp) Related Amino Acid Sequences

- Alignment No. 332

- gi No. 2245000

- Description: (Z97341) LET1 like protein

[Arabidopsis thaliana]

20 - % Identity: 31.4

- Alignment Length: 156

- Location of Alignment in SEQ ID NO 498: from 17
to 164

25 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 499

- Ceres seq_id 2053910

- Location of start within SEQ ID NO 497: at 168 nt.

30 - Location of Signal Peptide Cleavage Site within SEQ
ID NO 499: at 23 aa.(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

35 (Dp) Related Amino Acid Sequences

- Alignment No. 333

- gi No. 2245000

- Description: (Z97341) LET1 like protein

[Arabidopsis thaliana]

40 - % Identity: 31.4

- Alignment Length: 156

- Location of Alignment in SEQ ID NO 499: from 1 to
129

45 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 500

- Ceres seq_id 2053911

- Location of start within SEQ ID NO 497: at 216 nt.

50 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

283

- Alignment No. 334
 - gi No. 2245000
 - Description: (Z97341) LET1 like protein
 [Arabidopsis thaliana]
 - % Identity: 31.4
 - Alignment Length: 156
 - Location of Alignment in SEQ ID NO 500: from 1 to
 113

10 Maximum Length Sequence:
 Public Genomic DNA:

gi No: 4335711

Predicted Exons:

15	INTR	46239 ... 46470	OCKHAMG-CDNA
	INTR	46624 ... 46739	OCKHAMG-CDNA
	INTR	47125 ... 47428	OCKHAMG-CDNA
	INIT	46285 ... 46470	OCKHAMG-CDS
20	INTR	46624 ... 46739	OCKHAMG-CDS
	TERM	47125 ... 47413	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 501
 - Ceres seq_id 2056123

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 502
 - Ceres seq_id 2056124
 - Location of start within SEQ ID NO 501: at 47 nt.

(C) Nomination and Annotation of Domains within
 Predicted Polypeptide(s)

- Zinc finger, C3HC4 type (RING finger)
 - Location within SEQ ID NO 502: from 150 to 190
 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 335
 - gi No. 3790593
 - Description: (AF079185) RING-H2 finger protein
 RHY1a [Arabidopsis thaliana]
 - % Identity: 55.1
 - Alignment Length: 49
 - Location of Alignment in SEQ ID NO 502: from 146
 to 194

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 503
 - Ceres seq_id 2056125
 - Location of start within SEQ ID NO 501: at 56 nt.

284

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Zinc finger, C3HC4 type (RING finger)
 - Location within SEQ ID NO 503: from 147 to 187
- 5 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 336
 - gi No. 3790593
 - Description: (AF079185) RING-H2 finger protein
- 10 RHY1a [Arabidopsis thaliana]
- % Identity: 55.1
 - Alignment Length: 49
 - Location of Alignment in SEQ ID NO 503: from 143
- 15 to 191

Maximum Length Sequence:

Public Genomic DNA:

20 gi No: 4432829

Predicted Exons:

	INTR	51185 ...	51056	OCKHAMG-CDNA
	INTR	50590 ...	50253	OCKHAMG-CDNA
25	INIT	56176 ...	55097	OCKHAMG-CDS
	INTR	55014 ...	54161	OCKHAMG-CDS
	INTR	54076 ...	54011	OCKHAMG-CDS
	INTR	51530 ...	51382	OCKHAMG-CDS
	INTR	51187 ...	51056	OCKHAMG-CDS
30	TERM	50590 ...	50418	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 504
 - Ceres seq_id 2056245
- 35

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 505
 - Ceres seq_id 2056246
 - Location of start within SEQ ID NO 504: at 1 nt.
- 40

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 337
 - gi No. 4938484
 - Description: (AL078464) transcription factor-like
- 45 protein [Arabidopsis thaliana]
- % Identity: 56.2
 - Alignment Length: 661
- 50

285

644 - Location of Alignment in SEQ ID NO 505: from 4 to

(B) Polypeptide Sequence

- 5 - Pat. Appln. SEQ ID NO 506
- Ceres seq_id 2056247
- Location of start within SEQ ID NO 504: at 55 nt.

(C) Nomination and Annotation of Domains within

10 Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 15 protein [Arabidopsis thaliana]
- Alignment No. 338
- gi No. 4938484
- Description: (AL078464) transcription factor-like
- % Identity: 56.2
- Alignment Length: 661
- Location of Alignment in SEQ ID NO 506: from 1 to

626

20

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 507
- Ceres seq_id 2056248
- Location of start within SEQ ID NO 504: at 751 nt.

25

(C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- 30 - Alignment No. 339
- gi No. 4938484
- Description: (AL078464) transcription factor-like
protein [Arabidopsis thaliana]
- % Identity: 56.2
- Alignment Length: 661
- Location of Alignment in SEQ ID NO 507: from 1 to

35

394

Maximum Length Sequence:

related to:

40 Clone IDs:

213322

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 508
- Ceres seq_id 1941142

45

(B) Polypeptide Sequence

- 50 - Pat. Appln. SEQ ID NO 509
- Ceres seq_id 1941143
- Location of start within SEQ ID NO 508: at 119 nt.

286

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein L24e
- Location within SEQ ID NO 509: from 3 to 73 aa.

5

(Dp) Related Amino Acid Sequences

- Alignment No. 340
- gi No. 1710521
- Description: 60S RIBOSOMAL PROTEIN L24

10 >gi|1154859|emb|CAA63960| (X94296) L24 ribosomal protein
[Hordeum vulgare]

- % Identity: 94.4
- Alignment Length: 162
- Location of Alignment in SEQ ID NO 509: from 1 to

15 161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 510
- Ceres seq_id 1941144
- Location of start within SEQ ID NO 508: at 284 nt.

20

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 341
- gi No. 1710521
- Description: 60S RIBOSOMAL PROTEIN L24

25

>gi|1154859|emb|CAA63960| (X94296) L24 ribosomal protein
[Hordeum vulgare]

30

- % Identity: 94.4
- Alignment Length: 162
- Location of Alignment in SEQ ID NO 510: from 1 to

106

35 Maximum Length Sequence:

related to:

Clone IDs:

241379

(Ac) cDNA Polynucleotide Sequence

40

- Pat. Appln. SEQ ID NO 511
- Ceres seq_id 1942975
- Alternative transcription start site(s) located in SEQ
ID NO 511:
29,30,31,32,33,36

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 512
- Ceres seq_id 1942976
- Location of start within SEQ ID NO 511: at 1 nt.

50

287

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S3, C-terminal domain.
- Location within SEQ ID NO 512: from 149 to 233

5 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 342
- gi No. 133940

10

- Description: 40S RIBOSOMAL PROTEIN S3A (S1A)

>gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed
frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a
[Xenopus laevis]

15

- % Identity: 82.5

- Alignment Length: 223

- Location of Alignment in SEQ ID NO 512: from 46
to 268

(B) Polypeptide Sequence

20

- Pat. Appln. SEQ ID NO 513

- Ceres seq_id 1942977

- Location of start within SEQ ID NO 511: at 136 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

25

- Ribosomal protein S3, C-terminal domain.

- Location within SEQ ID NO 513: from 104 to 188

aa.

(Dp) Related Amino Acid Sequences

30

- Alignment No. 343

- gi No. 133940

- Description: 40S RIBOSOMAL PROTEIN S3A (S1A)

35

>gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed
frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a
[Xenopus laevis]

- % Identity: 82.5

- Alignment Length: 223

- Location of Alignment in SEQ ID NO 513: from 1 to
223

40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 514

- Ceres seq_id 1942978

45

- Location of start within SEQ ID NO 511: at 205 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

50

- Ribosomal protein S3, C-terminal domain.

- Location within SEQ ID NO 514: from 81 to 165 aa.

288

(Dp) Related Amino Acid Sequences

- Alignment No. 344

- gi No. 133940

- Description: 40S RIBOSOMAL PROTEIN S3A (S1A)

5 >gi|70851|pir||R3XL3A ribosomal protein S3a - African clawed
frog >gi|65091|emb|CAA40592| (X57322) ribosomal protein S1a
[Xenopus laevis]

- % Identity: 82.5

- Alignment Length: 223

10 - Location of Alignment in SEQ ID NO 514: from 1 to
200

Maximum Length Sequence:

related to:

15 Clone IDs:

289536

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 515

- Ceres seq_id 1944349

20

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 516

- Ceres seq_id 1944350

25 - Location of start within SEQ ID NO 515: at 423 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein L24e

30 - Location within SEQ ID NO 516: from 3 to 73 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 345

- gi No. 1710521

- Description: 60S RIBOSOMAL PROTEIN L24

35 >gi|1154859|emb|CAA63960| (X94296) L24 ribosomal protein
[Hordeum vulgare]

- % Identity: 94.4

- Alignment Length: 162

40 - Location of Alignment in SEQ ID NO 516: from 1 to
161

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 517

45 - Ceres seq_id 1944351

- Location of start within SEQ ID NO 515: at 588 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

50 (Dp) Related Amino Acid Sequences

- Alignment No. 346

289

- gi No. 1710521
- Description: 60S RIBOSOMAL PROTEIN L24
>gi|1154859|emb|CAA63960| (X94296) L24 ribosomal protein
[Hordeum vulgare]
5 - % Identity: 94.4
 - Alignment Length: 162
 - Location of Alignment in SEQ ID NO 517: from 1 to
106

10 (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 518
 - Ceres seq_id 1944352
 - Location of start within SEQ ID NO 515: at 736 nt.

15 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
 (Dp) Related Amino Acid Sequences
 - Alignment No. 347
 - gi No. 1362587
20 - Description: spermatid-specific protein T2
precursor - longfin squid
 - % Identity: 55.8
 - Alignment Length: 52
 - Location of Alignment in SEQ ID NO 518: from 1 to
25 46

Maximum Length Sequence:

related to:

Clone IDs:

30 291258

(Ac) cDNA Polynucleotide Sequence

 - Pat. Appln. SEQ ID NO 519
 - Ceres seq_id 1964011
 - Alternative transcription start site(s) located in SEQ
35 ID NO 519:
 4,34,37,38,39,40,41

 (B) Polypeptide Sequence
 - Pat. Appln. SEQ ID NO 520
40 - Ceres seq_id 1964012
 - Location of start within SEQ ID NO 519: at 3 nt.

 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)
45 - Ribosomal protein S3, C-terminal domain.
 - Location within SEQ ID NO 520: from 150 to 234
aa.

 (Dp) Related Amino Acid Sequences
50 - Alignment No. 348
 - gi No. 1173253

290

- Description: 40S RIBOSOMAL PROTEIN S3

>gi|543317|pir||S41170 ribosomal protein S3 - mouse

>gi|57728|emb|CAA35916| (X51536) ribosomal protein S3 (AA 1-243) [Rattus rattus] >gi|439522|emb|CAA54167| (X76772)

5 ribosomal protein S3 [Mus musculus]

- % Identity: 81.1

- Alignment Length: 227

- Location of Alignment in SEQ ID NO 520: from 47
to 273

10

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 521

- Ceres seq_id 1964013

- Location of start within SEQ ID NO 519: at 141 nt.

15

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S3, C-terminal domain.

- Location within SEQ ID NO 521: from 104 to 188

20 aa.

(Dp) Related Amino Acid Sequences

- Alignment No. 349

- gi No. 1173253

25 - Description: 40S RIBOSOMAL PROTEIN S3

>gi|543317|pir||S41170 ribosomal protein S3 - mouse

>gi|57728|emb|CAA35916| (X51536) ribosomal protein S3 (AA 1-243) [Rattus rattus] >gi|439522|emb|CAA54167| (X76772)

ribosomal protein S3 [Mus musculus]

30 - % Identity: 81.1

- Alignment Length: 227

- Location of Alignment in SEQ ID NO 521: from 1 to
227

35 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 522

- Ceres seq_id 1964014

- Location of start within SEQ ID NO 519: at 210 nt.

40 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

- Ribosomal protein S3, C-terminal domain.

- Location within SEQ ID NO 522: from 81 to 165 aa.

45 (Dp) Related Amino Acid Sequences

- Alignment No. 350

- gi No. 1173253

- Description: 40S RIBOSOMAL PROTEIN S3

>gi|543317|pir||S41170 ribosomal protein S3 - mouse

50 >gi|57728|emb|CAA35916| (X51536) ribosomal protein S3 (AA 1-

291

243) [Rattus rattus] >gi|439522|emb|CAA54167| (X76772)
ribosomal protein S3 [Mus musculus]

- % Identity: 81.1

- Alignment Length: 227

- Location of Alignment in SEQ ID NO 522: from 1 to
204

Maximum Length Sequence:

related to:

Clone IDs:

207986

224937

227089

229580

241662

275880

278084

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 523

- Ceres seq_id 1983854

- Alternative transcription start site(s) located in SEQ
ID NO 523:

-1,2,6,30,31,32,33,34,36

- Clone 207986 starts at 31 and ends at 810 in cDNA.

- Clone 224937 starts at 31 and ends at 810 in cDNA.

- Clone 227089 starts at 33 and ends at 804 in cDNA.

- Clone 229580 starts at 31 and ends at 821 in cDNA.

- Clone 241662 starts at 34 and ends at 815 in cDNA.

- Clone 275880 starts at 1 and ends at 804 in cDNA.

- Clone 278084 starts at 31 and ends at 815 in cDNA.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 524

- Ceres seq_id 1983855

- Location of start within SEQ ID NO 523: at 315 nt.

(C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 351

- gi No. 1710521

- Description: 60S RIBOSOMAL PROTEIN L24

>gi|1154859|emb|CAA63960| (X94296) L24 ribosomal protein
[Hordeum vulgare]

- % Identity: 94

- Alignment Length: 150

- Location of Alignment in SEQ ID NO 524: from 1 to

106

Maximum Length Sequence:

related to:

292

Clone IDs:

221977
226126
293001

5 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 525
- Ceres seq_id 1990261
- Alternative transcription start site(s) located in SEQ

ID NO 525:

- 10 16,30,32
- Clone 226126 starts at 30 and ends at 772 in cDNA.
 - Clone 293001 starts at 32 and ends at 810 in cDNA.

15 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 526
- Ceres seq_id 2061972
- Location of start within SEQ ID NO 525: at 144 nt.

20 (C) Nomination and Annotation of Domains within

Predicted Polypeptide(s)

- Ribosomal protein L24e
- Location within SEQ ID NO 526: from 3 to 73 aa.

25 (Dp) Related Amino Acid Sequences

- Alignment No. 352
- gi No. 1710521
- Description: 60S RIBOSOMAL PROTEIN L24

>gi|1154859|emb|CAA63960| (X94296) L24 ribosomal protein
[Hordeum vulgare]

- 30 - % Identity: 94.4
- Alignment Length: 162
- Location of Alignment in SEQ ID NO 526: from 1 to
161

35 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 527
- Ceres seq_id 2061973
- Location of start within SEQ ID NO 525: at 309 nt.

40 (C) Nomination and Annotation of Domains within
Predicted Polypeptide(s)

(Dp) Related Amino Acid Sequences

- Alignment No. 353
- gi No. 1710521
- Description: 60S RIBOSOMAL PROTEIN L24

>gi|1154859|emb|CAA63960| (X94296) L24 ribosomal protein
[Hordeum vulgare]

- 45 - % Identity: 94.4
- Alignment Length: 162
- 50 - Location of Alignment in SEQ ID NO 527: from 1 to

106

REF TABLE 2

Maximum Length Sequence:

related to:

5 Clone IDs:

9458

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 1

- Ceres seq_id 1007802

10 - Alternative transcription start site(s) located in SEQ
ID NO 1:

2,3,4

(B) Polypeptide Sequence

15 - Pat. Appln. SEQ ID NO 2

- Ceres seq_id 1007803

- Location of start within SEQ ID NO 1: at 3 nt.

(B) Polypeptide Sequence

20 - Pat. Appln. SEQ ID NO 3

- Ceres seq_id 1007804

- Location of start within SEQ ID NO 1: at 2 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 3: at 29 aa.

25 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 4

- Ceres seq_id 1007805

- Location of start within SEQ ID NO 1: at 29 nt.

30 - Location of Signal Peptide Cleavage Site within SEQ
ID NO 4: at 20 aa.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot

35 specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

40 Clone IDs:

8458

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 5

- Ceres seq_id 1008556

45 - Alternative transcription start site(s) located in SEQ
ID NO 5:

80,103,134,135,136,137,138,139,152,153,157,166,168

(B) Polypeptide Sequence

50 - Pat. Appln. SEQ ID NO 6

- Ceres seq_id 1008557

294

- Location of start within SEQ ID NO 5: at 173 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene. specific gene, plant

Maximum Length Sequence:

related to:

Clone IDs:

8384

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 7

- Ceres seq_id 1008628

- Alternative transcription start site(s) located in SEQ
ID NO 7:

3,28

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 8

- Ceres seq_id 1008629

- Location of start within SEQ ID NO 7: at 41 nt.

(Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot
specific gene. specific gene, plant

Maximum Length Sequence:

related to:

Clone IDs:

7260

Public Genomic DNA:

gi No: 5733889

Predicted Exons:

INIT	21286	...	21509	GENBANK
------	-------	-----	-------	---------

INTR	21606	...	21832	GENBANK
------	-------	-----	-------	---------

TERM	21951	...	21958	GENBANK
------	-------	-----	-------	---------

INIT	21286	...	21509	OCKHAMG-CDS
------	-------	-----	-------	-------------

INTR	21606	...	21832	OCKHAMG-CDS
------	-------	-----	-------	-------------

TERM	21951	...	21958	OCKHAMG-CDS
------	-------	-----	-------	-------------

gi No: 6041810

Predicted Exons:

INIT	34915	...	35138	OCKHAMG-CDS
------	-------	-----	-------	-------------

INTR	35235	...	35461	OCKHAMG-CDS
------	-------	-----	-------	-------------

TERM	35580	...	35587	OCKHAMG-CDS
------	-------	-----	-------	-------------

gi No: 6091711

Predicted Exons:

INIT	100255...	100478	OCKHAMG-CDS
------	-----------	--------	-------------

INTR	100575...	100801	OCKHAMG-CDS
------	-----------	--------	-------------

295

TERM 100920... 100927 OCKHAMG-CDS

gi No: 6102641

Predicted Exons:

INIT 91941 ... 92164 OCKHAMG-CDS

INTR 92261 ... 92487 OCKHAMG-CDS

TERM 92606 ... 92613 OCKHAMG-CDS

gi No: 6453849

Predicted Exons:

INIT 19658 ... 19435 OCKHAMG-CDS

INTR 19338 ... 19112 OCKHAMG-CDS

TERM 18993 ... 18986 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 9

- Ceres seq_id 1009376

- Alternative transcription start site(s) located in SEQ
ID NO 9:

4,7,22,48,56,77

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 10

- Ceres seq_id 1009377

- Location of start within SEQ ID NO 9: at 238 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 10: at 76 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 11

- Ceres seq_id 1009378

- Location of start within SEQ ID NO 9: at 334 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 11: at 44 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 12

- Ceres seq_id 1009379

- Location of start within SEQ ID NO 9: at 245 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 12: at 47 aa.(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

4489

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 13

296

- Ceres seq_id 1011128
- Alternative transcription start site(s) located in SEQ
ID NO 13:
6,7

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 14
- Ceres seq_id 1011129
- Location of start within SEQ ID NO 13: at 41 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 15
- Ceres seq_id 1011130
- Location of start within SEQ ID NO 13: at 59 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

42241

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 16
- Ceres seq_id 1011718

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 17
- Ceres seq_id 1011719
- Location of start within SEQ ID NO 16: at 3 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 18
- Ceres seq_id 1011720
- Location of start within SEQ ID NO 16: at 78 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 18: at 21 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 19
- Ceres seq_id 1011721
- Location of start within SEQ ID NO 16: at 102 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

297

Maximum Length Sequence:

related to:

5 Clone IDs:
42200

(Ac) cDNA Polynucleotide Sequence

10 - Pat. Appln. SEQ ID NO 20
- Ceres seq_id 1011735

(B) Polypeptide Sequence

15 - Pat. Appln. SEQ ID NO 21
- Ceres seq_id 1011736
- Location of start within SEQ ID NO 20: at 75 nt.

(B) Polypeptide Sequence

20 - Pat. Appln. SEQ ID NO 22
- Ceres seq_id 1011737
- Location of start within SEQ ID NO 20: at 1 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 22: at 37 aa.

(B) Polypeptide Sequence

25 - Pat. Appln. SEQ ID NO 23
- Ceres seq_id 1011738
- Location of start within SEQ ID NO 20: at 2 nt.

30 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

Maximum Length Sequence:

35 related to:

Clone IDs:
42217

(Ac) cDNA Polynucleotide Sequence

40 - Pat. Appln. SEQ ID NO 24
- Ceres seq_id 1011755
- Alternative transcription start site(s) located in SEQ
ID NO 24:
34

45 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 25
- Ceres seq_id 1011756
- Location of start within SEQ ID NO 24: at 1 nt.

50 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 26

298

- Ceres seq_id 1011757
- Location of start within SEQ ID NO 24: at 19 nt.

5 (Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot
specific gene, plant
specific gene.

Maximum Length Sequence:

10 related to:

Clone IDs:

42034

(Ac) cDNA Polynucleotide Sequence

- 15 - Pat. Appln. SEQ ID NO 27
- Ceres seq_id 1011832

(B) Polypeptide Sequence

- 20 - Pat. Appln. SEQ ID NO 28
- Ceres seq_id 1011833
- Location of start within SEQ ID NO 27: at 97 nt.

(B) Polypeptide Sequence

- 25 - Pat. Appln. SEQ ID NO 29
- Ceres seq_id 1011834
- Location of start within SEQ ID NO 27: at 100 nt.

(B) Polypeptide Sequence

- 30 - Pat. Appln. SEQ ID NO 30
- Ceres seq_id 1011835
- Location of start within SEQ ID NO 27: at 106 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot

35 specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

40 Clone IDs:

41812

Public Genomic DNA:

gi No: 6434227

Predicted Exons:

45 INIT 65854 ... 65974 OCKHAMG-CDS
TERM 66067 ... 66206 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- 50 - Pat. Appln. SEQ ID NO 31
- Ceres seq_id 1011907

(B) Polypeptide Sequence

299

- Pat. Appln. SEQ ID NO 32
- Ceres seq_id 1011908
- Location of start within SEQ ID NO 31: at 218 nt.
- Location of Signal Peptide Cleavage Site within SEQ

5 ID NO 32: at 30 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 33
- Ceres seq_id 1011909
- Location of start within SEQ ID NO 31: at 239 nt.
- Location of Signal Peptide Cleavage Site within SEQ

10

ID NO 33: at 23 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 34
- Ceres seq_id 1011910
- Location of start within SEQ ID NO 31: at 3 nt.
- Location of Signal Peptide Cleavage Site within SEQ

15

ID NO 34: at 17 aa.

20

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot

specific gene, plant

specific gene.

25

Maximum Length Sequence:

related to:

Clone IDs:

41828

30

Public Genomic DNA:

gi No: 4159707

Predicted Exons:

INTR 15084 ... 15201 OCKHAMG-CDNA

INTR 15295 ... 15324 OCKHAMG-CDNA

35

INTR 15414 ... 15533 OCKHAMG-CDNA

INTR 15648 ... 15956 OCKHAMG-CDNA

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 35

- Ceres seq_id 1011911

40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 36
- Ceres seq_id 1011912
- Location of start within SEQ ID NO 35: at 194 nt.

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 37
- Ceres seq_id 1011913
- Location of start within SEQ ID NO 35: at 230 nt.
- Location of Signal Peptide Cleavage Site within SEQ

50

ID NO 37: at 22 aa.

300

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 38
- Ceres seq_id 1011914
- Location of start within SEQ ID NO 35: at 2 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 38: at 28 aa.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

41723

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 39
- Ceres seq_id 1011954

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 40
- Ceres seq_id 1011955
- Location of start within SEQ ID NO 39: at 1 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 40: at 40 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 41
- Ceres seq_id 1011956
- Location of start within SEQ ID NO 39: at 107 nt.

(Ba) Polypeptide Activities: Similar to DNAJ Protein
Activities

Maximum Length Sequence:

related to:

Clone IDs:

41730

Public Genomic DNA:

gi No: 4678371

Predicted Exons:

SINGLE 48996 ... 49184 GENBANK

SINGLE 48996 ... 49184 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 42
- Ceres seq_id 1011960

301

- Alternative transcription start site(s) located in SEQ
ID NO 42:
20,22,25,43

5 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 43
- Ceres seq_id 1011961
- Location of start within SEQ ID NO 42: at 69 nt.

10 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 44
- Ceres seq_id 1011962
- Location of start within SEQ ID NO 42: at 78 nt.

15 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 45
- Ceres seq_id 1011963
- Location of start within SEQ ID NO 42: at 90 nt.

20 (Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot
specific gene, plant specific gene, similar to
serine rich protein
activities.

25 Maximum Length Sequence:
related to:
Clone IDs:
38977

30 (Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 46
- Ceres seq_id 1014075
- Alternative transcription start site(s) located in SEQ
ID NO 46:
35 -3,-2,-1,2,3,4,5,6,7,8,10,15,103

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 47
- Ceres seq_id 1014076
40 - Location of start within SEQ ID NO 46: at 1 nt.

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 48
- Ceres seq_id 1014077
45 - Location of start within SEQ ID NO 46: at 84 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 48: at 22 aa.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
50 dicot

302

specific gene.

specific gene, plant

Maximum Length Sequence:

5 related to:

Clone IDs:

37081

Public Genomic DNA:

gi No: 4159707

10 Predicted Exons:

INIT 15458 ... 15533 OCKHAMG-CDS

TERM 15648 ... 15751 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 49

15 - Ceres seq_id 1015865

- Alternative transcription start site(s) located in SEQ
ID NO 49:

-29

20 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 50

- Ceres seq_id 1015866

- Location of start within SEQ ID NO 49: at 281 nt.

25 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 51

- Ceres seq_id 1015867

- Location of start within SEQ ID NO 49: at 317 nt.

- Location of Signal Peptide Cleavage Site within SEQ

30 ID NO 51: at 22 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 52

- Ceres seq_id 1015868

35 - Location of start within SEQ ID NO 49: at 3 nt.

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 52: at 15 aa.

40 (Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot

specific gene, plant

specific gene.

Maximum Length Sequence:

45 related to:

Clone IDs:

29375

Public Genomic DNA:

gi No: 4159707

50 Predicted Exons:

INTR 15158 ... 15201 OCKHAMG-CDNA

303
INTR 15449 ... 15533 OCKHAMG-CDNA
INTR 15648 ... 15947 OCKHAMG-CDNA
(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 53
5 - Ceres seq_id 1021371
- Alternative transcription start site(s) located in SEQ
ID NO 53:
-74

10 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 54
- Ceres seq_id 1021372
- Location of start within SEQ ID NO 53: at 3 nt.

15 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 55
- Ceres seq_id 1021373
- Location of start within SEQ ID NO 53: at 54 nt.

20 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 56
- Ceres seq_id 1021374
- Location of start within SEQ ID NO 53: at 90 nt.
- Location of Signal Peptide Cleavage Site within SEQ
25 ID NO 56: at 22 aa.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
30 specific gene.

Maximum Length Sequence:
related to:
Clone IDs:
35 27064
(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 57
- Ceres seq_id 1022578

40 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 58
- Ceres seq_id 1022579
- Location of start within SEQ ID NO 57: at 1 nt.

45 (B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 59
- Ceres seq_id 1022580
- Location of start within SEQ ID NO 57: at 157 nt.

50 (B) Polypeptide Sequence

304

- Pat. Appln. SEQ ID NO 60
- Ceres seq_id 1022581
- Location of start within SEQ ID NO 57: at 10 nt.

5 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

10 Maximum Length Sequence:
related to:
Clone IDs:
23773

Public Genomic DNA:

15 gi No: 6136357
Predicted Exons:
INTR 51972 ... 51830 OCKHAMG-CDNA
INTR 51129 ... 51055 OCKHAMG-CDNA
INTR 50948 ... 50806 OCKHAMG-CDNA
20 INTR 50706 ... 50608 OCKHAMG-CDNA
INTR 50326 ... 50147 OCKHAMG-CDNA
gi No: 6143858
Predicted Exons:
INTR 51972 ... 51830 OCKHAMG-CDNA
25 INTR 51129 ... 51055 OCKHAMG-CDNA
INTR 50948 ... 50806 OCKHAMG-CDNA
INTR 50706 ... 50608 OCKHAMG-CDNA
INTR 50326 ... 50147 OCKHAMG-CDNA

(Ac) cDNA Polynucleotide Sequence

30 - Pat. Appln. SEQ ID NO 61
- Ceres seq_id 1024240

(B) Polypeptide Sequence

35 - Pat. Appln. SEQ ID NO 62
- Ceres seq_id 1024241
- Location of start within SEQ ID NO 61: at 54 nt.

(B) Polypeptide Sequence

40 - Pat. Appln. SEQ ID NO 63
- Ceres seq_id 1024242
- Location of start within SEQ ID NO 61: at 66 nt.

(B) Polypeptide Sequence

45 - Pat. Appln. SEQ ID NO 64
- Ceres seq_id 1024243
- Location of start within SEQ ID NO 61: at 404 nt.

(Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot
specific gene, plant
specific gene.

305

Maximum Length Sequence:

related to:

Clone IDs:

5 2030

Public Genomic DNA:

gi No: 5441914

Predicted Exons:

SINGLE 4802 ... 4449 OCKHAMG-CDS

10 gi No: 5881519

Predicted Exons:

SINGLE 4802 ... 4449 GENBANK

SINGLE 4802 ... 4449 OCKHAMG-CDS

15 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 65

- Ceres seq_id 1026562

- Alternative transcription start site(s) located in SEQ

ID NO 65:

20 36,41,43,44,88,90,94,102

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 66

- Ceres seq_id 1026563

25 - Location of start within SEQ ID NO 65: at 1 nt.

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 66: at 51 aa.

(B) Polypeptide Sequence

30 - Pat. Appln. SEQ ID NO 67

- Ceres seq_id 1026564

- Location of start within SEQ ID NO 65: at 109 nt.

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 67: at 15 aa.

35

(Ba) Polypeptide Activities: Similar to cytochrome c
oxidase II

activities.

40 Maximum Length Sequence:

related to:

Clone IDs:

20097

Public Genomic DNA:

45 gi No: 5733893

Predicted Exons:

INTR 66948 ... 67429 OCKHAMG-CDNA

SINGLE 66986 ... 67324 OCKHAMG-CDS

50 gi No: 5748882

Predicted Exons:

306

INTR 41416 ... 40935 OCKHAMG-CDNA

SINGLE 41380 ... 41042 OCKHAMG-CDS

gi No: 5801671

5 Predicted Exons:

INTR 51184 ... 50703 OCKHAMG-CDNA

SINGLE 51148 ... 50810 OCKHAMG-CDS

gi No: 5809708

10 Predicted Exons:

INTR 41416 ... 40935 OCKHAMG-CDNA

SINGLE 41380 ... 41042 OCKHAMG-CDS

gi No: 5836114

15 Predicted Exons:

INTR 42487 ... 42006 OCKHAMG-CDNA

SINGLE 42451 ... 42113 OCKHAMG-CDS

gi No: 5923662

20 Predicted Exons:

INTR 43106 ... 43587 OCKHAMG-CDNA

SINGLE 43144 ... 43482 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

25 - Pat. Appln. SEQ ID NO 68

- Ceres seq_id 1026648

- Alternative transcription start site(s) located in SEQ

ID NO 68:

-74,-72,-48,-42,76

30

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 69

- Ceres seq_id 1026649

- Location of start within SEQ ID NO 68: at 39 nt.

35 - Location of Signal Peptide Cleavage Site within SEQ

ID NO 69: at 59 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 70

40 - Ceres seq_id 1026650

- Location of start within SEQ ID NO 68: at 78 nt.

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 70: at 46 aa.

(B) Polypeptide Sequence

45 - Pat. Appln. SEQ ID NO 71

- Ceres seq_id 1026651

- Location of start within SEQ ID NO 68: at 81 nt.

- Location of Signal Peptide Cleavage Site within SEQ

50 ID NO 71: at 45 aa.

307

(Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot
specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

18274

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 72

- Ceres seq_id 1027881

- Alternative transcription start site(s) located in SEQ
ID NO 72:

-8,-4,2

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 73

- Ceres seq_id 1027882

- Location of start within SEQ ID NO 72: at 3 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 74

- Ceres seq_id 1027883

- Location of start within SEQ ID NO 72: at 36 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 75

- Ceres seq_id 1027884

- Location of start within SEQ ID NO 72: at 105 nt.

- Location of Signal Peptide Cleavage Site within SEQ
ID NO 75: at 18 aa.

(Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot
specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

121894

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 76

- Ceres seq_id 1381797

- Alternative transcription start site(s) located in SEQ
ID NO 76:

-41,18,19,22,26

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 77

308

- Ceres seq_id 1381798
- Location of start within SEQ ID NO 76: at 70 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 78
- Ceres seq_id 1381799
- Location of start within SEQ ID NO 76: at 82 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 79
- Ceres seq_id 1381800
- Location of start within SEQ ID NO 76: at 109 nt.

(Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

31667

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 80
- Ceres seq_id 1442747
- Alternative transcription start site(s) located in SEQ
ID NO 80:
3,5,6,11,62,64,65,66,69,70,71,72,74

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 81
- Ceres seq_id 1442748
- Location of start within SEQ ID NO 80: at 2 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 82
- Ceres seq_id 1442749
- Location of start within SEQ ID NO 80: at 140 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 83
- Ceres seq_id 1442750
- Location of start within SEQ ID NO 80: at 224 nt.

(Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

309

Clone IDs:

270354

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 84

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- Ceres seq_id 1459199
```

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 85

```
- Ceres seq_id 1459200
```

- Location of start within SEQ ID NO 84: at 2 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 86

```
- Ceres seq_id 1459201
```

- Location of start within SEQ ID NO 84: at 56 nt.

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 86: at 20 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 87

- Ceres seq id 1459202

- Location of start within SEQ ID NO 84: at 80 nt.

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 87: at 17 aa.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot

specific gene, plant

specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

12250

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 88

- Ceres seq id 1565605

- Alternative transcription start site(s) located in SEO

ID NO 88:

-17

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 89

- Ceres seq id 1565606

- Location of start within SEQ ID NO 88: at 133 nt.

(B) Polypeptide Sequence

310

- Pat. Appln. SEQ ID NO 90
- Ceres seq_id 1565607
- Location of start within SEQ ID NO 88: at 181 nt.

5 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant
specific gene.

10 Maximum Length Sequence:
related to:

Clone IDs:

97883

(Ac) cDNA Polynucleotide Sequence

- 15 - Pat. Appln. SEQ ID NO 91
- Ceres seq_id 1566686
 - Alternative transcription start site(s) located in SEQ
ID NO 91:
58,61

20

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 92
- Ceres seq_id 1566687
- Location of start within SEQ ID NO 91: at 137 nt.

25

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant
specific gene.

30

Maximum Length Sequence:
related to:

Clone IDs:

12408

35 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 93
- Ceres seq_id 1567367
- Alternative transcription start site(s) located in SEQ
ID NO 93:

40

-39,6,11,14,17,25,32,33,34,35,60

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 94
- Ceres seq_id 1567368
- Location of start within SEQ ID NO 93: at 1 nt.

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 95
- Ceres seq_id 1567369
- Location of start within SEQ ID NO 93: at 2 nt.

50

311

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 96
- Ceres seq_id 1567370
- Location of start within SEQ ID NO 93: at 65 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

Maximum Length Sequence:

related to:

Clone IDs:

19528

Public Genomic DNA:

gi No: 6091770

Predicted Exons:

INIT	21323	...	21390	OCKHAMG-CDS
INTR	21467	...	21564	OCKHAMG-CDS
INTR	21995	...	22027	OCKHAMG-CDS
TERM	22386	...	22468	OCKHAMG-CDS

gi No: 6102636

Predicted Exons:

INIT	21323	...	21390	OCKHAMG-CDS
INTR	21467	...	21564	OCKHAMG-CDS
INTR	21995	...	22027	OCKHAMG-CDS
TERM	22386	...	22468	OCKHAMG-CDS

gi No: 6137907

Predicted Exons:

INIT	21252	...	21319	OCKHAMG-CDS
INTR	21396	...	21493	OCKHAMG-CDS
INTR	21924	...	21956	OCKHAMG-CDS
TERM	22315	...	22397	OCKHAMG-CDS

gi No: 6437519

Predicted Exons:

INIT	14107	...	14174	OCKHAMG-CDS
INTR	14251	...	14348	OCKHAMG-CDS
INTR	14779	...	14811	OCKHAMG-CDS
TERM	15170	...	15252	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 97
- Ceres seq_id 1570101
- Alternative transcription start site(s) located in SEQ ID NO 97:

9,29,30,31,32,39,40,43,44,61,62,64,65,198

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 98
- Ceres seq_id 1570102
- Location of start within SEQ ID NO 97: at 116 nt.

312

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

5

Maximum Length Sequence:
related to:
Clone IDs:

42399

10 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 99

- Ceres seq_id 1571051

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 100

- Ceres seq_id 1571052

- Location of start within SEQ ID NO 99: at 1 nt.

20

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 101

- Ceres seq_id 1571053

- Location of start within SEQ ID NO 99: at 16 nt.

- Location of Signal Peptide Cleavage Site within SEQ

25 ID NO 101: at 30 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 102

- Ceres seq_id 1571054

- Location of start within SEQ ID NO 99: at 139 nt.

30

(Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot

specific gene, plant

specific gene.

35

Maximum Length Sequence:
related to:

Clone IDs:

6487

40 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 103

- Ceres seq_id 1571100

- Alternative transcription start site(s) located in SEQ
ID NO 103:

45 5,6

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 104

- Ceres seq_id 1571101

50 - Location of start within SEQ ID NO 103: at 1 nt.

313

- Location of Signal Peptide Cleavage Site within SEQ ID NO 104: at 19 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 105

- Ceres seq_id 1571102

- Location of start within SEQ ID NO 103: at 82 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene, dicot

specific gene. specific gene, plant

Maximum Length Sequence:

related to:

Clone IDs:

39977

14890

34623

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 106

- Ceres seq_id 1665272

- Alternative transcription start site(s) located in SEQ ID NO 106:

3,15,32,33,34,35,37,38,39,40,41,42,43,44,45,46,47,48,49,50
51,60,61,63,66,69,70,71,72,74,75,76,78,79,84,85

- Clone 39977 starts at 35 and ends at 636 in cDNA.

- Clone 14890 starts at 43 and ends at in cDNA.

- Clone 34623 starts at 1 and ends at 598 in cDNA.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 107

- Ceres seq_id 1665273

- Location of start within SEQ ID NO 106: at 90 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene, dicot

specific gene. specific gene, plant

Maximum Length Sequence:

related to:

Clone IDs:

24562

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 108

- Ceres seq_id 1713895

- Alternative transcription start site(s) located in SEQ ID NO 108:

-7,2,3,5,7,8,13,17,29,30,32,34

314

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 109
- Ceres seq_id 1713896
- Location of start within SEQ ID NO 108: at 3 nt.

5

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 110
- Ceres seq_id 1713897
- Location of start within SEQ ID NO 108: at 57 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 110: at 20 aa.

10

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 111
- Ceres seq_id 1713898
- Location of start within SEQ ID NO 108: at 81 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 111: at 17 aa.

15

20 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant
specific gene.

25 Maximum Length Sequence:

related to:

Clone IDs:

41879

(Ac) cDNA Polynucleotide Sequence

30

- Pat. Appln. SEQ ID NO 112
- Ceres seq_id 1923752

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 113
- Ceres seq_id 1923753
- Location of start within SEQ ID NO 112: at 2 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 113: at 19 aa.

35

40 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 114
- Ceres seq_id 1923754
- Location of start within SEQ ID NO 112: at 292 nt.

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 115
- Ceres seq_id 1923755
- Location of start within SEQ ID NO 112: at 384 nt.
- Location of Signal Peptide Cleavage Site within SEQ

50

ID NO 115: at 27 aa.

315

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

Maximum Length Sequence:
related to:
Clone IDs:

150069

(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 116
- Ceres seq_id 1976816
- Alternative transcription start site(s) located in SEQ
ID NO 116:
20,30,32

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 117
- Ceres seq_id 1976817
- Location of start within SEQ ID NO 116: at 2 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 117: at 61 aa.

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 118
- Ceres seq_id 1976818
- Location of start within SEQ ID NO 116: at 3 nt.

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 119
- Ceres seq_id 1976819
- Location of start within SEQ ID NO 116: at 52 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

Maximum Length Sequence:
related to:
Clone IDs:

109997

Public Genomic DNA:

gi No: 4263813

Predicted Exons:

INIT 82737 ... 82740 OCKHAMG-CDS

TERM 83475 ... 83623 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 120
- Ceres seq_id 2025128

316

- Alternative transcription start site(s) located in SEQ ID NO 120:

-5,5,61,88

- Clone 109997 starts at 5 and ends at 566 in cDNA.

5

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 121

- Ceres seq_id 2025129

- Location of start within SEQ ID NO 120: at 1 nt.

10

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 122

- Ceres seq_id 2025130

- Location of start within SEQ ID NO 120: at 3 nt.

15

- Location of Signal Peptide Cleavage Site within SEQ

ID NO 122: at 21 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 123

- Ceres seq_id 2025131

- Location of start within SEQ ID NO 120: at 316 nt.

20

(Ba) Polypeptide Activities: Arabidopsis specific gene, dicot

25

specific gene, plant

specific gene.

Maximum Length Sequence:

related to:

30

Clone IDs:

41792

Public Genomic DNA:

gi No: 5762549

Predicted Exons:

35

INTR 41272 ... 41749 OCKHAMG-CDNA

gi No: 5776585

Predicted Exons:

INTR 55175 ... 55652 OCKHAMG-CDNA

gi No: 5801669

40

Predicted Exons:

INTR 97802 ... 98279 OCKHAMG-CDNA

gi No: 5809709

Predicted Exons:

INTR 97803 ... 98280 OCKHAMG-CDNA

45

gi No: 5932531

Predicted Exons:

INTR 90652 ... 91129 OCKHAMG-CDNA

gi No: 6013612

Predicted Exons:

50

INTR 9143 ... 9620 OCKHAMG-CDNA

gi No: 6016671

317

Predicted Exons:

INTR 9266 ... 9743 OCKHAMG-CDNA

gi No: 6041828

Predicted Exons:

5 INTR 9266 ... 9743 OCKHAMG-CDNA

gi No: 6175159

Predicted Exons:

INTR 92644 ... 92167 OCKHAMG-CDNA

(Ac) cDNA Polynucleotide Sequence

10 - Pat. Appln. SEQ ID NO 124

- Ceres seq_id 2025402

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 125

15 - Ceres seq_id 2025403

- Location of start within SEQ ID NO 124: at 186 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 126

20 - Ceres seq_id 2025404

- Location of start within SEQ ID NO 124: at 2 nt.

(Ba) Polypeptide Activities: Similar to ribose 5-phosphate isomerase

25

Maximum Length Sequence:

related to:

Clone IDs:

28572

30 Public Genomic DNA:

gi No: 4725940

Predicted Exons:

INIT 99197 ... 99167 OCKHAMG-CDS

INTR 99060 ... 98960 OCKHAMG-CDS

35 INTR 98863 ... 98753 OCKHAMG-CDS

INTR 98654 ... 97823 OCKHAMG-CDS

INTR 97730 ... 97477 OCKHAMG-CDS

INTR 96772 ... 96683 OCKHAMG-CDS

TERM 96157 ... 96086 OCKHAMG-CDS

40 gi No: 5823567

Predicted Exons:

INIT 99197 ... 99167 OCKHAMG-CDS

INTR 99060 ... 98960 OCKHAMG-CDS

INTR 98863 ... 98753 OCKHAMG-CDS

45 INTR 98654 ... 97823 OCKHAMG-CDS

INTR 97730 ... 97477 OCKHAMG-CDS

INTR 96772 ... 96683 OCKHAMG-CDS

TERM 96157 ... 96086 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

50 - Pat. Appln. SEQ ID NO 127

- Ceres seq_id 2025479

318

- Alternative transcription start site(s) located in SEQ ID NO 127:

1419

- Clone 28572 starts at 1419 and ends at 1955 in cDNA.

5

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 128

- Ceres seq_id 2025480

- Location of start within SEQ ID NO 127: at 1 nt.

10

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 129

- Ceres seq_id 2025481

- Location of start within SEQ ID NO 127: at 226 nt.

15

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 130

- Ceres seq_id 2025482

- Location of start within SEQ ID NO 127: at 271 nt.

20

(Ba) Polypeptide Activities: Similar Cell Wall Plasma Membrane disconnecting CLCT Protein activities, and proline rich protein activities.

25

Maximum Length Sequence:

Public Genomic DNA:

gi No: 6:34247

Predicted Exons:

30

INTR 46663 ... 46055 OCKHAMG-CDNA

SINGLE 46579 ... 46103 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

35

- Pat. Appln. SEQ ID NO 131

- Ceres seq_id 2032963

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 132

40

- Ceres seq_id 2032964

- Location of start within SEQ ID NO 131: at 85 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene, dicot

45

specific gene. specific gene, plant

Maximum Length Sequence:

Public Genomic DNA:

50

gi No: 6449509

Predicted Exons:

319

	INIT	32110	...	32118	OCKHAMG-CDS
	INTR	32363	...	32538	OCKHAMG-CDS
	INTR	33006	...	33084	OCKHAMG-CDS
	TERM	33182	...	33247	OCKHAMG-CDS

5 gi No: 6453848

 Predicted Exons:

	INIT	34795	...	34803	OCKHAMG-CDS
	INTR	35048	...	35223	OCKHAMG-CDS
	INTR	35691	...	35769	OCKHAMG-CDS
10	TERM	35867	...	35932	OCKHAMG-CDS

 gi No: 6456153

 Predicted Exons:

	INIT	32305	...	32313	OCKHAMG-CDS
	INTR	32558	...	32733	OCKHAMG-CDS
15	INTR	33201	...	33279	OCKHAMG-CDS
	TERM	33377	...	33442	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

20 - Pat. Appln. SEQ ID NO 133

 - Ceres seq_id 2033706

(B) Polypeptide Sequence

 - Pat. Appln. SEQ ID NO 134

 - Ceres seq_id 2033707

25 - Location of start within SEQ ID NO 133: at 1 nt.

(B) Polypeptide Sequence

 - Pat. Appln. SEQ ID NO 135

 - Ceres seq_id 2033708

30 - Location of start within SEQ ID NO 133: at 34 nt.

(B) Polypeptide Sequence

 - Pat. Appln. SEQ ID NO 136

 - Ceres seq_id 2033709

35 - Location of start within SEQ ID NO 133: at 160 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot

40 specific gene. specific gene, plant

Maximum Length Sequence:

Public Genomic DNA:

45 gi No: 4512646

 Predicted Exons:

	INTR	43130	...	43387	OCKHAMG-CDNA
	INTR	43479	...	43638	OCKHAMG-CDNA
	INIT	43224	...	43387	OCKHAMG-CDS
50	TERM	43479	...	43494	OCKHAMG-CDS

320

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 137

- Ceres seq_id 2043118

5 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 138

- Ceres seq_id 2043119

- Location of start within SEQ ID NO 137: at 65 nt.

10 - Location of Signal Peptide Cleavage Site within SEQ ID NO 138: at 22 aa.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 139

- Ceres seq_id 2043120

15 - Location of start within SEQ ID NO 137: at 1 nt.

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 140

- Ceres seq_id 2043121

20 - Location of start within SEQ ID NO 137: at 95 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot

25 specific gene. specific gene, plant

Maximum Length Sequence:

Public Genomic DNA:

gi No: 3985934

30 Predicted Exons:

INTR 40094 ... 40516 OCKHAMG-CDNA

INTR 40861 ... 41275 OCKHAMG-CDNA

INIT 40233 ... 40516 OCKHAMG-CDS

35 TERM 40861 ... 41077 OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 141

- Ceres seq_id 2047214

40

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 142

- Ceres seq_id 2047215

- Location of start within SEQ ID NO 141: at 140 nt.

45

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 143

- Ceres seq_id 2047216

- Location of start within SEQ ID NO 141: at 224 nt.

50

(B) Polypeptide Sequence

321

- Pat. Appln. SEQ ID NO 144
 - Ceres seq_id 2047217
 - Location of start within SEQ ID NO 141: at 153 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
- 5 ID NO 144: at 18 aa.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant

10 specific gene.

Maximum Length Sequence:

Public Genomic DNA:

gi No: 3985958

15 Predicted Exons:

INTR	8598	...	8696	OCKHAMG-CDNA
INTR	8960	...	9035	OCKHAMG-CDNA
INTR	9202	...	9513	OCKHAMG-CDNA
INTR	9628	...	9669	OCKHAMG-CDNA

20

INIT	8997	...	9035	OCKHAMG-CDS
INTR	9202	...	9513	OCKHAMG-CDS
TERM	9628	...	9822	OCKHAMG-CDS

25 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 145
- Ceres seq_id 2047438

(B) Polypeptide Sequence

- 30
- Pat. Appln. SEQ ID NO 146
 - Ceres seq_id 2047439
 - Location of start within SEQ ID NO 145: at 137 nt.

Maximum Length Sequence:

35 Public Genomic DNA:

gi No: 4757403

Predicted Exons:

INTR	35281	...	34781	OCKHAMG-CDNA
------	-------	-----	-------	--------------

40

SINGLE	35235	...	35005	OCKHAMG-CDS
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(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 147
- Ceres seq_id 2049056

45

(B) Polypeptide Sequence

- 50
- Pat. Appln. SEQ ID NO 148
 - Ceres seq_id 2049057
 - Location of start within SEQ ID NO 147: at 47 nt.
 - Location of Signal Peptide Cleavage Site within SEQ
- ID NO 148: at 22 aa.

322

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 149
- Ceres seq_id 2049058
- 5 - Location of start within SEQ ID NO 147: at 59 nt.
- Location of Signal Peptide Cleavage Site within SEQ ID NO 149: at 18 aa.

Maximum Length Sequence:

10 Public Genomic DNA:

gi No: 4538972

Predicted Exons:

	INTR	32316	...	32561	OCKHAMG-CDNA
	INTR	32643	...	32715	OCKHAMG-CDNA
15	INTR	33489	...	33697	OCKHAMG-CDNA
	INTR	33789	...	33935	OCKHAMG-CDNA
	INTR	34034	...	34365	OCKHAMG-CDNA
	INIT	32328	...	32561	OCKHAMG-CDS
20	INTR	32643	...	32715	OCKHAMG-CDS
	INTR	33489	...	33697	OCKHAMG-CDS
	INTR	33789	...	33935	OCKHAMG-CDS
	TERM	34034	...	34159	OCKHAMG-CDS

25 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 150
- Ceres seq_id 2050386

(B) Polypeptide Sequence

- 30 - Pat. Appln. SEQ ID NO 151
- Ceres seq_id 2050387
- Location of start within SEQ ID NO 150: at 1 nt.

(B) Polypeptide Sequence

- 35 - Pat. Appln. SEQ ID NO 152
- Ceres seq_id 2050388
- Location of start within SEQ ID NO 150: at 13 nt.

(B) Polypeptide Sequence

- 40 - Pat. Appln. SEQ ID NO 153
- Ceres seq_id 2050389
- Location of start within SEQ ID NO 150: at 151 nt.

- 45 (Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot specific gene, plant
specific gene.

Maximum Length Sequence:

50 Public Genomic DNA:

gi No: 4878038

323

Predicted Exons:

5	INTR	22640 ...	22509	OCKHAMG-CDNA
	INTR	22412 ...	22340	OCKHAMG-CDNA
	INTR	22122 ...	21728	OCKHAMG-CDNA
	INTR	22674 ...	22509	OCKHAMG-CDNA
	INTR	22412 ...	22340	OCKHAMG-CDNA
	INTR	22122 ...	21766	OCKHAMG-CDNA
10	INIT	22587 ...	22509	OCKHAMG-CDS
	INTR	22412 ...	22340	OCKHAMG-CDS
	TERM	22122 ...	21852	OCKHAMG-CDS

gi No: 6143825

15	INTR	22639 ...	22508	OCKHAMG-CDNA
	INTR	22411 ...	22339	OCKHAMG-CDNA
	INTR	22121 ...	21727	OCKHAMG-CDNA
20	INTR	22673 ...	22508	OCKHAMG-CDNA
	INTR	22411 ...	22339	OCKHAMG-CDNA
	INTR	22121 ...	21765	OCKHAMG-CDNA
25	INIT	22586 ...	22508	OCKHAMG-CDS
	INTR	22411 ...	22339	OCKHAMG-CDS
	TERM	22121 ...	21851	OCKHAMG-CDS

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 154
- Ceres seq_id 2053353

(B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 155
- Ceres seq_id 2053354
- Location of start within SEQ ID NO 154: at 88 nt.

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene. specific gene, plant

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4115352

Predicted Exons:

45	INIT	29289 ...	29287	OCKHAMG-CDS
	INTR	27681 ...	27485	OCKHAMG-CDS
	INTR	27312 ...	27193	OCKHAMG-CDS
	INTR	26979 ...	26916	OCKHAMG-CDS
50	TERM	26654 ...	26646	OCKHAMG-CDS

324

(Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 156

- Ceres seq_id 2055693

5 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 157

- Ceres seq_id 2055694

- Location of start within SEQ ID NO 156: at 1 nt.

10 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 158

- Ceres seq_id 2055695

- Location of start within SEQ ID NO 156: at 46 nt.

15 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 159

- Ceres seq_id 2055696

- Location of start within SEQ ID NO 156: at 2 nt.

- Location of Signal Peptide Cleavage Site within SEQ

20 ID NO 159: at 28 aa.

(Ba) Polypeptide Activities: Arabidopsis specific
gene, dicot

specific gene, plant

25 specific gene.

Maximum Length Sequence:

Public Genomic DNA:

gi No: 4406790

30 Predicted Exons:

INTR 81640 ... 81247 OCKHAMG-CDNA

SINGLE 81603 ... 81367 OCKHAMG-CDS

35 (Ac) cDNA Polynucleotide Sequence

- Pat. Appln. SEQ ID NO 160

- Ceres seq_id 2056405

40 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 161

- Ceres seq_id 2056406

- Location of start within SEQ ID NO 160: at 38 nt.

45 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 162

- Ceres seq_id 2056407

- Location of start within SEQ ID NO 160: at 56 nt.

50 (B) Polypeptide Sequence

- Pat. Appln. SEQ ID NO 163

325

- Ceres seq_id 2056408
- Location of start within SEQ ID NO 160: at 177 nt.
- Location of Signal Peptide Cleavage Site within SEQ
ID NO 163: at 14 aa.

5

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

10

Maximum Length Sequence:
related to:
Clone IDs:
233233

15

(Ac) cDNA Polynucleotide Sequence
- Pat. Appln. SEQ ID NO 164
- Ceres seq_id 2065747

20

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 165
- Ceres seq_id 2065748
- Location of start within SEQ ID NO 164: at 114 nt.

25

(B) Polypeptide Sequence
- Pat. Appln. SEQ ID NO 166
- Ceres seq_id 2065749
- Location of start within SEQ ID NO 164: at 279 nt.

30

(Ba) Polypeptide Activities: Arabidopsis specific gene,
dicot
specific gene, plant
specific gene.

326

SEQ TABLE 1

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..601
 (D) OTHER INFORMATION: / Ceres Seq. ID 1007546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

gacgaacagg ccacgcgtga ctacatacat aatttggttt ctcttttttt ttttggttctt      60
cttggttcctc ttttggttttt gacattgggt ctggagaaga tgagttcggg agaaccagac      120
atggaagatc tgttccagga gaagaagcgt gtcaggaatc ctctcggtcc tctcgggtgca      180
cttatgaccg cgggagtgct cacggctggg ttgattagtt tcagaagagg caattctcag      240
ttgggtcagg ttttgatgag agctagggtg gtcgtccagg gtgctactgt cgctttaatg      300
gttggaaaccg gttattacta cgggtgataat ccgtggaaga agtgagctcc aactacttgt      360
tcgtttttcac ataattgaga tgacactcgg gaaatctgcg ggcaaagggtg tgtgtgctct      420
cgctctgagt gtagaaatat gcggtcctgc taggatttag taagggtaca ttacatgatt      480
tgaataattt gaagaacgaa caagtatcgt tgtatcttga tcaattgatt agattgatt      540
aaggaaattc tccgaaaacc atctttactc tatctgtcaa aatctcatta tctttctgcc      600

```

g

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..114

(D) OTHER INFORMATION: / Ceres Seq. ID 1007547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Asp Glu Gln Ala Thr Arg Asp Tyr Ile His Asn Leu Val Ser Leu Phe
1      5      10      15
Phe Phe Val Leu Leu Val Pro Leu Trp Phe Leu Thr Leu Val Leu Glu
20      25      30
Lys Met Ser Ser Val Glu Pro Asp Met Glu Asp Leu Phe Gln Glu Lys
35      40      45
Lys Arg Val Arg Asn Pro Leu Val Pro Leu Gly Ala Leu Met Thr Ala
50      55      60
Gly Val Leu Thr Ala Gly Leu Ile Ser Phe Arg Arg Gly Asn Ser Gln
65      70      75      80
Leu Gly Gln Val Leu Met Arg Ala Arg Val Val Val Gln Gly Ala Thr
85      90      95
Val Ala Leu Met Val Gly Thr Gly Tyr Tyr Tyr Gly Asp Asn Pro Trp
100      105      110
Lys Lys

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..81

327

(D) OTHER INFORMATION: / Ceres Seq. ID 1007548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ser Ser Val Glu Pro Asp Met Glu Asp Leu Phe Gln Glu Lys Lys
 1 5 10 15
 5 Arg Val Arg Asn Pro Leu Val Pro Leu Gly Ala Leu Met Thr Ala Gly
 20 25 30
 Val Leu Thr Ala Gly Leu Ile Ser Phe Arg Arg Gly Asn Ser Gln Leu
 35 40 45
 Gly Gln Val Leu Met Arg Ala Arg Val Val Val Gln Gly Ala Thr Val
 50 55 60
 10 Ala Leu Met Val Gly Thr Gly Tyr Tyr Tyr Gly Asp Asn Pro Trp Lys
 65 70 75 80
 Lys

15 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

25 (D) OTHER INFORMATION: / Ceres Seq. ID 1007549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Glu Asp Leu Phe Gln Glu Lys Lys Arg Val Arg Asn Pro Leu Val
 1 5 10 15
 30 Pro Leu Gly Ala Leu Met Thr Ala Gly Val Leu Thr Ala Gly Leu Ile
 20 25 30
 Ser Phe Arg Arg Gly Asn Ser Gln Leu Gly Gln Val Leu Met Arg Ala
 35 40 45
 Arg Val Val Val Gln Gly Ala Thr Val Ala Leu Met Val Gly Thr Gly
 50 55 60
 35 Tyr Tyr Tyr Gly Asp Asn Pro Trp Lys Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 970 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

45 (A) NAME/KEY: -

(B) LOCATION: 1..970

(D) OTHER INFORMATION: / Ceres Seq. ID 1007583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

aacgccgctc atttttaggg ttccagatat aggcagattc tcacatttgc aaacatgacg 60
 50 actcagatca gcaagaagag aaagtttgta gcggacggtg tgttctacgc tgaattgaat 120
 gaggttctta caagagagct agcagaggat ggttactctg gtgttgaggt tagggttact 180
 cctatgagga ctgagattat catcagagct acacgtactc agaatgttct cggtgagaag 240
 gggaggagaa ttagggaatt gacttccctt gttcagaaga gattcaagtt tccagttgac 300
 agtggtgagc tttatgccga gaagggttaac aacagagggtc tctgtgccat cgctcaggct 360
 55 gagtctttac gttacaagct tcttggtggt ctgctgttc gtagggttg ctatggtgtg 420
 ttgaggtttg ttatggagag tggagctaag ggatgcgagg ttatcgtgag tggaaagctt 480
 cgtgctgccg gagccaagtc tatgaagttc aaagatggct acatggtgtc atctggtcaa 540
 ccaactaagg aatacataga ctctgcagtg agacatgttt tgcttagaca aggtgtgttg 600
 ggaatcaagg tgaaggttat gcttgattgg gaccctaagg gcatatcagg accaaagaca 660
 60 ccattgcctg atgttgtgat cattcattct cctaaagaag aagaggccat ctacgcacct 720
 gctcaggttg ctgccccggc tgctctcgta gcagatgcac cactcacagc cgtagattac 780
 cctgcgatga tcccagtcgc ctaaaagaat cctttgtact agtcgatgtg attttgtttt 840

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caactgtttct tgctctttttg acagattata gctttctcgta ttttcgaatc agacacgttt 900
 cctctgtttct tattcgaaaa ttatctcaag ttccattgt tgaaaaagcc ctttttagtt 960
 tcataaatcg

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..249
- (D) OTHER INFORMATION: / Ceres Seq. ID 1007584

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Thr	Thr	Gln	Ile	Ser	Lys	Lys	Arg	Lys	Phe	Val	Ala	Asp	Gly	Val	1	5	10	15
Phe	Tyr	Ala	Glu	Leu	Asn	Glu	Val	Leu	Thr	Arg	Glu	Leu	Ala	Glu	Asp	20	25	30	
Gly	Tyr	Ser	Gly	Val	Glu	Val	Arg	Val	Thr	Pro	Met	Arg	Thr	Glu	Ile	35	40	45	
Ile	Ile	Arg	Ala	Thr	Arg	Thr	Gln	Asn	Val	Leu	Gly	Glu	Lys	Gly	Arg	50	55	60	
Arg	Ile	Arg	Glu	Leu	Thr	Ser	Leu	Val	Gln	Lys	Arg	Phe	Lys	Phe	Pro	65	70	75	80
Val	Asp	Ser	Val	Glu	Leu	Tyr	Ala	Glu	Lys	Val	Asn	Asn	Arg	Gly	Leu	85	90	95	
Cys	Ala	Ile	Ala	Gln	Ala	Glu	Ser	Leu	Arg	Tyr	Lys	Leu	Leu	Gly	Gly	100	105	110	
Leu	Ala	Val	Arg	Arg	Ala	Cys	Tyr	Gly	Val	Leu	Arg	Phe	Val	Met	Glu	115	120	125	
Ser	Gly	Ala	Lys	Gly	Cys	Glu	Val	Ile	Val	Ser	Gly	Lys	Leu	Arg	Ala	130	135	140	
Ala	Arg	Ala	Lys	Ser	Met	Lys	Phe	Lys	Asp	Gly	Tyr	Met	Val	Ser	Ser	145	150	155	160
Gly	Gln	Pro	Thr	Lys	Glu	Tyr	Ile	Asp	Ser	Ala	Val	Arg	His	Val	Leu	165	170	175	
Leu	Arg	Gln	Gly	Val	Leu	Gly	Ile	Lys	Val	Lys	Val	Met	Leu	Asp	Trp	180	185	190	
Asp	Pro	Lys	Gly	Ile	Ser	Gly	Pro	Lys	Thr	Pro	Leu	Pro	Asp	Val	Val	195	200	205	
Ile	Ile	His	Ser	Pro	Lys	Glu	Glu	Glu	Ala	Ile	Tyr	Ala	Pro	Ala	Gln	210	215	220	
Val	Ala	Ala	Pro	Ala	Ala	Leu	Val	Ala	Asp	Ala	Pro	Leu	Thr	Ala	Val	225	230	235	240
Asp	Tyr	Pro	Ala	Met	Ile	Pro	Val	Ala								245			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..206
- (D) OTHER INFORMATION: / Ceres Seq. ID 1007585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Arg	Thr	Glu	Ile	Ile	Ile	Arg	Ala	Thr	Arg	Thr	Gln	Asn	Val	Leu	1	5	10	15
Gly	Glu	Lys	Gly	Arg	Arg	Ile	Arg	Glu	Leu	Thr	Ser	Leu	Val	Gln	Lys				

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20 25 30
 Arg Phe Lys Phe Pro Val Asp Ser Val Glu Leu Tyr Ala Glu Lys Val
 35 40 45
 Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr
 5 50 55 60
 Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu
 65 70 75 80
 Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser
 85 90 95
 10 Gly Lys Leu Arg Ala Ala Arg Ala Lys Ser Met Lys Phe Lys Asp Gly
 100 105 110
 Tyr Met Val Ser Ser Gly Gln Pro Thr Lys Glu Tyr Ile Asp Ser Ala
 115 120 125
 15 Val Arg His Val Leu Leu Arg Gln Gly Val Leu Gly Ile Lys Val Lys
 130 135 140
 Val Met Leu Asp Trp Asp Pro Lys Gly Ile Ser Gly Pro Lys Thr Pro
 145 150 155 160
 Leu Pro Asp Val Val Ile Ile His Ser Pro Lys Glu Glu Glu Ala Ile
 165 170 175
 20 Tyr Ala Pro Ala Gln Val Ala Ala Pro Ala Ala Leu Val Ala Asp Ala
 180 185 190
 Pro Leu Thr Ala Val Asp Tyr Pro Ala Met Ile Pro Val Ala
 195 200 205
 (2) INFORMATION FOR SEQ ID NO:8:
 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 768 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..768
 (D) OTHER INFORMATION: / Ceres Seq. ID 1008148
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
 aaaaaaaccc tagttttttg ctctctcgaa gttccgtgcg actctctgct cgagcaagat 60
 ctctaccga tacaatgatt atctcagagg ctaaccgcaa agaaatctgc aagtacctct 120
 tcaaagaagg agtttgcttt gcgaagaagg atttcaatct tgctaagcat ccgttgatcg 180
 atgtcccga cctacaagtg attaagctta tgcagagttt caaatccaag gagtatgtta 240
 40 gagagacatt tgcctggatg cactactatt ggtttttgac caatgaaggg atcgagttct 300
 tgagaactta tcttaatctt ccactctgatg ttgttctgct tactttgaag aagtcagcta 360
 agcctggtgg tcgtccattt ggtggcccac ctggtgatcg ctcaagagga cctcgccatg 420
 aaggaggaga ccgtcccagg tttggtgacc gtgatgggta ccgtgcaggt cctcgagctg 480
 gtggtgagtt tggaggtgaa aagggtggag ctctgcaga ttaccagcca tctttccaag 540
 45 gaagtgggcg tggttttggc cgtggtgctg gtggctacag cgcagctgca ccactctggtt 600
 caggtttgcc ttgaaaaaga aatgtcttta ggtgacagta agaccatgga ggagttttca 660
 gctttaaatt ttgcttttgt aattcagatt ccggaatcct tcataatctc tatctgagtt 720
 tagttttggt gttgaatcaa acatccgatt taaagttatg ttcattcc
 (2) INFORMATION FOR SEQ ID NO:9:
 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..203
 (D) OTHER INFORMATION: / Ceres Seq. ID 1008149
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
 Lys Asn Pro Ser Phe Leu Leu Ser Arg Ser Ser Val Arg Leu Ser Ala
 1 5 10 15

330

Arg Ala Arg Ser Pro Thr Asp Thr Met Ile Ile Ser Glu Ala Asn Arg
 20 25 30
 Lys Glu Ile Cys Lys Tyr Leu Phe Lys Glu Gly Val Cys Phe Ala Lys
 35 40 45
 5 Lys Asp Phe Asn Leu Ala Lys His Pro Leu Ile Asp Val Pro Asn Leu
 50 55 60
 Gln Val Ile Lys Leu Met Gln Ser Phe Lys Ser Lys Glu Tyr Val Arg
 65 70 75 80
 10 Glu Thr Phe Ala Trp Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly
 85 90 95
 Ile Glu Phe Leu Arg Thr Tyr Leu Asn Leu Pro Ser Asp Val Val Pro
 100 105 110
 Ala Thr Leu Lys Lys Ser Ala Lys Pro Gly Gly Arg Pro Phe Gly Gly
 115 120 125
 15 Pro Pro Gly Asp Arg Ser Arg Gly Pro Arg His Glu Gly Gly Asp Arg
 130 135 140
 Pro Arg Phe Gly Asp Arg Asp Gly Tyr Arg Ala Gly Pro Arg Ala Gly
 145 150 155 160
 20 Gly Glu Phe Gly Gly Glu Lys Gly Gly Ala Pro Ala Asp Tyr Gln Pro
 165 170 175
 Ser Phe Gln Gly Ser Gly Arg Gly Phe Gly Arg Gly Ala Gly Gly Tyr
 180 185 190
 Ser Ala Ala Pro Ser Gly Ser Gly Leu Pro
 195 200
 25 (2) INFORMATION FOR SEQ ID NO:10:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 179 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..179
 35 (D) OTHER INFORMATION: / Ceres Seq. ID 1008150
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
 Met Ile Ile Ser Glu Ala Asn Arg Lys Glu Ile Cys Lys Tyr Leu Phe
 1 5 10 15
 40 Lys Glu Gly Val Cys Phe Ala Lys Lys Asp Phe Asn Leu Ala Lys His
 20 25 30
 Pro Leu Ile Asp Val Pro Asn Leu Gln Val Ile Lys Leu Met Gln Ser
 35 40 45
 Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Phe Ala Trp Met His Tyr
 50 55 60
 45 Tyr Trp Phe Leu Thr Asn Glu Gly Ile Glu Phe Leu Arg Thr Tyr Leu
 65 70 75 80
 Asn Leu Pro Ser Asp Val Val Pro Ala Thr Leu Lys Lys Ser Ala Lys
 85 90 95
 50 Pro Gly Gly Arg Pro Phe Gly Gly Pro Pro Gly Asp Arg Ser Arg Gly
 100 105 110
 Pro Arg His Glu Gly Gly Asp Arg Pro Arg Phe Gly Asp Arg Asp Gly
 115 120 125
 Tyr Arg Ala Gly Pro Arg Ala Gly Gly Glu Phe Gly Gly Glu Lys Gly
 130 135 140
 55 Gly Ala Pro Ala Asp Tyr Gln Pro Ser Phe Gln Gly Ser Gly Arg Gly
 145 150 155 160
 Phe Gly Arg Gly Ala Gly Gly Tyr Ser Ala Ala Pro Ser Gly Ser
 165 170 175
 60 Gly Leu Pro
 (2) INFORMATION FOR SEQ ID NO:11:
 (i) SEQUENCE CHARACTERISTICS:

331

- (A) LENGTH: 134 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..134
 (D) OTHER INFORMATION: / Ceres Seq. ID 1008151
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Ser | Phe | Lys | Ser | Lys | Glu | Tyr | Val | Arg | Glu | Thr | Phe | Ala | Trp |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Met | His | Tyr | Tyr | Trp | Phe | Leu | Thr | Asn | Glu | Gly | Ile | Glu | Phe | Leu | Arg |
| | | 20 | | | | | | 25 | | | | | 30 | | |
| 15 | Thr | Tyr | Leu | Asn | Leu | Pro | Ser | Asp | Val | Val | Pro | Ala | Thr | Leu | Lys |
| | | 35 | | | | | | 40 | | | | | 45 | | |
| | Ser | Ala | Lys | Pro | Gly | Gly | Arg | Pro | Phe | Gly | Gly | Pro | Pro | Gly | Asp |
| | | 50 | | | | | 55 | | | | | 60 | | | |
| | Ser | Arg | Gly | Pro | Arg | His | Glu | Gly | Gly | Asp | Arg | Pro | Arg | Phe | Gly |
| 20 | | 65 | | | | 70 | | | | 75 | | | | 80 | |
| | Arg | Asp | Gly | Tyr | Arg | Ala | Gly | Pro | Arg | Ala | Gly | Gly | Glu | Phe | Gly |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| | Glu | Lys | Gly | Gly | Ala | Pro | Ala | Asp | Tyr | Gln | Pro | Ser | Phe | Gln | Gly |
| | | | 100 | | | | | 105 | | | | | | 110 | |
| 25 | Gly | Arg | Gly | Phe | Gly | Arg | Gly | Ala | Gly | Gly | Tyr | Ser | Ala | Ala | Pro |
| | | 115 | | | | | 120 | | | | | | 125 | | |
| | Ser | Gly | Ser | Gly | Leu | Pro | | | | | | | | | |
| | | 130 | | | | | | | | | | | | | |
- (2) INFORMATION FOR SEQ ID NO:12:
- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 995 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: ~
 (B) LOCATION: 1..995
 (D) OTHER INFORMATION: / Ceres Seq. ID 1008334
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
- | | | | | | | |
|---------------|------------|------------|------------|------------|------------|-----|
| atatctaaaa | gactcaaaaa | cctatcgtca | tttatcttca | acaggcggaa | gaacggcgat | 60 |
| ggccgcccatt | acagctctca | ctctccgctc | tcctgttttt | cttcttcctc | catcgctcgt | 120 |
| cacaagccct | agattccatg | gcttcaccaa | tcaaccacca | ccagctcgtc | tcttctttcc | 180 |
| tcttaacccc | ttcccttctc | tatcaatcca | aaaccctaaa | tccatccgaa | tttccgcatt | 240 |
| cgcttcgccc | ataacaacac | caatcctcca | gacggagaag | tcaacagctc | ggtcacogac | 300 |
| actcaccggg | tccactcggt | ctctcgctac | tctcgcggt | ttagcaatcg | ctgtaaccag | 360 |
| agtccctagct | cagaaactct | ctctcgcaat | ccagacttca | agtcccgtaa | tgcgcgacgg | 420 |
| gttacgattc | tctctcagta | cgcccggaac | tgtcttcttc | gcgtctctcc | gggatcgtcc | 480 |
| tccgggatac | ttgaacacgc | cgctgacggt | tgttgcggtg | gggataaaga | agtggctaga | 540 |
| 50 catttacagt | ggggtattga | tgggtagggt | tttgctgagt | tggttccta | atatcccttg | 600 |
| ggaaagacag | cctttgtctg | ccattagaga | tctctgtgat | ccttacttga | atctcttcag | 660 |
| aaacatcatt | cctcctatct | tgcatacgt | tgatgttagt | ccattgcttg | ctttcgcggt | 720 |
| tcttggtaca | cttggtatga | ttgttcattg | cagcactggg | tagaaattgg | aagacttgag | 780 |
| ctaattggtt | tgttgaaacg | ttcaattggg | aaatttctgc | aacttgtttc | ccaagattag | 840 |
| 55 ggaaaaatca | gaatttgatg | ctgtgttgga | tgctcgatga | gagttgtgag | ctttatcggt | 900 |
| tttggtgttc | tctttttgac | tttgattctg | aataatgaga | ttttgggttg | ttgtttatct | 960 |
| cctaattaca | tgttcagact | acagtttatt | gatgg | | | |
- (2) INFORMATION FOR SEQ ID NO:13:
- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

332

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

5 (A) NAME/KEY: peptide
(B) LOCATION: 1..253
(D) OTHER INFORMATION: / Ceres Seq. ID 1008335
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Tyr Leu Lys Asp Ser Lys Thr Tyr Arg His Leu Ser Ser Thr Gly Gly
1 5 10 15
10 Arg Thr Ala Met Ala Ala Ile Thr Ala Leu Thr Leu Arg Ser Pro Val
20 25 30
Phe Leu Leu Pro Pro Ser Ser Val Thr Ser Pro Arg Phe His Gly Phe
35 40 45
15 Thr Asn Gln Pro Pro Pro Ala Arg Leu Phe Phe Pro Leu Asn Pro Phe
50 55 60
Pro Ser Leu Ser Ile Gln Asn Pro Lys Ser Ile Arg Ile Ser Ala Ser
65 70 75 80
Ala Ser Pro Ile Thr Thr Pro Ile Leu Gln Thr Glu Lys Ser Thr Ala
85 90 95
20 Arg Ser Ser Thr Leu Thr Gly Ser Thr Arg Ser Leu Ala Thr Leu Ala
100 105 110
Ala Leu Ala Ile Ala Val Thr Arg Val Leu Ala Gln Lys Leu Ser Leu
115 120 125
25 Ala Ile Gln Thr Ser Ser Pro Val Ile Ala Asp Gly Leu Arg Phe Ser
130 135 140
Leu Ser Thr Ala Gly Pro Val Phe Phe Ala Ser Leu Arg Asp Arg Pro
145 150 155 160
Pro Gly Tyr Leu Asn Thr Pro Leu Thr Val Val Ala Val Gly Ile Lys
165 170 175
30 Lys Trp Leu Asp Ile Tyr Ser Gly Val Leu Met Val Arg Val Leu Leu
180 185 190
Ser Trp Phe Pro Asn Ile Pro Trp Glu Arg Gln Pro Leu Ser Ala Ile
195 200 205
35 Arg Asp Leu Cys Asp Pro Tyr Leu Asn Leu Phe Arg Asn Ile Ile Pro
210 215 220
Pro Ile Phe Asp Thr Leu Asp Val Ser Pro Leu Leu Ala Phe Ala Val
225 230 235 240
Leu Gly Thr Leu Gly Ser Ile Val His Gly Ser Thr Gly
245 250

40 (2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..234
50 (D) OTHER INFORMATION: / Ceres Seq. ID 1008336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Ala Ala Ile Thr Ala Leu Thr Leu Arg Ser Pro Val Phe Leu Leu
1 5 10 15
55 Pro Pro Ser Ser Val Thr Ser Pro Arg Phe His Gly Phe Thr Asn Gln
20 25 30
Pro Pro Pro Ala Arg Leu Phe Phe Pro Leu Asn Pro Phe Pro Ser Leu
35 40 45
Ser Ile Gln Asn Pro Lys Ser Ile Arg Ile Ser Ala Ser Ala Ser Pro
50 55 60
60 Ile Thr Thr Pro Ile Leu Gln Thr Glu Lys Ser Thr Ala Arg Ser Ser
65 70 75 80
Thr Leu Thr Gly Ser Thr Arg Ser Leu Ala Thr Leu Ala Ala Leu Ala

333

	85	90	95
	Ile Ala Val Thr Arg Val Leu Ala Gln Lys Leu Ser Leu Ala Ile Gln		
	100	105	110
5	Thr Ser Ser Pro Val Ile Ala Asp Gly Leu Arg Phe Ser Leu Ser Thr		
	115	120	125
	Ala Gly Pro Val Phe Phe Ala Ser Leu Arg Asp Arg Pro Pro Gly Tyr		
	130	135	140
	Leu Asn Thr Pro Leu Thr Val Val Ala Val Gly Ile Lys Lys Trp Leu		
	145	150	155
10	Asp Ile Tyr Ser Gly Val Leu Met Val Arg Val Leu Leu Ser Trp Phe		
	165	170	175
	Pro Asn Ile Pro Trp Glu Arg Gln Pro Leu Ser Ala Ile Arg Asp Leu		
	180	185	190
	Cys Asp Pro Tyr Leu Asn Leu Phe Arg Asn Ile Ile Pro Pro Ile Phe		
15	195	200	205
	Asp Thr Leu Asp Val Ser Pro Leu Leu Ala Phe Ala Val Leu Gly Thr		
	210	215	220
	Leu Gly Ser Ile Val His Gly Ser Thr Gly		
	225	230	
20	(2) INFORMATION FOR SEQ ID NO:15:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 520 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEDNESS: single		
25	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: DNA (genomic)		
	(ix) FEATURE:		
	(A) NAME/KEY: -		
	(B) LOCATION: 1..520		
30	(D) OTHER INFORMATION: / Ceres Seq. ID 1008701		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:		
	acacataacc ctcttggaag gagtctcaac acttgcagag aaaaagaaga aggaagatcc		60
	cggaaaatgg caacggcgat tgtacgttca gctctttccc gagcagcgac tcgcgagct		120
	ccgaagacat ccgtcgctcc taagcgaaac ttttctctt ccgcccggcca tgacgatgct		180
35	tatgaagctg cgaagtggga gaagataact tatctgggta ttgctagttg cactgctcta		240
	gctgtctatg ttttatccaa gggccatcat cccggcgaag accctcctgc ctatccgcat		300
	atgcacatcc gcaacaagga gtttccttgg ggtccggatg gtctgtttga ggtgaagcac		360
	aacaaagagc actgagtctt gcgtgggtcat aataacgtct tcttggttta tttgaaaggc		420
40	taaaatgttt taccgtatatt gttctcaccg ttgtgcaacg attttctact ccaatctctt		480
	ttcttttggtt gggaaataaa agttaatact ttgcttggtc		
	(2) INFORMATION FOR SEQ ID NO:16:		
	(i) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 124 amino acids		
	(B) TYPE: amino acid		
45	(C) STRANDEDNESS:		
	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: peptide		
	(ix) FEATURE:		
	(A) NAME/KEY: peptide		
50	(B) LOCATION: 1..124		
	(D) OTHER INFORMATION: / Ceres Seq. ID 1008702		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:		
	Thr His Asn Pro Leu Gly Lys Ser Leu Asn Thr Cys Arg Glu Lys Glu		
	1	5	10
55	Glu Gly Arg Ser Arg Lys Met Ala Thr Ala Ile Val Arg Ser Ala Leu		
	20	25	30
	Ser Arg Ala Ala Thr Arg Ala Ala Pro Lys Thr Ser Val Ala Pro Lys		
	35	40	45
	Arg Asn Phe Ser Ser Ser Ala Gly His Asp Asp Ala Tyr Glu Ala Ala		
60	50	55	60
	Lys Trp Glu Lys Ile Thr Tyr Leu Gly Ile Ala Ser Cys Thr Ala Leu		
	65	70	75
			80

334

Ala Val Tyr Val Leu Ser Lys Gly His His Pro Gly Glu Asp Pro Pro

85

90

95

Ala Tyr Pro His Met His Ile Arg Asn Lys Glu Phe Pro Trp Gly Pro

100

105

110

5 Asp Gly Leu Phe Glu Val Lys His Asn Lys Glu His

115

120

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1008703

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Thr Ala Ile Val Arg Ser Ala Leu Ser Arg Ala Ala Thr Arg

1

5

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Ala Ala Pro Lys Thr Ser Val Ala Pro Lys Arg Asn Phe Ser Ser Ser

20

25

30

Ala Gly His Asp Asp Ala Tyr Glu Ala Ala Lys Trp Glu Lys Ile Thr

35

40

45

25 Tyr Leu Gly Ile Ala Ser Cys Thr Ala Leu Ala Val Tyr Val Leu Ser

50

55

60

Lys Gly His His Pro Gly Glu Asp Pro Pro Ala Tyr Pro His Met His

65

70

75

80

Ile Arg Asn Lys Glu Phe Pro Trp Gly Pro Asp Gly Leu Phe Glu Val

30

85

90

95

Lys His Asn Lys Glu His

100

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1008704

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

His Ile Thr Leu Leu Glu Arg Val Ser Thr Leu Ala Glu Lys Lys Lys

1

5

10

15

Lys Glu Asp Pro Gly Lys Trp Gln Arg Arg Leu Tyr Val Gln Leu Phe

20

25

30

Pro Glu Gln Arg Leu Ala Gln Leu Arg Arg His Pro Ser Leu Leu Ser

35

40

45

50 Glu Thr Phe Pro Leu Pro Pro Ala Met Thr Met Leu Met Lys Leu Arg

50

55

60

Ser Gly Arg Arg

65

55 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 662 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

60

335

(A) NAME/KEY: -

(B) LOCATION: 1..662

(D) OTHER INFORMATION: / Ceres Seq. ID 1009003

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```

5  catttttttct ttctctctct cctccctaag caaaactaaa acaagctatg gctggtatgc      60
   ttcccggagt tgagtgtgca aggaggcggc gcttccacgg tgggtgctcct ccgattgaat      120
   cctcgaacac agcttctgtg gcggctgcgg cgggacacgt ctggacacgg cgaccatcgt      180
   tctctcttta cactaccaat catgagagcc accaggccca tgtctccttc tcggagagaa      240
   gtgttaggaa taaatcttat ggagaagaca acgatgagaa acttgacgga gcagccaaaag      300
10  aggcaaagca gaggcttaac aagcggctga gaatcccacc acgtacaaagt tcaggcaaaa      360
   tggtaaagac aaagggaata aattggagca aggaaagggt aaacctctcg gggacttacc      420
   gaccgaggtg gtcgggttaa agaagagccg aggaagggtg atggaatggt tcaagcggcg      480
   agttagggaa caacaagatt gtgctatatg tctagaccgg ttcaagaagg gtgagacctt      540
   ggtacaccta ccatgtgccc ataagtttca ctccatatgc ttattgcctt ggctagacac      600
15  taatgtttat tgcccatatt gtagaactga tatttggaa taaatgttat atttttgatg      660
   cc

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1009004

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

30  Met Ala Gly Met Leu Pro Gly Val Glu Cys Ala Arg Arg Arg Arg Phe
   1          5          10          15
   His Gly Gly Ala Pro Pro Ile Glu Ser Ser Asn Thr Ala Ser Val Ala
   20          25          30
   Ala Ala Ala Gly His Val Trp Thr Arg Arg Pro Ser Phe Ser Leu Tyr
   35  35          40          45
   Thr Thr Asn His Glu Ser His Gln Ala His Val Ser Phe Ser Glu Arg
   50          55          60
   Ser Val Arg Asn Lys Ser Tyr Gly Glu Asp Asn Asp Glu Lys Leu Asp
   65  70          75          80
   Gly Ala Ala Lys Glu Ala Lys Gln Arg Leu Asn Lys Arg Leu Arg Ile
   85          90          95
   Pro Pro Arg Thr Ser Ser Gly Lys Met Val Lys Thr Lys Gly Ile Asn
   100          105          110
   Trp Ser Lys Glu Arg Val Asn Leu Ser Gly Thr Tyr Arg Pro Arg Trp
   115          120          125
45  Ser Gly
   130

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1009005

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

60  Met Leu Pro Gly Val Glu Cys Ala Arg Arg Arg Arg Phe His Gly Gly
   1          5          10          15
   Ala Pro Pro Ile Glu Ser Ser Asn Thr Ala Ser Val Ala Ala Ala Ala
   20          25          30

```

336

Gly His Val Trp Thr Arg Arg Pro Ser Phe Ser Leu Tyr Thr Thr Asn
 35 40 45
 His Glu Ser His Gln Ala His Val Ser Phe Ser Glu Arg Ser Val Arg
 50 55 60
 5 Asn Lys Ser Tyr Gly Glu Asp Asn Asp Glu Lys Leu Asp Gly Ala Ala
 65 70 75 80
 Lys Glu Ala Lys Gln Arg Leu Asn Lys Arg Leu Arg Ile Pro Pro Arg
 85 90 95
 10 Thr Ser Ser Gly Lys Met Val Lys Thr Lys Gly Ile Asn Trp Ser Lys
 100 105 110
 Glu Arg Val Asn Leu Ser Gly Thr Tyr Arg Pro Arg Trp Ser Gly
 115 120 125

(2) INFORMATION FOR SEQ ID NO:22:
 (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 504 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 20 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..504
 (D) OTHER INFORMATION: / Ceres Seq. ID 1009345
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:
 25 aagaaacaaa ggtgtcaaga agaaggatca acatattaat tgactaaaaa tgaatgcatg 60
 gatgataatc ttgttggtga tttgtgtcgc tgtggtggtg gagcaatcag aggctcgcaa 120
 aggtcgaaaag tatttaaatac caggcgtgct tgaccggtgt cgtggctcta atcctccagc 180
 gggatgtcat cctcacaatt cccaccacaa acctcgcgtc cctgttcaca attatagtcg 240
 30 tggttgtagt agaattaccc ggtgcagacg agatgcctag gtttaacctc acatgacgac 300
 gacgtccctt tatattgatac cttctttctac atgagacttg caatgatatt atatattcat 360
 atatatacac attacgctgt atatgataat tccagttgat taatatataa atcttactga 420
 tttcaattca atacacaaga tcctgtaact gaaataattt tgtccatggt ttgtgcttat 480
 aataatggta tgactcttat tatt

(2) INFORMATION FOR SEQ ID NO:23:
 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..76
 (D) OTHER INFORMATION: / Ceres Seq. ID 1009346
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:
 Met Asn Ala Trp Met Ile Ile Leu Leu Val Ile Cys Val Ala Val Val
 1 5 10 15
 Val Glu Gln Ser Glu Ala Arg Lys Gly Arg Lys Tyr Leu Asn Pro Gly
 20 25 30
 50 Val Leu Asp Arg Cys Arg Gly Pro Asn Pro Pro Ala Gly Cys His Pro
 35 40 45
 His Asn Ser His His Lys Pro Arg Val Pro Val His Asn Tyr Ser Arg
 50 55 60
 Gly Cys Ser Arg Ile Thr Arg Cys Arg Arg Asp Ala
 55 65 70 75

(2) INFORMATION FOR SEQ ID NO:24:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 60 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide

337

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..72

(D) OTHER INFORMATION: / Ceres Seq. ID 1009347

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ile Ile Leu Leu Val Ile Cys Val Ala Val Val Val Glu Gln Ser
 1 5 10 15
 Glu Ala Arg Lys Gly Arg Lys Tyr Leu Asn Pro Gly Val Leu Asp Arg
 20 25 30
 10 Cys Arg Gly Pro Asn Pro Pro Ala Gly Cys His Pro His Asn Ser His
 35 40 45
 His Lys Pro Arg Val Pro Val His Asn Tyr Ser Arg Gly Cys Ser Arg
 50 55 60
 Ile Thr Arg Cys Arg Arg Asp Ala
 15 65 70

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 967 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

25 (B) LOCATION: 1..967

(D) OTHER INFORMATION: / Ceres Seq. ID 1010140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

attttatttc ttctccaacc attctcaatc ctctctctcc aatggcttcc ttatccttcg 60
 ttctctcttc tcaccttacg ctacgcactc cttctattgc cctacgcagc actggctctt 120
 30 ctctcgaac ctccgtttca ttctccgtca aggctcaatc cgtcgcgctt tcacaggacg 180
 atttgaagaa gctcgcggcg gagaaagctg tggaggcaat taaacctggg atggttctag 240
 ggctcggaa cggatccacc gcagcttttc ctgttgatca gatcgggaaa ctactctctt 300
 ccggtgaact ctacgatatt gtcggtatcc caacgtcgaa acgaacggag gaacaagcac 360
 ggctcgttagg gattcctctt gttggggttag atacacatcc gagaatcgat ctcgctattg 420
 35 acggagcaga cgaggtagat ccgaatcttg atttagtcaa aggtcgtgga ggtgctcttc 480
 tccgtgagaa aatggtggaa gctgtggctg acaagtttat tgttggtggt gatgatacca 540
 aactcgttac aggactcggg ggaagtggat tagctatgcc ggtggaagtt gttcaattct 600
 gctggaactt taatttgatt agattgcaag agctcttcaa ggaatttgga tgtgaatcaa 660
 agcttagagt tgatggtgat ggcaagcctt atgtgactga taacagtaat tacattattg 720
 40 atttgtattt taagactcct ttgaaggatg gattcgctgc ggctaaagag attgggaagt 780
 ttcaaggagt ggtggagcat ggtctgtttc tcggaatggc tacttctgtc attatcgtcg 840
 gaaagaatgg cgttgaagtt atgaccaagt gaggttaaaa gttcaatctt tctcttcttc 900
 tttgattgac aaatttttct cctttgtaaa attatcaatt gagtttttat gtgagatcat 960
 ttcaatc

45 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 289 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..289

(D) OTHER INFORMATION: / Ceres Seq. ID 1010141

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Phe Ile Ser Ser Pro Thr Ile Leu Asn Pro Leu Ser Pro Met Ala Ser
 1 5 10 15
 60 Leu Ser Phe Val Ser Ser Ser His Leu Thr Leu Arg Thr Pro Ser Ile
 20 25 30
 Ala Leu Arg Ser Thr Gly Ser Ser Pro Arg Thr Ser Val Ser Phe Ser
 35 40 45

338

Val Lys Ala Gln Ser Val Ala Leu Ser Gln Asp Asp Leu Lys Lys Leu
 50 55 60
 Ala Ala Glu Lys Ala Val Glu Ala Ile Lys Pro Gly Met Val Leu Gly
 65 70 75 80
 5 Leu Gly Thr Gly Ser Thr Ala Ala Phe Ala Val Asp Gln Ile Gly Lys
 85 90 95
 Leu Leu Ser Ser Gly Glu Leu Tyr Asp Ile Val Gly Ile Pro Thr Ser
 100 105 110
 10 Lys Arg Thr Glu Glu Gln Ala Arg Ser Leu Gly Ile Pro Leu Val Gly
 115 120 125
 Leu Asp Thr His Pro Arg Ile Asp Leu Ala Ile Asp Gly Ala Asp Glu
 130 135 140
 Val Asp Pro Asn Leu Asp Leu Val Lys Gly Arg Gly Gly Ala Leu Leu
 145 150 155 160
 15 Arg Glu Lys Met Val Glu Ala Val Ala Asp Lys Phe Ile Val Val Ala
 165 170 175
 Asp Asp Thr Lys Leu Val Thr Gly Leu Gly Gly Ser Gly Leu Ala Met
 180 185 190
 20 Pro Val Glu Val Val Gln Phe Cys Trp Asn Phe Asn Leu Ile Arg Leu
 195 200 205
 Gln Glu Leu Phe Lys Glu Phe Gly Cys Glu Ser Lys Leu Arg Val Asp
 210 215 220
 Gly Asp Gly Lys Pro Tyr Val Thr Asp Asn Ser Asn Tyr Ile Ile Asp
 225 230 235 240
 25 Leu Tyr Phe Lys Thr Pro Leu Lys Asp Gly Phe Ala Ala Ala Lys Glu
 245 250 255
 Ile Gly Lys Phe Gln Gly Val Val Glu His Gly Leu Phe Leu Gly Met
 260 265 270
 30 Ala Thr Ser Val Ile Ile Ala Gly Lys Asn Gly Val Glu Val Met Thr
 275 280 285
 Lys

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..276

(D) OTHER INFORMATION: / Ceres Seq. ID 1010142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

45 Met Ala Ser Leu Ser Phe Val Ser Ser Ser His Leu Thr Leu Arg Thr
 1 5 10 15
 Pro Ser Ile Ala Leu Arg Ser Thr Gly Ser Ser Pro Arg Thr Ser Val
 20 25 30
 50 Ser Phe Ser Val Lys Ala Gln Ser Val Ala Leu Ser Gln Asp Asp Leu
 35 40 45
 Lys Lys Leu Ala Ala Glu Lys Ala Val Glu Ala Ile Lys Pro Gly Met
 50 55 60
 Val Leu Gly Leu Gly Thr Gly Ser Thr Ala Ala Phe Ala Val Asp Gln
 65 70 75 80
 55 Ile Gly Lys Leu Leu Ser Ser Gly Glu Leu Tyr Asp Ile Val Gly Ile
 85 90 95
 Pro Thr Ser Lys Arg Thr Glu Glu Gln Ala Arg Ser Leu Gly Ile Pro
 100 105 110
 60 Leu Val Gly Leu Asp Thr His Pro Arg Ile Asp Leu Ala Ile Asp Gly
 115 120 125
 Ala Asp Glu Val Asp Pro Asn Leu Asp Leu Val Lys Gly Arg Gly Gly
 130 135 140

339

Ala Leu Leu Arg Glu Lys Met Val Glu Ala Val Ala Asp Lys Phe Ile
 145 150 155 160
 Val Val Ala Asp Asp Thr Lys Leu Val Thr Gly Leu Gly Gly Ser Gly
 165 170 175
 5 Leu Ala Met Pro Val Glu Val Val Gln Phe Cys Trp Asn Phe Asn Leu
 180 185 190
 Ile Arg Leu Gln Glu Leu Phe Lys Glu Phe Gly Cys Glu Ser Lys Leu
 195 200 205
 10 Arg Val Asp Gly Asp Gly Lys Pro Tyr Val Thr Asp Asn Ser Asn Tyr
 210 215 220
 Ile Ile Asp Leu Tyr Phe Lys Thr Pro Leu Lys Asp Gly Phe Ala Ala
 225 230 235 240
 Ala Lys Glu Ile Gly Lys Phe Gln Gly Val Val Glu His Gly Leu Phe
 245 250 255
 15 Leu Gly Met Ala Thr Ser Val Ile Ile Ala Gly Lys Asn Gly Val Glu
 260 265 270
 Val Met Thr Lys
 275

(2) INFORMATION FOR SEQ ID NO:28:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..213

(D) OTHER INFORMATION: / Ceres Seq. ID 1010143

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Val Leu Gly Leu Gly Thr Gly Ser Thr Ala Ala Phe Ala Val Asp
 1 5 10 15
 Gln Ile Gly Lys Leu Leu Ser Ser Gly Glu Leu Tyr Asp Ile Val Gly
 20 25 30
 35 Ile Pro Thr Ser Lys Arg Thr Glu Glu Gln Ala Arg Ser Leu Gly Ile
 35 40 45
 Pro Leu Val Gly Leu Asp Thr His Pro Arg Ile Asp Leu Ala Ile Asp
 50 55 60
 40 Gly Ala Asp Glu Val Asp Pro Asn Leu Asp Leu Val Lys Gly Arg Gly
 65 70 75 80
 Gly Ala Leu Leu Arg Glu Lys Met Val Glu Ala Val Ala Asp Lys Phe
 85 90 95
 Ile Val Val Ala Asp Asp Thr Lys Leu Val Thr Gly Leu Gly Gly Ser
 100 105 110
 45 Gly Leu Ala Met Pro Val Glu Val Val Gln Phe Cys Trp Asn Phe Asn
 115 120 125
 Leu Ile Arg Leu Gln Glu Leu Phe Lys Glu Phe Gly Cys Glu Ser Lys
 130 135 140
 50 Leu Arg Val Asp Gly Asp Gly Lys Pro Tyr Val Thr Asp Asn Ser Asn
 145 150 155 160
 Tyr Ile Ile Asp Leu Tyr Phe Lys Thr Pro Leu Lys Asp Gly Phe Ala
 165 170 175
 Ala Ala Lys Glu Ile Gly Lys Phe Gln Gly Val Val Glu His Gly Leu
 180 185 190
 55 Phe Leu Gly Met Ala Thr Ser Val Ile Ile Ala Gly Lys Asn Gly Val
 195 200 205
 Glu Val Met Thr Lys
 210

(2) INFORMATION FOR SEQ ID NO:29:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 623 base pairs

(B) TYPE: nucleic acid

340

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..623

(D) OTHER INFORMATION: / Ceres Seq. ID 1010217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

gaaaaccctt aagctaagca aatttcaaag caattcaaaa accctagcct ctctctcttt      60
atctctcaca acaaaatctt tgaaatggcg atctctaagg cttccattgt tgttctcatg      120
atggtgatta tctccgtcgt tgcacgggca cagtcctgagg caccagcacc aagtcctact      180
tctggatcta gtgcgatctc agcgtctttc gtgtcagctg tgcagttatc accggcggag      240
aggggaagcaa gggttttgag gtatagagag aagaggaaga atcggaaatt tgagaagacg      300
attaggtatg cgtcgcgtaa agcttacgct gagatgaggc cgagaatcaa aggacgtttt      360
gctaagagaa cagattcgag agagaatgat ggtggagacg tcggagttaa ttgcggattc      420
gggtgtgttc cgagtttctg atatttcccg gttaaagaaa catggtagta gtatatcggt      480
taatagcaga ttaaggataa ttaaaactaa aatgtttcct gatttaatca ggggctaagt      540
tattgttaga agattgttgt tttttgaatt aattctcaca attgtatcct aaattatata      600
gtttacttaa tgttgaacta atg

```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1010218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Met Ala Ile Ser Lys Ala Ser Ile Val Val Leu Met Met Val Ile Ile
1          5          10          15
Ser Val Val Ala Ser Ala Gln Ser Glu Ala Pro Ala Pro Ser Pro Thr
35          20          25          30
Ser Gly Ser Ser Ala Ile Ser Ala Ser Phe Val Ser Ala Val Gln Leu
35          40          45
Ser Pro Ala Glu Arg Glu Ala Arg Val Leu Arg Tyr Arg Glu Lys Arg
50          55          60
Lys Asn Arg Lys Phe Glu Lys Thr Ile Arg Tyr Ala Ser Arg Lys Ala
40          65          70          75          80
Tyr Ala Glu Met Arg Pro Arg Ile Lys Gly Arg Phe Ala Lys Arg Thr
85          90          95
Asp Ser Arg Glu Asn Asp Gly Gly Asp Val Gly Val Tyr Cys Gly Phe
45          100          105          110
Gly Val Val Pro Ser Phe
115

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..107

(D) OTHER INFORMATION: / Ceres Seq. ID 1010219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

Met Met Val Ile Ile Ser Val Val Ala Ser Ala Gln Ser Glu Ala Pro
60          5          10          15
Ala Pro Ser Pro Thr Ser Gly Ser Ser Ala Ile Ser Ala Ser Phe Val

```

341

20 25 30
 Ser Ala Val Gln Leu Ser Pro Ala Arg Glu Ala Arg Val Leu Arg
 35 40 45
 Tyr Arg Glu Lys Arg Lys Asn Arg Lys Phe Glu Lys Thr Ile Arg Tyr
 50 55 60
 Ala Ser Arg Lys Ala Tyr Ala Glu Met Arg Pro Arg Ile Lys Gly Arg
 65 70 75 80
 Phe Ala Lys Arg Thr Asp Ser Arg Glu Asn Asp Gly Gly Asp Val Gly
 85 90 95
 Val Tyr Cys Gly Phe Gly Val Val Pro Ser Phe
 100 105

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1010220

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Val Ile Ile Ser Val Val Ala Ser Ala Gln Ser Glu Ala Pro Ala
 1 5 10 15
 Pro Ser Pro Thr Ser Gly Ser Ser Ala Ile Ser Ala Ser Phe Val Ser
 20 25 30
 Ala Val Gln Leu Ser Pro Ala Glu Arg Glu Ala Arg Val Leu Arg Tyr
 35 40 45
 Arg Glu Lys Arg Lys Asn Arg Lys Phe Glu Lys Thr Ile Arg Tyr Ala
 50 55 60
 Ser Arg Lys Ala Tyr Ala Glu Met Arg Pro Arg Ile Lys Gly Arg Phe
 65 70 75 80
 Ala Lys Arg Thr Asp Ser Arg Glu Asn Asp Gly Gly Asp Val Gly Val
 85 90 95
 Tyr Cys Gly Phe Gly Val Val Pro Ser Phe
 100 105

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 568 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..568

(D) OTHER INFORMATION: / Ceres Seq. ID 1010302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

50 aaaacaaatc attcaaagac atacaaaata attgagtttt ttttttaatt agaaacaaat 60
 ggggttgagt ggtgttcttc atgtggaggt tgaggttaag tctccggctg aaaagtctctg 120
 ggtagccctc ggagacggca tcaatctctt ccccaaagct ttccctaacg actacaaaac 180
 catccaagtt ctagccggcg acggcaacgc tcttggtctc attgcctca ttacttatgg 240
 agaaggatct ccaactggtga agatatcgcc ggagaggatc gaagcagtgg atttgagaa 300
 55 caaaagcatg tcatcacgca tcattggcgg cgaaatgttg gagtactaca aaacgttcaa 360
 aggaaccatc accgttattc ctaagaacgg tggcagcctt ctgaaatggg ctggtgagtt 420
 tgagaagacc gcccatgaga ttgatgacct acacgtcatc aaggactttg ctgtcaagaa 480
 cttcaaagag atagatgagt atctccttaa gcaaactagt gcctaacact agaaccctta 540
 aattatataa gagggttcga tcgtctct

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

342

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..155
 (D) OTHER INFORMATION: / Ceres Seq. ID 1010303
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

10 Met Gly Leu Ser Gly Val Leu His Val Glu Val Glu Val Lys Ser Pro
 1 5 10 15
 Ala Glu Lys Phe Trp Val Ala Leu Gly Asp Gly Ile Asn Leu Phe Pro
 20 25 30
 Lys Ala Phe Pro Asn Asp Tyr Lys Thr Ile Gln Val Leu Ala Gly Asp
 15 35 40 45
 Gly Asn Ala Pro Gly Ser Ile Arg Leu Ile Thr Tyr Gly Glu Gly Ser
 50 55 60
 Pro Leu Val Lys Ile Ser Ala Glu Arg Ile Glu Ala Val Asp Leu Glu
 65 70 75 80
 20 Asn Lys Ser Met Ser Tyr Ser Ile Ile Gly Gly Glu Met Leu Glu Tyr
 85 90 95
 Tyr Lys Thr Phe Lys Gly Thr Ile Thr Val Ile Pro Lys Asn Gly Gly
 100 105 110
 Ser Leu Leu Lys Trp Ser Gly Glu Phe Glu Lys Thr Ala His Glu Ile
 115 120 125
 25 Asp Asp Pro His Val Ile Lys Asp Phe Ala Val Lys Asn Phe Lys Glu
 130 135 140
 Ile Asp Glu Tyr Leu Leu Lys Gln Thr Ser Ala
 145 150 155

30 (2) INFORMATION FOR SEQ ID NO:35:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 531 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..531
 40 (D) OTHER INFORMATION: / Ceres Seq. ID 1010815
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

gcgcgcgcgcg aacccgaaga agaactctct cttgtaaacc tgcgatctga atcttcccg 60
 cggtgaaaaa tgggtgcgga gaagaaggcg aagaagtccc atgaaggaat caacagcaga 120
 ttagctcttg tgatgaagag tggaaagtac actcttggat acaagtctgt tctcaaatcc 180
 45 cttcgcagct ccaaaggtaa gctgatattg atatctagca attgccacc gttgagaagg 240
 tcagagattg aatactatgc gatgcttgct aaagttggag ttcacgccta caatggcaac 300
 aatggttgatt tgggtactgc ttgtggtaaa tacttccgag tttcttgccct cagcatcggt 360
 gatcctggtg attccgacat catcaagaca cttcctggag atcagtgatt ctgattttga 420
 tgattttgcc atggtgttct ctatgcttga ttatgctttg tgttcttcaa agacttaatg 480
 50 ttagatttct ttggtttccc gacttctct taatggttat aattaattac t

(2) INFORMATION FOR SEQ ID NO:36:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 55 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 60 (B) LOCATION: 1..112
 (D) OTHER INFORMATION: / Ceres Seq. ID 1010816
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

343

Met Val Ala Glu Lys Lys Ala Lys Lys Ser His Glu Gly Ile Asn Ser
 1 5 10 15
 Arg Leu Ala Leu Val Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys
 20 25 30
 5 Ser Val Leu Lys Ser Leu Arg Ser Ser Lys Gly Lys Leu Ile Leu Ile
 35 40 45
 Ser Ser Asn Cys Pro Pro Leu Arg Arg Ser Glu Ile Glu Tyr Tyr Ala
 50 55 60
 10 Met Leu Ala Lys Val Gly Val His Arg Tyr Asn Gly Asn Asn Val Asp
 65 70 75 80
 Leu Gly Thr Ala Cys Gly Lys Tyr Phe Arg Val Ser Cys Leu Ser Ile
 85 90 95
 Val Asp Pro Gly Asp Ser Asp Ile Ile Lys Thr Leu Pro Gly Asp Gln
 100 105 110

15 (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

25 (D) OTHER INFORMATION: / Ceres Seq. ID 1010817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys Ser Val Leu Lys Ser
 1 5 10 15
 Leu Arg Ser Ser Lys Gly Lys Leu Ile Leu Ile Ser Ser Asn Cys Pro
 20 25 30
 Pro Leu Arg Arg Ser Glu Ile Glu Tyr Tyr Ala Met Leu Ala Lys Val
 35 40 45
 Gly Val His Arg Tyr Asn Gly Asn Asn Val Asp Leu Gly Thr Ala Cys
 50 55 60
 35 Gly Lys Tyr Phe Arg Val Ser Cys Leu Ser Ile Val Asp Pro Gly Asp
 65 70 75 80
 Ser Asp Ile Ile Lys Thr Leu Pro Gly Asp Gln
 85 90

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..73

(D) OTHER INFORMATION: / Ceres Seq. ID 1010818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Arg Cys Leu Leu Lys Leu Glu Phe Ile Ala Thr Met Ala Thr Met
 1 5 10 15
 Leu Ile Trp Val Leu Leu Val Val Asn Thr Ser Glu Phe Leu Ala Ser
 20 25 30
 55 Ala Ser Leu Ile Leu Val Ile Pro Thr Ser Ser Arg His Phe Leu Glu
 35 40 45
 Ile Ser Asp Ser Asp Phe Asp Asp Phe Ala Met Leu Phe Ser Met Leu
 50 55 60
 Asp Tyr Ala Leu Cys Ser Ser Lys Thr
 65 70

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

344

(A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..494
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011437

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
 acaatcggaa gaaaggagaa gacgaagatg tcgttggtat ggctggaagc gatgttgccct 60
 ctcggaatca tcggtgggat gctctgtatc atgggcaatt ctcagtacta catccacaaa 120
 gcttatcatg gccgtcctaa gcacatcggc cacgatgaat gggatgtttc tatggaaaga 180
 cgcgacaaga aagtcgtcga gaaagctgca gctccttcct catgattcgc tttatctcct 240
 15 ttgtgttcct caggggctta aggtgaccac ttgtgggtgac aaataaagtg cattccagaa 300
 gaagaagaag ctgggggatc tagtactttc attcccattt gatttttcctt ggacatatta 360
 aagctttcag aaatcagacc tcaataacat ttggtttatc aatatttctc tattcgtgat 420
 attttgatg cttttaagtt gcatgatata ctgaactact ctcttgctgt gtgagtgaat 480
 aaatgaatat ctgt

20 (2) INFORMATION FOR SEQ ID NO:40:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..94
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011438

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
 Gln Ser Glu Glu Arg Arg Arg Arg Arg Cys Arg Trp Tyr Gly Trp Lys
 1 5 10 15
 Arg Cys Cys Leu Ser Glu Ser Ser Val Gly Cys Ser Val Ser Trp Ala
 35 20 25 30
 Ile Leu Ser Thr Thr Ser Thr Lys Leu Ile Met Ala Val Leu Ser Thr
 35 40 45
 Ser Ala Thr Met Asn Gly Met Phe Leu Trp Lys Asp Ala Thr Arg Lys
 50 55 60
 40 Ser Ser Arg Lys Leu Gln Leu Leu Pro His Asp Ser Leu Tyr Leu Phe
 65 70 75 80
 Cys Val Pro Gln Gly Leu Lys Val Thr Thr Cys Gly Asp Lys
 85 90

45 (2) INFORMATION FOR SEQ ID NO:41:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..74
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011439

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
 Thr Ile Gly Arg Lys Glu Lys Thr Lys Met Ser Leu Val Trp Leu Glu
 1 5 10 15
 Ala Met Leu Pro Leu Gly Ile Ile Gly Gly Met Leu Cys Ile Met Gly
 20 25 30
 60 Asn Ser Gln Tyr Tyr Ile His Lys Ala Tyr His Gly Arg Pro Lys His
 35 40 45
 Ile Gly His Asp Glu Trp Asp Val Ser Met Glu Arg Arg Asp Lys Lys

345

50 55 60
Val Val Glu Lys Ala Ala Pro Ser Ser
65 70

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..65
(D) OTHER INFORMATION: / Ceres Seq. ID 1011440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ser Leu Val Trp Leu Glu Ala Met Leu Pro Leu Gly Ile Ile Gly
1 5 10 15
Gly Met Leu Cys Ile Met Gly Asn Ser Gln Tyr Tyr Ile His Lys Ala
20 25 30
Tyr His Gly Arg Pro Lys His Ile Gly His Asp Glu Trp Asp Val Ser
35 40 45
Met Glu Arg Arg Asp Lys Lys Val Val Glu Lys Ala Ala Ala Pro Ser
50 55 60
Ser
65

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1011 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..1011
(D) OTHER INFORMATION: / Ceres Seq. ID 1011616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ctgtttcttt ttgtttcctt agactttctc gtcgattaac ccttgccgag ggtcattttt 60
ttttcttgaa ttttttcacc aagtgttcgt tcacggcatt gcttgctctc cagtatgagt 120
40 atctccggtg ctgcagttgg ttcaggcaga aatttaagaa gagcggtaga gtttgggaaa 180
actcatgtgg ttaggcctaa agggaaacat caagcaacta ttgtctgggtt acatgggctt 240
ggggacaatg gctcgagctg gtcccagctt ttggagacct tcccccttcc aaatatcaaa 300
tggtttgccc cgactgctcc ttctcaacca ataagtttat ttggtggttt tccctccaca 360
gcttggtttg atgttggtga catcaatgaa gatggacctg atgatatgga aggattggat 420
45 gtggctgctg cacatgttgc aaatctgttg tcgaatgagc ctgctgacat taaattaggt 480
gttgaggatg tcagcatggg tgcggcgaca tctctatatt ctgcaacttg ttttgctctc 540
ggtaaatatg gaaatggcaa tccataacct atcaatttaa gcgcaatcat aggcttaagc 600
ggctggcttc cttgtgcaaa gacattggct ggcaaacatg aagaggaaca gatcaagaac 660
cgagctgcat cgttacccat tggtgtctgt catggaaaag ctgatgatgt ggtaccgttc 720
50 aagtttgggg agaaatcttc acaggctttg ctttcaaagt gggttaagaa ggtgaccttc 780
aaaccttaca gtgcacttgg tcaccacaca atcccacagg agttggatga gttgtgcgca 840
tggttgacat ccacgctcag cctcgaaggt tgatacttcc tatgatgtag ctttctgatg 900
aaaacccttc aactcttgag agtttgattg aattggatgt ttcaggattt cacaatgttt 960
tcattggaat atttgtgtaa gacacattcg tctagtagca aatcttctcc c

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

346

(A) NAME/KEY: peptide

(B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1011617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

5  Met Ser Ile Ser Gly Ala Ala Val Gly Ser Gly Arg Asn Leu Arg Arg
   1          5          10          15
   Ala Val Glu Phe Gly Lys Thr His Val Val Arg Pro Lys Gly Lys His
           20          25          30
10  Gln Ala Thr Ile Val Trp Leu His Gly Leu Gly Asp Asn Gly Ser Ser
   35          40          45
   Trp Ser Gln Leu Leu Glu Thr Leu Pro Leu Pro Asn Ile Lys Trp Ile
   50          55          60
   Cys Pro Thr Ala Pro Ser Gln Pro Ile Ser Leu Phe Gly Gly Phe Pro
   65          70          75          80
15  Ser Thr Ala Trp Phe Asp Val Val Asp Ile Asn Glu Asp Gly Pro Asp
           85          90          95
   Asp Met Glu Gly Leu Asp Val Ala Ala Ala His Val Ala Asn Leu Leu
           100          105          110
   Ser Asn Glu Pro Ala Asp Ile Lys Leu Gly Val Gly Gly Phe Ser Met
   115          120          125
20  Gly Ala Ala Thr Ser Leu Tyr Ser Ala Thr Cys Phe Ala Leu Gly Lys
   130          135          140
   Tyr Gly Asn Gly Asn Pro Tyr Pro Ile Asn Leu Ser Ala Ile Ile Gly
   145          150          155          160
25  Leu Ser Gly Trp Leu Pro Cys Ala Lys Thr Leu Ala Gly Lys Leu Glu
           165          170          175
   Glu Glu Gln Ile Lys Asn Arg Ala Ala Ser Leu Pro Ile Val Val Cys
           180          185          190
   His Gly Lys Ala Asp Asp Val Val Pro Phe Lys Phe Gly Glu Lys Ser
   195          200          205
30  Ser Gln Ala Leu Leu Ser Asn Gly Phe Lys Lys Val Thr Phe Lys Pro
   210          215          220
   Tyr Ser Ala Leu Gly His His Thr Ile Pro Gln Glu Leu Asp Glu Leu
   225          230          235          240
35  Cys Ala Trp Leu Thr Ser Thr Leu Ser Leu Glu Gly
           245          250

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: .

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1011618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

50  Met Glu Gly Leu Asp Val Ala Ala Ala His Val Ala Asn Leu Leu Ser
   1          5          10          15
   Asn Glu Pro Ala Asp Ile Lys Leu Gly Val Gly Gly Phe Ser Met Gly
           20          25          30
   Ala Ala Thr Ser Leu Tyr Ser Ala Thr Cys Phe Ala Leu Gly Lys Tyr
           35          40          45
55  Gly Asn Gly Asn Pro Tyr Pro Ile Asn Leu Ser Ala Ile Ile Gly Leu
   50          55          60
   Ser Gly Trp Leu Pro Cys Ala Lys Thr Leu Ala Gly Lys Leu Glu Glu
   65          70          75          80
   Glu Gln Ile Lys Asn Arg Ala Ala Ser Leu Pro Ile Val Val Cys His
           85          90          95
60  Gly Lys Ala Asp Asp Val Val Pro Phe Lys Phe Gly Glu Lys Ser Ser
           100          105          110

```

347

Gln Ala Leu Leu Ser Asn Gly Phe Lys Lys Val Thr Phe Lys Pro Tyr
 115 120 125
 Ser Ala Leu Gly His His Thr Ile Pro Gln Glu Leu Asp Glu Leu Cys
 130 135 140
 5 Ala Trp Leu Thr Ser Thr Leu Ser Leu Glu Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..643

(D) OTHER INFORMATION: / Ceres Seq. ID 1011631

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

agaatgtgat	ggagatggga	gtgaatgaga	tgagtgggtg	gattaaagaa	gagaagaagg	60
agaaggctct	tatgcttaga	ttggactatg	aatcagtcac	ttccacttgg	ggaggccaag	120
ggatcccatg	gaccgcccgg	gtgccatctg	aaatagacct	cgacatgggt	tgtttcccaa	180
cccataccat	gggtgaaagt	ggagcagagg	ctcatcatca	caaccacttc	cgcggcctag	240
ggttacacct	aggagatgct	ggggatggag	gaagagaggc	tagggtttca	agataccgag	300
agaaaaggag	gacaagggtg	ttctccaaga	agataaggta	cgaggtagct	aaattgaatg	360
25 cagagaaaag	gcctcgcatg	aaaggaaggt	tcgtcaagag	atcttcaatt	ggtgttgctc	420
actaaagaac	ttaattaatt	atggatatta	aattactttg	ctctcatctt	gcttttttgt	480
tgctatagtt	ttggtgattg	ttagctttct	ttttctgcat	tcatagagaa	ttttgcacgt	540
ttttgtgagc	tacgtatgta	cataaatata	tcacccaaaa	aatgtgacta	tcttgtaagc	600
actgatttat	atagtcgata	taacgtgaat	tttgattgct	ggc		

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1011632

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asn Val Met Glu Met Gly Val Asn Glu Met Ser Gly Gly Ile Lys Glu	
1 5 10 15	
Glu Lys Lys Glu Lys Ala Leu Met Leu Arg Leu Asp Tyr Glu Ser Val	
20 25 30	
Ile Ser Thr Trp Gly Gly Gln Gly Ile Pro Trp Thr Ala Arg Val Pro	
35 40 45	
Ser Glu Ile Asp Leu Asp Met Val Cys Phe Pro Thr His Thr Met Gly	
50 55 60	
50 Glu Ser Gly Ala Glu Ala His His His Asn His Phe Arg Gly Leu Gly	
65 70 75 80	
Leu His Leu Gly Asp Ala Gly Asp Gly Gly Arg Glu Ala Arg Val Ser	
85 90 95	
Arg Tyr Arg Glu Lys Arg Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg	
100 105 110	
Tyr Glu Val Arg Lys Leu Asn Ala Glu Lys Arg Pro Arg Met Lys Gly	
115 120 125	
Arg Phe Val Lys Arg Ser Ser Ile Gly Val Ala His	
130 135 140	

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

348

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..138
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011633
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

10	Met	Glu	Met	Gly	Val	Asn	Glu	Met	Ser	Gly	Gly	Ile	Lys	Glu	Glu	Lys
	1				5					10				15		
	Lys	Glu	Lys	Ala	Leu	Met	Leu	Arg	Leu	Asp	Tyr	Glu	Ser	Val	Ile	Ser
				20					25					30		
	Thr	Trp	Gly	Gly	Gln	Gly	Ile	Pro	Trp	Thr	Ala	Arg	Val	Pro	Ser	Glu
15			35					40					45			
	Ile	Asp	Leu	Asp	Met	Val	Cys	Phe	Pro	Thr	His	Thr	Met	Gly	Glu	Ser
		50					55					60				
	Gly	Ala	Glu	Ala	His	His	His	Asn	His	Phe	Arg	Gly	Leu	Gly	Leu	His
	65				70					75					80	
20	Leu	Gly	Asp	Ala	Gly	Asp	Gly	Gly	Arg	Glu	Ala	Arg	Val	Ser	Arg	Tyr
					85				90					95		
	Arg	Glu	Lys	Arg	Arg	Thr	Arg	Leu	Phe	Ser	Lys	Lys	Ile	Arg	Tyr	Glu
				100					105					110		
	Val	Arg	Lys	Leu	Asn	Ala	Glu	Lys	Arg	Pro	Arg	Met	Lys	Gly	Arg	Phe
25			115					120					125			
	Val	Lys	Arg	Ser	Ser	Ile	Gly	Val	Ala	His						
		130					135									

(2) INFORMATION FOR SEQ ID NO:49:
 (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 136 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 35 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..136
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011634
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

40	Met	Gly	Val	Asn	Glu	Met	Ser	Gly	Gly	Ile	Lys	Glu	Glu	Lys	Lys	Glu
	1				5					10				15		
	Lys	Ala	Leu	Met	Leu	Arg	Leu	Asp	Tyr	Glu	Ser	Val	Ile	Ser	Thr	Trp
				20					25					30		
	Gly	Gly	Gln	Gly	Ile	Pro	Trp	Thr	Ala	Arg	Val	Pro	Ser	Glu	Ile	Asp
45			35					40					45			
	Leu	Asp	Met	Val	Cys	Phe	Pro	Thr	His	Thr	Met	Gly	Glu	Ser	Gly	Ala
		50					55					60				
	Glu	Ala	His	His	His	Asn	His	Phe	Arg	Gly	Leu	Gly	Leu	His	Leu	Gly
	65				70					75					80	
50	Asp	Ala	Gly	Asp	Gly	Gly	Arg	Glu	Ala	Arg	Val	Ser	Arg	Tyr	Arg	Glu
					85				90					95		
	Lys	Arg	Arg	Thr	Arg	Leu	Phe	Ser	Lys	Lys	Ile	Arg	Tyr	Glu	Val	Arg
				100					105					110		
	Lys	Leu	Asn	Ala	Glu	Lys	Arg	Pro	Arg	Met	Lys	Gly	Arg	Phe	Val	Lys
55			115					120					125			
	Arg	Ser	Ser	Ile	Gly	Val	Ala	His								
		130					135									

(2) INFORMATION FOR SEQ ID NO:50:
 (i) SEQUENCE CHARACTERISTICS:
 60 (A) LENGTH: 663 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

349

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..663

(D) OTHER INFORMATION: / Ceres Seq. ID 1011714

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

gtgttcgata ataatgtcga caggagaagc gataccaaga gtcgccgctcg tcgtttttcat      60
tctcaacgga aactcaatct tattaggtcg ccgccgttcc tcaatcggca actccacttt      120
cgctcttccc ggtggccacc tcgaattcgg agagagcttt gaagaatgtg cagcgagaga      180
agtaatggag gaaacaggtc taaagattga aaagatgaag cttttgactg ttacaaacaa      240
tgtcttcaaa gaagcaccaa cgccatcaca ctacgtctct gtttcgatac gtgcggtggt      300
ggtggatcca agtcaagaac cgaagaatat ggaaccagag aagtgtgaag gatgggattg      360
gtatgattgg gagaatctac caaagccttt gttttggcca cttgagaaat tgtttggaag      420
tggtttcaat cctttcactc atggtggtgg agactaatag atgtaagagt taatgattga      480
tttgggattg aatgttgcaa attgggcatt tgggtctagt gtatgattct cgcttagggg      540
gcgagaggtc ccgagttcaa ttctcggaat gccctctct tttactcttt tttattgtat      600
ttttggtttc tgttttccta attagtaata aacttatcat gtgtcctatc gattttattt      660
ctc

```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1011715

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Cys Ser Ile Ile Met Ser Thr Gly Glu Ala Ile Pro Arg Val Ala Val
1      5      10      15
Val Val Phe Ile Leu Asn Gly Asn Ser Ile Leu Leu Gly Arg Arg Arg
20      25      30
Ser Ser Ile Gly Asn Ser Thr Phe Ala Leu Pro Gly Gly His Leu Glu
35      40      45
Phe Gly Glu Ser Phe Glu Glu Cys Ala Ala Arg Glu Val Met Glu Glu
50      55      60
Thr Gly Leu Lys Ile Glu Lys Met Lys Leu Leu Thr Val Thr Asn Asn
65      70      75      80
Val Phe Lys Glu Ala Pro Thr Pro Ser His Tyr Val Ser Val Ser Ile
85      90      95
Arg Ala Val Leu Val Asp Pro Ser Gln Glu Pro Lys Asn Met Glu Pro
100      105      110
Glu Lys Cys Glu Gly Trp Asp Trp Tyr Asp Trp Glu Asn Leu Pro Lys
115      120      125
Pro Leu Phe Trp Pro Leu Glu Lys Leu Phe Gly Ser Gly Phe Asn Pro
130      135      140
Phe Thr His Gly Gly Gly Asp
145      150

```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1011716

350

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Met Ser Thr Gly Glu Ala Ile Pro Arg Val Ala Val Val Val Phe Ile
 1 5 10 15
 5 Leu Asn Gly Asn Ser Ile Leu Leu Gly Arg Arg Arg Ser Ser Ile Gly
 20 25 30
 Asn Ser Thr Phe Ala Leu Pro Gly Gly His Leu Glu Phe Gly Glu Ser
 35 40 45
 Phe Glu Glu Cys Ala Ala Arg Glu Val Met Glu Glu Thr Gly Leu Lys
 50 55 60
 10 Ile Glu Lys Met Lys Leu Thr Val Thr Asn Asn Val Phe Lys Glu
 65 70 75 80
 Ala Pro Thr Pro Ser His Tyr Val Ser Val Ser Ile Arg Ala Val Leu
 85 90 95
 15 Val Asp Pro Ser Gln Glu Pro Lys Asn Met Glu Pro Glu Lys Cys Glu
 100 105 110
 Gly Trp Asp Trp Tyr Asp Trp Glu Asn Leu Pro Lys Pro Leu Phe Trp
 115 120 125
 Pro Leu Glu Lys Leu Phe Gly Ser Gly Phe Asn Pro Phe Thr His Gly
 130 135 140
 20 Gly Gly Asp
 145

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

30 (A) NAME/KEY: peptide
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

35 Met Glu Glu Thr Gly Leu Lys Ile Glu Lys Met Lys Leu Leu Thr Val
 1 5 10 15
 Thr Asn Asn Val Phe Lys Glu Ala Pro Thr Pro Ser His Tyr Val Ser
 20 25 30
 Val Ser Ile Arg Ala Val Leu Val Asp Pro Ser Gln Glu Pro Lys Asn
 35 40 45
 40 Met Glu Pro Glu Lys Cys Glu Gly Trp Asp Trp Tyr Asp Trp Glu Asn
 50 55 60
 Leu Pro Lys Pro Leu Phe Trp Pro Leu Glu Lys Leu Phe Gly Ser Gly
 65 70 75 80
 Phe Asn Pro Phe Thr His Gly Gly Gly Asp
 85 90
 45

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 524 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

55 (A) NAME/KEY: -
 (B) LOCATION: 1..524
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

aaaacagaac aaacacaaac acaaacagag aatcaacgaa gaagaaaaat ggtgaagggtg 60
 atgtgggttt ccgttttagc tctggcggcg gcgattctcc ttttgacggt cccggtggca 120
 60 gaaggggtga cgtgctcgcc tatgcagctg gcttcatgtg cggcggcgat gacgtcatct 180
 tgcgcccat cggaggcgtg ttgcacaaag ctgagagagc agcagccatg cctttgtggg 240
 tacatgagga accctaccct ccgccaatac gttagctccc ctaacgcaag gaaagtctcc 300

351

aacagtttgc agattccttc cccaagctgt taaggaaatg ttaatcatga ttaattagtg 360
 acaagtttgc ctgattatag tggtaaatgc tggctcttgc ttcgtcagta ctacttaaaa 420
 taataaatga gtgatgatga ttgatgatta tcatcatcat gcttgaatgt tatgttttct 480
 atcttataaa atatgaaata tacttttagaa atatgtttcg tcgt

5 (2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

15

(D) OTHER INFORMATION: / Ceres Seq. ID 1011785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Lys	Thr	Glu	Gln	Thr	Gln	Thr	Gln	Thr	Glu	Asn	Gln	Arg	Arg	Arg	Lys
1			5					10				15			
Met	Val	Lys	Val	Met	Trp	Val	Ser	Val	Leu	Ala	Leu	Ala	Ala	Ala	Ile
			20					25				30			
Leu	Leu	Leu	Thr	Val	Pro	Val	Ala	Glu	Gly	Val	Thr	Cys	Ser	Pro	Met
			35				40					45			
Gln	Leu	Ala	Ser	Cys	Ala	Ala	Ala	Met	Thr	Ser	Ser	Ser	Pro	Pro	Ser
			50				55					60			
Glu	Ala	Cys	Cys	Thr	Lys	Leu	Arg	Glu	Gln	Gln	Pro	Cys	Leu	Cys	Gly
							70				75				80
Tyr	Met	Arg	Asn	Pro	Thr	Leu	Arg	Gln	Tyr	Val	Ser	Ser	Pro	Asn	Ala
							85				90			95	
Arg	Lys	Val	Ser	Asn	Ser	Cys	Lys	Ile	Pro	Ser	Pro	Ser	Cys		
							100				105			110	

20

25

30

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

40

(D) OTHER INFORMATION: / Ceres Seq. ID 1011786

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met	Val	Lys	Val	Met	Trp	Val	Ser	Val	Leu	Ala	Leu	Ala	Ala	Ala	Ile
1				5					10					15	
Leu	Leu	Leu	Thr	Val	Pro	Val	Ala	Glu	Gly	Val	Thr	Cys	Ser	Pro	Met
				20				25				30			
Gln	Leu	Ala	Ser	Cys	Ala	Ala	Ala	Met	Thr	Ser	Ser	Ser	Pro	Pro	Ser
				35			40					45			
Glu	Ala	Cys	Cys	Thr	Lys	Leu	Arg	Glu	Gln	Gln	Pro	Cys	Leu	Cys	Gly
				50			55				60				
Tyr	Met	Arg	Asn	Pro	Thr	Leu	Arg	Gln	Tyr	Val	Ser	Ser	Pro	Asn	Ala
							70				75				80
Arg	Lys	Val	Ser	Asn	Ser	Cys	Lys	Ile	Pro	Ser	Pro	Ser	Cys		
							85				90				

45

50

55

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

352

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 1011787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

5  Asn Arg Thr Asn Thr Asn Thr Asn Arg Glu Ser Thr Lys Lys Lys Asn
   1             5             10             15
   Gly Glu Gly Asp Val Gly Phe Arg Phe Ser Ser Gly Gly Gly Asp Ser
   20             25             30
10  Pro Phe Asp Gly Pro Gly Gly Arg Arg Gly Asp Val Leu Ala Tyr Ala
   35             40             45
   Ala Gly Phe Met Cys Gly Gly Asp Asp Val Ile Phe Ala Ala Ile Gly
   50             55             60
   Gly Val Leu His Lys Ala Glu Arg Ala Ala Ala Met Pro Leu Trp Val
   65             70             75             80
15  His Glu Glu Pro Tyr Pro Pro Pro Ile Arg
   85             90

```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1007 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1007

(D) OTHER INFORMATION: / Ceres Seq. ID 1011820

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

30  ccaaatttct ccatggatcg ttctttgaat ctctctgatt tagccttagg gttcgatgag      60
   cagctagcta ttccatcgcc actaaatgga aaagtaatac taatagaaga ctgtgtagag      120
   acgagtgggt cctttgtact tcaccagcta atgaaacgtg ttctctcctc taactcctcc      180
   gacgcaactta tctttctcgc ttttgctcgc cctttctctc attatgatcg aatcttgctg      240
   aaactgggat gtaatttagc tacccataag tcgaataatc gattggtggt ctttgacatg      300
   ctcatgggta agtggttcaga tggggatcaa atggaagaca atgtgagtgc agttgacgaaa      360
35  ctatttcggg agatacaaga aaccgttcga aagctacaga gtgtaacaag tggtaacata      420
   actgttatgg tggatgacat gtctctgctg gaaattgcta ctaccggcag caactcagat      480
   cacgtattgg acttcttgca ttattgccac acattaagtt ctgaaagcaa ttgttcattg      540
   gtcacacctc atcatgaaga tatatacgcg agcatggaga gacctgcatt tttgctacag      600
   atggtatgcc ttgcagatgt tgtgataaag gcagagcctt tagcctctgg tttagcaaat      660
40  gatgtacatg gccaatggac tgttctgaac aaagggataa gcaactcagg tagaggaagc      720
   tcgaggaaca agttgcagaa ttttcaattc aggatcaagg aaaatggtat cgactatttc      780
   taccctgggt gcagaagctg aggattagac accgttctga gcattagcat ggtagtgaga      840
   tgcacttaga cagttttggt atttgcgttt aggttaaaca gagacactct gttcaacatt      900
   ttacttttag tgtctcttct ggttgtaact tgatgactta gctaaagttg aatgcttgag      960
45  acacagaaac ttgtagacat ggaaaattag taacattcta tatcttt

```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 1011821

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

60  Pro Asn Phe Ser Met Asp Arg Ser Leu Asn Leu Leu Asp Leu Ala Leu
   1             5             10             15
   Gly Phe Asp Glu Gln Leu Ala Ile Pro Ser Pro Leu Asn Gly Lys Val
   20             25             30
   Ile Leu Ile Glu Asp Cys Val Glu Thr Ser Gly Ser Phe Val Leu His

```


353

35 40 45
 Gln Leu Met Lys Arg Val Leu Ser Ser Asn Ser Ser Asp Ala Leu Ile
 50 55 60
 Phe Leu Ala Phe Ala Arg Pro Phe Ser His Tyr Asp Arg Ile Leu Arg
 65 70 75 80
 Lys Leu Gly Cys Asn Leu Ala Thr His Lys Ser Asn Asn Arg Leu Val
 85 90 95
 Phe Phe Asp Met Leu Met Val Lys Cys Ser Asp Gly Asp Gln Met Glu
 100 105 110
 10 Asp Asn Val Ser Ala Val Ala Lys Leu Phe Arg Glu Ile Gln Glu Thr
 115 120 125
 Val Arg Lys Leu Gln Ser Val Thr Ser Gly Asn Ile Thr Val Met Val
 130 135 140
 Asp Asp Met Ser Leu Leu Glu Ile Ala Thr Thr Gly Ser Asn Ser Asp
 145 150 155 160
 15 His Val Leu Asp Phe Leu His Tyr Cys His Thr Leu Ser Ser Glu Ser
 165 170 175
 Asn Cys Ser Leu Val Ile Leu Asn His Glu Asp Ile Tyr Ala Ser Met
 180 185 190
 20 Glu Arg Pro Ala Phe Leu Leu Gln Met Val Cys Leu Ala Asp Val Val
 195 200 205
 Ile Lys Ala Glu Pro Leu Ala Ser Gly Leu Ala Asn Asp Val His Gly
 210 215 220
 25 Gln Leu Thr Val Leu Asn Lys Gly Ile Ser Asn Ser Gly Arg Gly Ser
 225 230 235 240
 Ser Arg Asn Lys Leu Gln Asn Phe Gln Phe Arg Ile Lys Glu Asn Gly
 245 250 255
 Ile Asp Tyr Phe Tyr Pro Gly Cys Arg Ser
 260 265
 30 (2) INFORMATION FOR SEQ ID NO:60:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 35 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..262
 40 (D) OTHER INFORMATION: / Ceres Seq. ID 1011822
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
 Met Asp Arg Ser Leu Asn Leu Leu Asp Leu Ala Leu Gly Phe Asp Glu
 1 5 10 15
 45 Gln Leu Ala Ile Pro Ser Pro Leu Asn Gly Lys Val Ile Leu Ile Glu
 20 25 30
 Asp Cys Val Glu Thr Ser Gly Ser Phe Val Leu His Gln Leu Met Lys
 35 40 45
 Arg Val Leu Ser Ser Asn Ser Ser Asp Ala Leu Ile Phe Leu Ala Phe
 50 55 60
 50 Ala Arg Pro Phe Ser His Tyr Asp Arg Ile Leu Arg Lys Leu Gly Cys
 65 70 75 80
 Asn Leu Ala Thr His Lys Ser Asn Asn Arg Leu Val Phe Phe Asp Met
 85 90 95
 55 Leu Met Val Lys Cys Ser Asp Gly Asp Gln Met Glu Asp Asn Val Ser
 100 105 110
 Ala Val Ala Lys Leu Phe Arg Glu Ile Gln Glu Thr Val Arg Lys Leu
 115 120 125
 Gln Ser Val Thr Ser Gly Asn Ile Thr Val Met Val Asp Asp Met Ser
 130 135 140
 60 Leu Leu Glu Ile Ala Thr Thr Gly Ser Asn Ser Asp His Val Leu Asp
 145 150 155 160
 Phe Leu His Tyr Cys His Thr Leu Ser Ser Glu Ser Asn Cys Ser Leu

354

				165					170					175		
	Val	Ile	Leu	Asn	His	Glu	Asp	Ile	Tyr	Ala	Ser	Met	Glu	Arg	Pro	Ala
				180					185					190		
5	Phe	Leu	Leu	Gln	Met	Val	Cys	Leu	Ala	Asp	Val	Val	Ile	Lys	Ala	Glu
			195					200					205			
	Pro	Leu	Ala	Ser	Gly	Leu	Ala	Asn	Asp	Val	His	Gly	Gln	Leu	Thr	Val
			210				215					220				
	Leu	Asn	Lys	Gly	Ile	Ser	Asn	Ser	Gly	Arg	Gly	Ser	Ser	Arg	Asn	Lys
	225					230					235				240	
10	Leu	Gln	Asn	Phe	Gln	Phe	Arg	Ile	Lys	Glu	Asn	Gly	Ile	Asp	Tyr	Phe
				245						250					255	
	Tyr	Pro	Gly	Cys	Arg	Ser										
				260												

(2) INFORMATION FOR SEQ ID NO:61:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1011823

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Met	Lys	Arg	Val	Leu	Ser	Ser	Asn	Ser	Ser	Asp	Ala	Leu	Ile	Phe	Leu
1				5				10						15	
Ala	Phe	Ala	Arg	Pro	Phe	Ser	His	Tyr	Asp	Arg	Ile	Leu	Arg	Lys	Leu
			20					25					30		
30	Gly	Cys	Asn	Leu	Ala	Thr	His	Lys	Ser	Asn	Asn	Arg	Leu	Val	Phe
			35					40					45		
	Asp	Met	Leu	Met	Val	Lys	Cys	Ser	Asp	Gly	Asp	Gln	Met	Glu	Asp
	50						55					60			
	Val	Ser	Ala	Val	Ala	Lys	Leu	Phe	Arg	Glu	Ile	Gln	Glu	Thr	Val
35	65					70				75				80	
	Lys	Leu	Gln	Ser	Val	Thr	Ser	Gly	Asn	Ile	Thr	Val	Met	Val	Asp
				85						90				95	
	Met	Ser	Leu	Leu	Glu	Ile	Ala	Thr	Thr	Gly	Ser	Asn	Ser	Asp	His
				100					105					110	
40	Leu	Asp	Phe	Leu	His	Tyr	Cys	His	Thr	Leu	Ser	Ser	Glu	Ser	Asn
			115					120					125		
	Ser	Leu	Val	Ile	Leu	Asn	His	Glu	Asp	Ile	Tyr	Ala	Ser	Met	Glu
	130					135						140			
	Pro	Ala	Phe	Leu	Leu	Gln	Met	Val	Cys	Leu	Ala	Asp	Val	Val	Ile
45	145					150					155				160
	Ala	Glu	Pro	Leu	Ala	Ser	Gly	Leu	Ala	Asn	Asp	Val	His	Gly	Gln
				165						170				175	
	Thr	Val	Leu	Asn	Lys	Gly	Ile	Ser	Asn	Ser	Gly	Arg	Gly	Ser	Ser
				180					185					190	
50	Asn	Lys	Leu	Gln	Asn	Phe	Gln	Phe	Arg	Ile	Lys	Glu	Asn	Gly	Ile
			195					200					205		
	Tyr	Phe	Tyr	Pro	Gly	Cys	Arg	Ser							
			210				215								

(2) INFORMATION FOR SEQ ID NO:62:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 584 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

355

(B) LOCATION: 1..584

(D) OTHER INFORMATION: / Ceres Seq. ID 1011874

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

	tcaattaaca	taaccttcgc	cgtcgatgaa	gctttccctt	caattccac	taccttcagc	60
5	gtcgcaacga	aacaacacta	cgacgtaaaa	ccaatccacc	atgaagttaa	tgacggagaa	120
	aggaagatat	acgacatcag	ccaccagtac	acgccggagt	tgccggtttg	ggagtcttca	180
	gaaggactag	ggaactttct	tagacttgcc	gtgagtatga	agaatggatc	cgatgctaata	240
	atctcgaaga	tggaaactatc	tgttcactct	ggaactcatg	ttgatgcacc	aggccatttc	300
	catgaccatt	attatgagtc	tggttttgat	actgattcac	ttgatcttca	aatccttaata	360
10	ggtaaacatt	tttggaactc	tttttttttt	ttttttttta	gtagctagt	atcggttttg	420
	aaattgggtt	ctgtgaattt	aatttatagg	tctgtcttta	ttggttgatg	ttccaagaga	480
	taagaacatt	tcaggtttgt	tgagagtttt	ctaaccattga	aatttttaca	aatcttcat	540
	taaatgtttg	ttacaaaatt	tttgtgtaata	gatttggttg	ttgt		

(2) INFORMATION FOR SEQ ID NO:63:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1011875

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

	Ser	Ile	Asn	Ile	Thr	Phe	Ala	Val	Asp	Glu	Ala	Phe	Pro	Ser	Ile	Pro	
	1				5					10					15		
	Thr	Thr	Phe	Ser	Val	Ala	Thr	Lys	Gln	His	Tyr	Asp	Val	Lys	Pro	Ile	
				20					25					30			
30	His	His	Glu	Val	Tyr	Asp	Gly	Glu	Arg	Lys	Ile	Tyr	Asp	Ile	Ser	His	
			35					40					45				
	Gln	Tyr	Thr	Pro	Glu	Leu	Pro	Val	Trp	Glu	Ser	Ser	Glu	Gly	Leu	Gly	
		50				55						60					
	Asn	Phe	Leu	Arg	Leu	Ala	Val	Ser	Met	Lys	Asn	Gly	Ser	Asp	Ala	Asn	
35		65				70					75				80		
	Ile	Ser	Lys	Met	Glu	Leu	Ser	Val	His	Ser	Gly	Thr	His	Val	Asp	Ala	
				85						90					95		
	Pro	Gly	His	Phe	His	Asp	His	Tyr	Tyr	Glu	Ser	Gly	Phe	Asp	Thr	Asp	
				100					105					110			
40	Ser	Leu	Asp	Leu	Gln	Ile	Leu	Asn	Gly	Lys	His	Phe	Trp	Asn	Ser	Phe	
			115				120						125				
	Phe	Phe	Phe	Phe	Leu	Ser	Ser										
		130				135											

(2) INFORMATION FOR SEQ ID NO:64:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 626 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..626

(D) OTHER INFORMATION: / Ceres Seq. ID 1011981

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

	acatcctaata	cgaaaaaaac	cctagcaaaa	acctctctct	ctctctcaat	tcacttctcc	60
	tcctacaatg	gcttggcgca	acgcaggatc	tgctgctcgt	tccttctgtc	ccgccaccgc	120
	aagatcacca	tctctccggt	ctccaccac	ggcgcttcct	cgctcccgtc	ctcctcaatc	180
	ctccttacct	agccgtcgct	tcaccttctc	gtcaccttcc	aggaatctag	gagccctagg	240
60	ttgcacacag	tcgttcttgc	ctctgtacag	tggtgtggct	acttctcaac	tgacatctca	300
	ccttaacgtt	aatttgcgag	ctttctgcga	gctgtctaac	ggtacttgaa	gaggcaaaag	360
	agtgtaat	cactgcgc	gcgtgaatca	gtactttgaa	gggatgtgag	atcgaaattg	420

356

tgggattacc tcagcaaaaaa cttgcttaat gtgttgccctg ttttagaagt tttagtttca 480
 caatgtgtgg atttattagt ttagagactt ttctgatgct tggcacaatg gttttttctc 540
 agagaacctt tttttgtttt ggagaaatgc atagcagcat taataagtgt attggatcag 600
 aactgaaaca atgttggttac tgattc

5 (2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

15

(D) OTHER INFORMATION: / Ceres Seq. ID 1011982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Ala Trp Arg Asn Ala Gly Ser Ala Ala Arg Ser Phe Val Ser Ala
 1 5 10 15
 Thr Ala Arg Ser Pro Ser Leu Arg Ser Pro Thr Thr Ala Leu Pro Arg
 20 25 30
 Leu Arg Pro Pro Gln Ser Ser Leu Pro Ser Arg Arg Phe Thr Phe Ser
 35 40 45
 Ser Pro Ser Arg Asn Leu Gly Ala Leu Gly Cys Thr Gln Ser Phe Leu
 50 55 60
 25 Pro Leu Tyr Ser Val Val Ala Thr Ser Gln Leu Thr Ser His Leu Asn
 65 70 75 80
 Val Asn Leu Arg Ala Phe Cys Glu Leu Ser Asn Gly Thr
 85 90

30 (2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1011983

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ile Leu Ile Glu Lys Asn Pro Ser Lys Asn Leu Ser Leu Ser Leu Asn
 1 5 10 15
 Ser Leu Leu Leu Leu Gln Trp Leu Gly Ala Thr Gln Asp Leu Leu Leu
 20 25 30
 45 Val Leu Ser Ser Pro Pro Pro Gln Asp His His Leu Ser Val Leu Pro
 35 40 45
 Pro Arg Arg Phe Leu Ala Ser Val Leu Leu Asn Pro Pro Tyr Leu Ala
 50 55 60
 50 Val Ala Ser Pro Ser Arg His Leu Pro Gly Ile
 65 70 75

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..46

60

(D) OTHER INFORMATION: / Ceres Seq. ID 1011984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

357

Met Cys Gly Phe Ile Ser Cys Arg Ala Phe Arg Met Leu Gly Thr Met
 1 5 10 15
 Val Phe Ser Gln Arg Thr Phe Phe Cys Phe Gly Glu Met His Ser Ser
 20 25 30
 5 Ile Asn Lys Cys Ile Gly Ser Glu Leu Lys Gln Cys Cys Tyr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..468
 (D) OTHER INFORMATION: / Ceres Seq. ID 1014547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

atagaatata accatattcc ggacatgaag atcgtgacat tggactcgt cgtcttcgtc 60
 atacttttcga catcattccc ggctgccatc aaagccgaag acacgggaga tacaggaaat 120
 gtgggagtga catgtgacgc aaggcagctt cagccttgcc ttgccgcgat tacgggagga 180
 ggacaaccct cgggtgcatg ttgtgcaaag cttacagagc aacagtcatg cctatgtggt 240
 ttcgctaaga accctgcgtt cgcacagtac attagctctc caaacgctcg caaagtgtc 300
 cttgcttgca atgttgctta tcccacttgt tgaaacttat ctagatttta taaataaata 360
 25 aacgaaagga aataaattac attatatcaa acgttatgat acaattcaac cgtttggtg 420
 aatgtactgg cttacatggt taaataaagt ttaatttctt ggttgctc

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..110
 (D) OTHER INFORMATION: / Ceres Seq. ID 1014548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ile Glu Tyr Asn His Ile Pro Asp Met Lys Ile Val Thr Leu Val Leu
 1 5 10 15
 Val Val Phe Val Ile Leu Ser Thr Ser Phe Pro Ala Ala Ile Lys Ala
 20 25 30
 Glu Asp Thr Gly Asp Thr Gly Asn Val Gly Val Thr Cys Asp Ala Arg
 35 40 45
 Gln Leu Gln Pro Cys Leu Ala Ala Ile Thr Gly Gly Gly Gln Pro Ser
 50 55 60
 Gly Ala Cys Cys Ala Lys Leu Thr Glu Gln Gln Ser Cys Leu Cys Gly
 65 70 75 80
 Phe Ala Lys Asn Pro Ala Phe Ala Gln Tyr Ile Ser Ser Pro Asn Ala
 85 90 95
 Arg Lys Val Leu Leu Ala Cys Asn Val Ala Tyr Pro Thr Cys
 100 105 110

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..102

358

(D) OTHER INFORMATION: / Ceres Seq. ID 1014549

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Lys Ile Val Thr Leu Val Leu Val Val Phe Val Ile Leu Ser Thr
 1 5 10 15
 5 Ser Phe Pro Ala Ala Ile Lys Ala Glu Asp Thr Gly Asp Thr Gly Asn
 20 25 30
 Val Gly Val Thr Cys Asp Ala Arg Gln Leu Gln Pro Cys Leu Ala Ala
 35 40 45
 10 Ile Thr Gly Gly Gly Gln Pro Ser Gly Ala Cys Cys Ala Lys Leu Thr
 50 55 60
 Glu Gln Gln Ser Cys Leu Cys Gly Phe Ala Lys Asn Pro Ala Phe Ala
 65 70 75 80
 Gln Tyr Ile Ser Ser Pro Asn Ala Arg Lys Val Leu Leu Ala Cys Asn
 85 90 95
 15 Val Ala Tyr Pro Thr Cys
 100

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 1303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

25 (A) NAME/KEY: -
 (B) LOCATION: 1..1303

(D) OTHER INFORMATION: / Ceres Seq. ID 1014995

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

aaaactcaag tttcttgcaa ttacctactt acaacaaagc aactcgactc gaacaaacac 60
 30 atccatggct ccttctgctc aacctcttcc tgtgagtgtt tcggatgaaa aatatgcaa 120
 tgtcaagtgg gaagagttgg cattcaagtt tgttcgtacg gattatatgt atgttgcgaa 180
 gtgcaatcat ggagagagtt ttcaagaggg gaagattcct ccttttgctg atttgcaact 240
 taacccttgc gctgctgttc ttcagtatgg ccaggggttta tatgaaggac tgaaagctta 300
 caggacagaa gatggctcga ttctgctatt ccgaccagac caaaacggtc tccgccttca 360
 35 agccggagct gacagactct atatgcctta tcttcggctc gatcaattcg tctccgccat 420
 caaacaagtt gctcttgcca acaagaaatg gattcctcct ccgggggaaag gaacattgta 480
 tattaggcct atcttgtttg ggagtgggtcc gattccttgt tcatttccca ttcctgagac 540
 caccttcaca gcttttgctt gtcctgttgg acgttatcat aaggataact ctggtttgaa 600
 tctgaaaatc gaagatcagt ttctgctgagc ttttcctagt ggaactgggtg gtgtgaagag 660
 40 catcacaacac tattgtcctg ttggataacc attggcagag gcgaaaaaac aaggtttctc 720
 tgatattttg tttttggatg ctgcaactgg caaaaacatt gaagaacttt tcgcagctaa 780
 tgttttttat ctcaagggca atgttgtatc gacaccaaca attgcaggaa ctattttgcc 840
 cggagtcact cgaaactgcg taatggaatt gtgtcgtgat ttcggctacc aggtcgagga 900
 acgtacgatt cctctagtgg acttttctga tgcggacgaa gctttctgta ctggcactgc 960
 45 ttccattgtg actagtattg catccgtaac ctttaaagac aaaaagaccg gattcaaac 1020
 aggggaagaaa cattggctgc gaagctatac gagacgttaa gtgatatcca gacgggtcgg 1080
 gtgcaggata ccaagggatg gacggtggag attgaccgcc agggctgaaa gttgaaactg 1140
 taacttgatg ctaaataatgt gtgtgtgtgt atacaaaact tatgtaagaa acatctgaag 1200
 atgtctctga tctttgtgat tgtgatgatc atgcatgtcc tatcgttgcg atgtatttta 1260
 50 taaatgttcg tctgtaagtt atttaataac tatggctttt tgc

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 352 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

60 (A) NAME/KEY: peptide
 (B) LOCATION: 1..352

(D) OTHER INFORMATION: / Ceres Seq. ID 1014996

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

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	Lys	Leu	Lys	Phe	Leu	Ala	Ile	Thr	Tyr	Leu	Gln	Gln	Ser	Asn	Ser	Thr
	1				5					10					15	
	Arg	Thr	Asn	Thr	Ser	Met	Ala	Pro	Ser	Ala	Gln	Pro	Leu	Pro	Val	Ser
				20					25					30		
5	Val	Ser	Asp	Glu	Lys	Tyr	Ala	Asn	Val	Lys	Trp	Glu	Glu	Leu	Ala	Phe
			35					40					45			
	Lys	Phe	Val	Arg	Thr	Asp	Tyr	Met	Tyr	Val	Ala	Lys	Cys	Asn	His	Gly
		50					55					60				
10	Glu	Ser	Phe	Gln	Glu	Gly	Lys	Ile	Leu	Pro	Phe	Ala	Asp	Leu	Gln	Leu
	65					70					75					80
	Asn	Pro	Cys	Ala	Ala	Val	Leu	Gln	Tyr	Gly	Gln	Gly	Leu	Tyr	Glu	Gly
				85						90					95	
	Leu	Lys	Ala	Tyr	Arg	Thr	Glu	Asp	Gly	Arg	Ile	Leu	Leu	Phe	Arg	Pro
				100					105						110	
15	Asp	Gln	Asn	Gly	Leu	Arg	Leu	Gln	Ala	Gly	Ala	Asp	Arg	Leu	Tyr	Met
			115					120					125			
	Pro	Tyr	Pro	Ser	Val	Asp	Gln	Phe	Val	Ser	Ala	Ile	Lys	Gln	Val	Ala
		130					135						140			
20	Leu	Ala	Asn	Lys	Lys	Trp	Ile	Pro	Pro	Pro	Gly	Lys	Gly	Thr	Leu	Tyr
	145					150					155					160
	Ile	Arg	Pro	Ile	Leu	Phe	Gly	Ser	Gly	Pro	Ile	Leu	Gly	Ser	Phe	Pro
				165						170					175	
	Ile	Pro	Glu	Thr	Thr	Phe	Thr	Ala	Phe	Ala	Cys	Pro	Val	Gly	Arg	Tyr
				180					185					190		
25	His	Lys	Asp	Asn	Ser	Gly	Leu	Asn	Leu	Lys	Ile	Glu	Asp	Gln	Phe	Arg
			195					200					205			
	Arg	Ala	Phe	Pro	Ser	Gly	Thr	Gly	Gly	Val	Lys	Ser	Ile	Thr	Asn	Tyr
		210					215					220				
30	Cys	Pro	Val	Trp	Ile	Pro	Leu	Ala	Glu	Ala	Lys	Lys	Gln	Gly	Phe	Ser
	225					230					235					240
	Asp	Ile	Leu	Phe	Leu	Asp	Ala	Ala	Thr	Gly	Lys	Asn	Ile	Glu	Glu	Leu
				245						250					255	
	Phe	Ala	Ala	Asn	Val	Phe	Met	Leu	Lys	Gly	Asn	Val	Val	Ser	Thr	Pro
				260					265						270	
35	Thr	Ile	Ala	Gly	Thr	Ile	Leu	Pro	Gly	Val	Thr	Arg	Asn	Cys	Val	Met
			275					280						285		
	Glu	Leu	Cys	Arg	Asp	Phe	Gly	Tyr	Gln	Val	Glu	Glu	Arg	Thr	Ile	Pro
		290					295					300				
40	Leu	Val	Asp	Phe	Leu	Asp	Ala	Asp	Glu	Ala	Phe	Cys	Thr	Gly	Thr	Ala
	305					310					315					320
	Ser	Ile	Val	Thr	Ser	Ile	Ala	Ser	Val	Thr	Phe	Lys	Asp	Lys	Lys	Thr
				325						330					335	
	Gly	Phe	Lys	Thr	Gly	Lys	Lys	His	Trp	Leu	Arg	Ser	Tyr	Thr	Arg	Arg
				340					345					350		
45	(2) INFORMATION FOR SEQ ID NO:73:															
	(i) SEQUENCE CHARACTERISTICS:															
	(A) LENGTH: 331 amino acids															
	(B) TYPE: amino acid															
	(C) STRANDEDNESS:															
50	(D) TOPOLOGY: linear															
	(ii) MOLECULE TYPE: peptide															
	(ix) FEATURE:															
	(A) NAME/KEY: peptide															
	(B) LOCATION: 1..331															
55	(D) OTHER INFORMATION: / Ceres Seq. ID 1014997															
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:															
	Met	Ala	Pro	Ser	Ala	Gln	Pro	Leu	Pro	Val	Ser	Val	Ser	Asp	Glu	Lys
	1				5					10					15	
	Tyr	Ala	Asn	Val	Lys	Trp	Glu	Glu	Leu	Ala	Phe	Lys	Phe	Val	Arg	Thr
60				20					25					30		
	Asp	Tyr	Met	Tyr	Val	Ala	Lys	Cys	Asn	His	Gly	Glu	Ser	Phe	Gln	Glu
			35					40						45		

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	Gly	Lys	Ile	Leu	Pro	Phe	Ala	Asp	Leu	Gln	Leu	Asn	Pro	Cys	Ala	Ala
	50					55					60					
	Val	Leu	Gln	Tyr	Gly	Gln	Gly	Leu	Tyr	Glu	Gly	Leu	Lys	Ala	Tyr	Arg
	65				70					75					80	
5	Thr	Glu	Asp	Gly	Arg	Ile	Leu	Leu	Phe	Arg	Pro	Asp	Gln	Asn	Gly	Leu
				85					90					95		
	Arg	Leu	Gln	Ala	Gly	Ala	Asp	Arg	Leu	Tyr	Met	Pro	Tyr	Pro	Ser	Val
			100				105						110			
10	Asp	Gln	Phe	Val	Ser	Ala	Ile	Lys	Gln	Val	Ala	Leu	Ala	Asn	Lys	Lys
		115					120					125				
	Trp	Ile	Pro	Pro	Pro	Gly	Lys	Gly	Thr	Leu	Tyr	Ile	Arg	Pro	Ile	Leu
	130					135						140				
	Phe	Gly	Ser	Gly	Pro	Ile	Leu	Gly	Ser	Phe	Pro	Ile	Pro	Glu	Thr	Thr
	145				150					155					160	
15	Phe	Thr	Ala	Phe	Ala	Cys	Pro	Val	Gly	Arg	Tyr	His	Lys	Asp	Asn	Ser
				165					170					175		
	Gly	Leu	Asn	Leu	Lys	Ile	Glu	Asp	Gln	Phe	Arg	Arg	Ala	Phe	Pro	Ser
			180					185					190			
20	Gly	Thr	Gly	Gly	Val	Lys	Ser	Ile	Thr	Asn	Tyr	Cys	Pro	Val	Trp	Ile
		195					200						205			
	Pro	Leu	Ala	Glu	Ala	Lys	Lys	Gln	Gly	Phe	Ser	Asp	Ile	Leu	Phe	Leu
	210					215						220				
	Asp	Ala	Ala	Thr	Gly	Lys	Asn	Ile	Glu	Glu	Leu	Phe	Ala	Ala	Asn	Val
	225				230					235					240	
25	Phe	Met	Leu	Lys	Gly	Asn	Val	Val	Ser	Thr	Pro	Thr	Ile	Ala	Gly	Thr
				245					250					255		
	Ile	Leu	Pro	Gly	Val	Thr	Arg	Asn	Cys	Val	Met	Glu	Leu	Cys	Arg	Asp
			260				265						270			
30	Phe	Gly	Tyr	Gln	Val	Glu	Glu	Arg	Thr	Ile	Pro	Leu	Val	Asp	Phe	Leu
		275					280					285				
	Asp	Ala	Asp	Glu	Ala	Phe	Cys	Thr	Gly	Thr	Ala	Ser	Ile	Val	Thr	Ser
	290					295					300					
	Ile	Ala	Ser	Val	Thr	Phe	Lys	Asp	Lys	Lys	Thr	Gly	Phe	Lys	Thr	Gly
	305				310					315					320	
35	Lys	Lys	His	Trp	Leu	Arg	Ser	Tyr	Thr	Arg	Arg					
				325					330							

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 297 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..297

(D) OTHER INFORMATION: / Ceres Seq. ID 1014998

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

50	Met	Tyr	Val	Ala	Lys	Cys	Asn	His	Gly	Glu	Ser	Phe	Gln	Glu	Gly	Lys
	1			5					10				15			
	Ile	Leu	Pro	Phe	Ala	Asp	Leu	Gln	Leu	Asn	Pro	Cys	Ala	Ala	Val	Leu
			20				25					30				
	Gln	Tyr	Gly	Gln	Gly	Leu	Tyr	Glu	Gly	Leu	Lys	Ala	Tyr	Arg	Thr	Glu
		35				40						45				
55	Asp	Gly	Arg	Ile	Leu	Leu	Phe	Arg	Pro	Asp	Gln	Asn	Gly	Leu	Arg	Leu
	50				55				60							
	Gln	Ala	Gly	Ala	Asp	Arg	Leu	Tyr	Met	Pro	Tyr	Pro	Ser	Val	Asp	Gln
	65				70				75					80		
	Phe	Val	Ser	Ala	Ile	Lys	Gln	Val	Ala	Leu	Ala	Asn	Lys	Lys	Trp	Ile
60				85					90					95		
	Pro	Pro	Pro	Gly	Lys	Gly	Thr	Leu	Tyr	Ile	Arg	Pro	Ile	Leu	Phe	Gly
				100				105						110		

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Ser Gly Pro Ile Leu Gly Ser Phe Pro Ile Pro Glu Thr Thr Phe Thr
 115 120 125
 Ala Phe Ala Cys Pro Val Gly Arg Tyr His Lys Asp Asn Ser Gly Leu
 130 135 140
 5 Asn Leu Lys Ile Glu Asp Gln Phe Arg Arg Ala Phe Pro Ser Gly Thr
 145 150 155 160
 Gly Gly Val Lys Ser Ile Thr Asn Tyr Cys Pro Val Trp Ile Pro Leu
 165 170 175
 10 Ala Glu Ala Lys Lys Gln Gly Phe Ser Asp Ile Leu Phe Leu Asp Ala
 180 185 190
 Ala Thr Gly Lys Asn Ile Glu Glu Leu Phe Ala Ala Asn Val Phe Met
 195 200 205
 Leu Lys Gly Asn Val Val Ser Thr Pro Thr Ile Ala Gly Thr Ile Leu
 210 215 220
 15 Pro Gly Val Thr Arg Asn Cys Val Met Glu Leu Cys Arg Asp Phe Gly
 225 230 235 240
 Tyr Gln Val Glu Glu Arg Thr Ile Pro Leu Val Asp Phe Leu Asp Ala
 245 250 255
 20 Asp Glu Ala Phe Cys Thr Gly Thr Ala Ser Ile Val Thr Ser Ile Ala
 260 265 270
 Ser Val Thr Phe Lys Asp Lys Lys Thr Gly Phe Lys Thr Gly Lys Lys
 275 280 285
 His Trp Leu Arg Ser Tyr Thr Arg Arg
 290 295
 25 (2) INFORMATION FOR SEQ ID NO:75:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..789
 35 (D) OTHER INFORMATION: / Ceres Seq. ID 1015323
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:
 ggggttaggtt tgtcttcaaa atcgtcagaa gaagaagaag aagtcaaaga cgataacaat 60
 gacgtcatca tcgtacctcc gatttgcgat cgccgtcgta gctttcctct caatcaccac 120
 catcaccacc gcacgtcctt gcaaaacctt cctaattctcc tcatattccc tctcaataac 180
 40 cccagaaaac cctaacctcg aatccgattt cacctccaca cgattcgtca ccgttttcac 240
 aatccgctgt ctaaattcctc accacgtggt tcctttcttc gtcaatcgtc gtcacgagaa 300
 gccacagatc caatcggatc gttccctccc ttgatctct gataacatca attcgtttag 360
 agatcgaacc agagatatct ttagcgtcgt cgtcgcgctt ttgttcggtg ttggttgtgg 420
 tgctttaacc gctgctacta tgtatcttgt ttgggctctt gttgtgaatc gtcaaagcta 480
 45 tgattttgag gaagaagaag atgattatga gaatgatgaa tctgatgctg ctagcttgaa 540
 gaaattgggt tatgttaaga ttccagctcc agctcctgct cctgtgaagg aagctgcttg 600
 atttgaggtt gtgaatttca gtttctgcat attatcatga tttacgttgt tgcttatcta 660
 tgttggtgcg tacaagtaaa ttcgctctctg ttatggattt atctaaactt actatactct 720
 aagtatcagt gtttttacga tttgtagttg atgtttctta tatatatata taagtgtgat 780
 50 tatgatgct
 (2) INFORMATION FOR SEQ ID NO:76:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 55 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 60 (B) LOCATION: 1..180
 (D) OTHER INFORMATION: / Ceres Seq. ID 1015324
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

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Met Thr Ser Ser Ser Tyr Leu Arg Phe Ala Ile Ala Val Val Ala Phe
 1 5 10 15
 Leu Ser Ile Thr Thr Ile Thr Thr Ala Arg Pro Cys Lys Thr Phe Leu
 20 25 30
 5 Ile Ser Ser Tyr Ser Leu Ser Ile Thr Pro Glu Asn Pro Asn Leu Glu
 35 40 45
 Ser Asp Phe Thr Ser Thr Arg Phe Val Thr Val Phe Thr Ile Arg Arg
 50 55 60
 10 Leu Asn Pro His His Val Val Pro Phe Phe Val Asn Arg Arg His Glu
 65 70 75 80
 Lys Pro Gln Ile Gln Ser Asp Arg Ser Leu Pro Leu Ile Ser Asp Asn
 85 90 95
 Ile Asn Ser Phe Arg Asp Arg Thr Arg Asp Ile Leu Ser Val Val Val
 100 105 110
 15 Ala Leu Leu Phe Gly Val Gly Cys Gly Ala Leu Thr Ala Ala Thr Met
 115 120 125
 Tyr Leu Val Trp Ala Leu Val Val Asn Arg Gln Ser Tyr Asp Phe Glu
 130 135 140
 20 Glu Glu Glu Asp Asp Tyr Glu Asn Asp Glu Ser Asp Ala Ala Ser Leu
 145 150 155 160
 Lys Lys Leu Gly Tyr Val Lys Ile Pro Ala Pro Ala Pro Ala Pro Val
 165 170 175
 Lys Glu Ala Ala
 180

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..495
 (D) OTHER INFORMATION: / Ceres Seq. ID 1016486

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

acttcctcat tagcattcta cagtctgcac acttatcact tctttcgaaa tctctctcta 60
 tccctctcaa aaatgaagct ctctgtgcgt tttatctcgc ctgctcttct ctgttcatg 120
 gtattcattg ccacagggat gggtccagtc accgtggagg cacgcacgtg tgagtcaaag 180
 40 agccataggt tcaagggtcc atgtgtgagc acacacaact gtgcaaactg gtgccacaac 240
 gaaggcttcg gcgagggtaa atgccgtgga ttccgtcgtc gttgctactg cacaagacac 300
 tgctgatcca tccattctca tgactcaaat ctctgatcca tcgtcagtgt gttacttctt 360
 tcttatctaa atcttccgta cgggtaccata tcgtaccgta catgagtgtt ttctcaaata 420
 agtcgttggt ttgtgtgttt ccggttttaa tgtaattgta aatcaattaa tggcttttaa 480
 45 tatattgtat tatgg

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
 (B) LOCATION: 1..101
 (D) OTHER INFORMATION: / Ceres Seq. ID 1016487

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Thr Ser Ser Leu Ala Phe Tyr Ser Leu His Thr Tyr His Phe Phe Arg
 1 5 10 15
 60 Asn Leu Ser Leu Ser Leu Ser Lys Met Lys Leu Ser Val Arg Phe Ile
 20 25 30
 Ser Ala Ala Leu Leu Leu Phe Met Val Phe Ile Ala Thr Gly Met Gly

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35 40 45
 Pro Val Thr Val Glu Ala Arg Thr Cys Glu Ser Lys Ser His Arg Phe
 50 55 60
 Lys Gly Pro Cys Val Ser Thr His Asn Cys Ala Asn Val Cys His Asn
 5 65 70 75 80
 Glu Gly Phe Gly Gly Gly Lys Cys Arg Gly Phe Arg Arg Arg Cys Tyr
 85 90 95
 Cys Thr Arg His Cys

10 (2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

20 (D) OTHER INFORMATION: / Ceres Seq. ID 1016488

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Lys Leu Ser Val Arg Phe Ile Ser Ala Ala Leu Leu Leu Phe Met
 1 5 10 15
 Val Phe Ile Ala Thr Gly Met Gly Pro Val Thr Val Glu Ala Arg Thr
 25 20 25 30
 Cys Glu Ser Lys Ser His Arg Phe Lys Gly Pro Cys Val Ser Thr His
 35 40 45
 Asn Cys Ala Asn Val Cys His Asn Glu Gly Phe Gly Gly Gly Lys Cys
 50 55 60
 Arg Gly Phe Arg Arg Arg Cys Tyr Cys Thr Arg His Cys
 30 65 70 75

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1016489

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Met Val Phe Ile Ala Thr Gly Met Gly Pro Val Thr Val Glu Ala Arg
 45 1 5 10 15
 Thr Cys Glu Ser Lys Ser His Arg Phe Lys Gly Pro Cys Val Ser Thr
 20 25 30
 His Asn Cys Ala Asn Val Cys His Asn Glu Gly Phe Gly Gly Gly Lys
 35 40 45
 Cys Arg Gly Phe Arg Arg Arg Cys Tyr Cys Thr Arg His Cys
 50 55 60

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..325

(D) OTHER INFORMATION: / Ceres Seq. ID 1018341

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

atcatcaaac acaaaacaat caatcaaaaa cataaaattc aaagtgtgtaag caaaaccaga      60
acgagagaaaa atggacaaca agcaaaacgc gagctaccaa gccggtcaag ccactggcca      120
gactaaggag aaggccggtg gaatgatgga caaggccaag gatgctgctg cttcagctca      180
5 agactccttg caacagactg gacaacaaat gaaggagaag gcgcaaggag ctgctgatgt      240
cgtcaaggac aagaccggca tgaacaaaag ccactaagca agcatcttgg acttcctttc      300
taattaattc ccctcttcga cttgt

```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 1018342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```

20 Met Asp Asn Lys Gln Asn Ala Ser Tyr Gln Ala Gly Gln Ala Thr Gly
   1           5           10           15
Gln Thr Lys Glu Lys Ala Gly Gly Met Met Asp Lys Ala Lys Asp Ala
   20           25           30
Ala Ala Ser Ala Gln Asp Ser Leu Gln Gln Thr Gly Gln Gln Met Lys
25   35           40           45
Glu Lys Ala Gln Gly Ala Ala Asp Val Val Lys Asp Lys Thr Gly Met
   50           55           60
Asn Lys Ser His
65

```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 44 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..44

(D) OTHER INFORMATION: / Ceres Seq. ID 1018343

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

40 Met Met Asp Lys Ala Lys Asp Ala Ala Ser Ala Gln Asp Ser Leu
   1           5           10           15
Gln Gln Thr Gly Gln Gln Met Lys Glu Lys Ala Gln Gly Ala Ala Asp
45   20           25           30
Val Val Lys Asp Lys Thr Gly Met Asn Lys Ser His
   35           40

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..43

(D) OTHER INFORMATION: / Ceres Seq. ID 1018344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

60 Met Asp Lys Ala Lys Asp Ala Ala Ser Ala Gln Asp Ser Leu Gln
   1           5           10           15
Gln Thr Gly Gln Gln Met Lys Glu Lys Ala Gln Gly Ala Ala Asp Val

```

365

Val Lys Asp Lys Thr Gly Met Asn Lys Ser His

30

(2) INFORMATION FOR SEO ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..540

(D) OTHER INFORMATION: / Ceres Seq. ID 1018382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

taaaagcaat	aaaaaacaaa	aatggcggtt	actccgaaga	tcatcacatg	cctcattgtc	60
cttacgatct	acatgacatc	cccaacagag	tcaaccatcc	agtgtgggac	agtgacgagc	120
acactggcac	agtgcgtgac	ctacttgacc	aacagtggtc	cattgccatc	acaatgctgc	180
gtgggagtca	agtcattgta	ccaattggct	cagaccacac	cggaccgtaa	acaagtatgt	240
gagtgcctta	aactagcggg	taaagaaaatc	aagggcctca	acaccgacct	tgtggccgca	300
cttcctacca	cttgtggtgt	ttcaattccc	taccccatca	gtttttagca	caattgcgac	360
agtatatcga	ctgccgtgtg	aaagaggcta	gtgatcagat	gtacgactaa	tcaaactttgc	420
cagctttttaa	cctaatttaa	taaaagttatt	ctgcttatat	tccccatctt	atgatttttat	480
cttcttatct	atgtaaccac	acgatttcat	atgctaataa	tqacaacgga	tctttctctc	540

(2) INFORMATION FOR SEO ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..119

(D) OTHER INFORMATION: / Ceres Seq. ID 1018383

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

[illegible]

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

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(D) OTHER INFORMATION: / Ceres Seq. ID 1018384

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Met Thr Ser Pro Thr Glu Ser Thr Ile Gln Cys Gly Thr Val Thr Ser
 1 5 10 15
 5 Thr Leu Ala Gln Cys Val Thr Tyr Leu Thr Asn Ser Gly Pro Leu Pro
 20 25 30
 Ser Gln Cys Cys Val Gly Val Lys Ser Leu Tyr Gln Leu Ala Gln Thr
 35 40 45
 Thr Pro Asp Arg Lys Gln Val Cys Glu Cys Leu Lys Leu Ala Gly Lys
 50 55 60
 10 Glu Ile Lys Gly Leu Asn Thr Asp Leu Val Ala Leu Pro Thr Thr
 65 70 75 80
 Cys Gly Val Ser Ile Pro Tyr Pro Ile Ser Phe Ser Thr Asn Cys Asp
 85 90 95
 15 Ser Ile Ser Thr Ala Val
 100

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 75 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

25 (A) NAME/KEY: peptide
 (B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1018385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Lys Ala Ile Lys Asn Lys Asn Gly Val Tyr Ser Glu Asp His His Met
 1 5 10 15
 30 Pro His Cys Pro Tyr Asp Leu His Asp Ile Pro Asn Arg Val Asn His
 20 25 30
 Pro Val Trp Asp Ser Asp Glu His Thr Gly Thr Val Arg Asp Leu Leu
 35 35 40 45
 Asp Gln Gln Trp Ser Ile Ala Ile Thr Met Leu Arg Gly Ser Gln Val
 50 55 60
 Ile Val Pro Ile Gly Ser Asp His Thr Gly Pro
 65 70 75

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 844 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..844

(D) OTHER INFORMATION: / Ceres Seq. ID 1020666

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

50 ctaaataattt aaagctttcc ttcaccagca ttgtattgcc tccctggaac accgaagctc 60
 tggattaacc tattttcacc ttctaagggt cttcgctcgtt cttattgata tgtgaagatg 120
 tattcgggtc agaacaagat ccacaaggat aagggtgttg caccaacaga gtttgaagag 180
 caagttactc aggctttgtt tgacttggag aacaccaacc aggagttgaa aagcgagttg 240
 55 aaagatctct acattaacca agctgttcag atggatatatt ctggcaaccg caaagctgtt 300
 gtgatctacg ttccattcag gctgaggaaa gctttccgca agattcatct tcgtctggtc 360
 agagagcttg agaagaagtt cagtggaaaa gatgtgatct ttgttgctac cagaagaatc 420
 atgcgcccac caaagaaagg ctcagctgtt cacagaccac gcaacagaac tcttacttct 480
 gtccatgaag ccatgctcga ggatgtcgtt taccctgctg agattgtagg aaagagaacc 540
 60 agataccgtc ttgatggcac caagatcatg aagggtatttt tggatagtaa gctaaagaac 600
 gacactgagt acaagctgga gacaatggtg ggtgtgtaca gaaaacttac agggaaagat 660
 gtagtttttcg agtaccacgt catagaagct tgaagagatg aatgtttgtt tcattctttt 720

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ttgtcggata gagagctttt gattctgttt gggagtaaaa ctctttgcaa agattttgtt 780
 atttcagcat ttcgcaatct ctctttcaaa gttcgattta tcgatacaat tcttttttcc 840
 tacc

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..191
 (D) OTHER INFORMATION: / Ceres Seq. ID 1020667

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Met	Tyr	Ser	Gly	Gln	Asn	Lys	Ile	His	Lys	Asp	Lys	Gly	Val	Ala	Pro
1				5					10					15	
Thr	Glu	Phe	Glu	Glu	Gln	Val	Thr	Gln	Ala	Leu	Phe	Asp	Leu	Glu	Asn
			20					25					30		
Thr	Asn	Gln	Glu	Leu	Lys	Ser	Glu	Leu	Lys	Asp	Leu	Tyr	Ile	Asn	Gln
		35					40					45			
Ala	Val	Gln	Met	Asp	Ile	Ser	Gly	Asn	Arg	Lys	Ala	Val	Val	Ile	Tyr
		50				55					60				
Val	Pro	Phe	Arg	Leu	Arg	Lys	Ala	Phe	Arg	Lys	Ile	His	Leu	Arg	Leu
25					70				75					80	
Val	Arg	Glu	Leu	Glu	Lys	Lys	Phe	Ser	Gly	Lys	Asp	Val	Ile	Phe	Val
				85					90					95	
Ala	Thr	Arg	Arg	Ile	Met	Arg	Pro	Pro	Lys	Lys	Gly	Ser	Ala	Val	Gln
			100					105					110		
Arg	Pro	Arg	Asn	Arg	Thr	Leu	Thr	Ser	Val	His	Glu	Ala	Met	Leu	Glu
		115				120					125				
Asp	Val	Ala	Tyr	Pro	Ala	Glu	Ile	Val	Gly	Lys	Arg	Thr	Arg	Tyr	Arg
		130				135					140				
Leu	Asp	Gly	Thr	Lys	Ile	Met	Lys	Val	Phe	Leu	Asp	Ser	Lys	Leu	Lys
35					150				155					160	
Asn	Asp	Thr	Glu	Tyr	Lys	Leu	Glu	Thr	Met	Val	Gly	Val	Tyr	Arg	Lys
				165				170						175	
Leu	Thr	Gly	Lys	Asp	Val	Val	Phe	Glu	Tyr	Pro	Val	Ile	Glu	Ala	
		180						185					190		

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1020668

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Met	Asp	Ile	Ser	Gly	Asn	Arg	Lys	Ala	Val	Val	Ile	Tyr	Val	Pro	Phe
1				5				10						15	
Arg	Leu	Arg	Lys	Ala	Phe	Arg	Lys	Ile	His	Leu	Arg	Leu	Val	Arg	Glu
			20					25					30		
Leu	Glu	Lys	Lys	Phe	Ser	Gly	Lys	Asp	Val	Ile	Phe	Val	Ala	Thr	Arg
		35				40						45			
Arg	Ile	Met	Arg	Pro	Pro	Lys	Lys	Gly	Ser	Ala	Val	Gln	Arg	Pro	Arg
		50				55					60				
Asn	Arg	Thr	Leu	Thr	Ser	Val	His	Glu	Ala	Met	Leu	Glu	Asp	Val	Ala
				70				75						80	
Tyr	Pro	Ala	Glu	Ile	Val	Gly	Lys	Arg	Thr	Arg	Tyr	Arg	Leu	Asp	Gly

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85 90 95

Thr Lys Ile Met Lys Val Phe Leu Asp Ser Lys Leu Lys Asn Asp Thr
 100 105 110

5 Glu Tyr Lys Leu Glu Thr Met Val Gly Val Tyr Arg Lys Leu Thr Gly
 115 120 125

Lys Asp Val Val Phe Glu Tyr Pro Val Ile Glu Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO:92:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

15 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..789
 (D) OTHER INFORMATION: / Ceres Seq. ID 1020784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

20 aggggttaggt ttgtcttcaa aatcgtcaga agaagaagaa gaagtcaaag acgataacaa 60
 tgacgtcatc atcgtacctc cgatttgcga tcgccgtcgt agctttcctc tcaatcacca 120
 ccatcaccac cgcacgtcct tgcaaaacct tcctaattct ctcataattcc ctctcaataa 180
 ccccagaaaa ccctaacctc gaatccgatt tcacctccac acgattcatc accgtttttca 240
 caatccgtcg tctaaatcct caccacgtgg ttccctttctt cgtcaatcgt cgtcacgaga 300
 25 agccacagat ccaatcggat cgttccctcc ctttgatctc tgataacatc aattcgttta 360
 gagatcgaac cagagatatt cttagcgtcg tcgtcgcgct tttggttcggt gttgggtgtg 420
 gtgctttaac cgctgctact atgtatcttg tttgggctct tgttgatgaat cgtcaaagct 480
 atgattttga ggaagaagaa gatgattatg agaatgatga atctgatgct gctagcttga 540
 agaaattggg ttatgttaag attccagctc cagctcctgc tcctgtgaag gaagctgctt 600
 30 gatttgaggt tgtgaatttc agtttctgca tattatcatg atttacgttg ttgcttatct 660
 atgttggtgc gtacaagtaa attcgtctct gttatggatt tatctaaact tactatactc 720
 taagtatcag tgtttttacg atttgtagtt gatgtttctt atatatatat ataagtgatga 780
 ttatgatgc

(2) INFORMATION FOR SEQ ID NO:93:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..180
 (D) OTHER INFORMATION: / Ceres Seq. ID 1020785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

45 Met Thr Ser Ser Ser Tyr Leu Arg Phe Ala Ile Ala Val Val Ala Phe
 1 5 10 15
 Leu Ser Ile Thr Thr Ile Thr Thr Ala Arg Pro Cys Lys Thr Phe Leu
 20 25 30

50 Ile Ser Ser Tyr Ser Leu Ser Ile Thr Pro Glu Asn Pro Asn Leu Glu
 35 40 45
 Ser Asp Phe Thr Ser Thr Arg Phe Ile Thr Val Phe Thr Ile Arg Arg
 50 55 60

55 Leu Asn Pro His His Val Val Pro Phe Phe Val Asn Arg Arg His Glu
 65 70 75 80
 Lys Pro Gln Ile Gln Ser Asp Arg Ser Leu Pro Leu Ile Ser Asp Asn
 85 90 95

Ile Asn Ser Phe Arg Asp Arg Thr Arg Asp Ile Leu Ser Val Val Val
 100 105 110

60 Ala Leu Leu Phe Gly Val Gly Cys Gly Ala Leu Thr Ala Ala Thr Met
 115 120 125

Tyr Leu Val Trp Ala Leu Val Val Asn Arg Gln Ser Tyr Asp Phe Glu

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130 135 140
 Glu Glu Glu Asp Asp Tyr Glu Asn Asp Glu Ser Asp Ala Ala Ser Leu
 145 150 155 160
 Lys Lys Leu Gly Tyr Val Lys Ile Pro Ala Pro Ala Pro Ala Pro Val
 5 165 170 175
 Lys Glu Ala Ala
 180

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..765
 (D) OTHER INFORMATION: / Ceres Seq. ID 1021525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

20 accctcactc acttttccgg tttcaaccat tagcacaaaa aatctgagct ccgacaaaa 60
 attggggaac gacgatggcg acgactcttc agaaactctc ctctcaaadc caccgactct 120
 ctccattcac cagatctcta atcgcttcga catccgcaac gtctgctcct tctccgtctc 180
 tgggatcgaa gaaagtctct gaccgaatcg tcaagcttct tgcgatcgat cccgatggat 240
 acaagcagga catcattgga ctctctggcc agactctcct tctgctgctc actcacactg 300
 25 gtctgataga tccagcatcg catagattgg atgacatcga ggcttgctca gcggagtgcg 360
 aggttcagat cgcagaggaa tggctcgaga agctcccgcc gcgtacttac gatgaggagt 420
 atgtgctgaa gcgtagctct agatccccta tcttgaacaa gcaactcgct cttggttgcc 480
 aagttgtgtt aacgcaggag cttcaaggta tggctcgctc tgtccctgaa gctaagcctt 540
 gggatattcc gtaagttttt gttcttgagg atctcataaa tgttggttcc gttctcaatt 600
 30 tggctaataa aattcgcttt ggaaatttcg gtactctgaa gataactcca tttgaatctg 660
 taattttcgt ttgcttacat ttaaattttg taatgtggta aagaactctg cttgttttaa 720
 cgattccctg cttcaagtat ggggtgaatgt tgttttcttg attcc

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..159
 (D) OTHER INFORMATION: / Ceres Seq. ID 1021526

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

45 Met Ala Thr Thr Leu Gln Lys Leu Ser Ser Gln Ile His Arg Leu Ser
 1 5 10 15
 Pro Phe Thr Arg Ser Leu Ile Val Arg Thr Ser Ala Thr Ser Ala Pro
 20 25 30
 50 Ser Pro Ser Leu Gly Ser Lys Lys Val Ser Asp Arg Ile Val Lys Leu
 35 40 45
 Ser Ala Ile Asp Pro Asp Gly Tyr Lys Gln Asp Ile Ile Gly Leu Ser
 50 55 60
 Gly Gln Thr Leu Leu Arg Ala Leu Thr His Thr Gly Leu Ile Asp Pro
 65 70 75 80
 55 Ala Ser His Arg Leu Asp Asp Ile Glu Ala Cys Ser Ala Glu Cys Glu
 85 90 95
 Val Gln Ile Ala Glu Glu Trp Leu Glu Lys Leu Pro Pro Arg Thr Tyr
 100 105 110
 60 Asp Glu Glu Tyr Val Leu Lys Arg Ser Ser Arg Ser Arg Ile Leu Asn
 115 120 125
 Lys His Ser Arg Leu Gly Cys Gln Val Val Leu Thr Gln Glu Leu Gln
 130 135 140

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Gly Met Val Val Ala Val Pro Glu Ala Lys Pro Trp Asp Ile Pro
 145 150 155

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..588
 (D) OTHER INFORMATION: / Ceres Seq. ID 1021563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

atcttcggaa	agtcctcattt	ctcgatcccc	aattcgtgga	ttaggggttaa	agaaccatt	60
tttattctcg	tcgcgcaaca	acaaatccag	atcgaaaaag	gaagaagaga	tcgaaatggc	120
tttgagaagg	gtttacagtg	aaatcagagg	gaagaagggtg	acggagcttc	caggctatat	180
caaatcgact	ttttcaatgg	agaccgtgaa	gacctctgtg	aagagaggac	tcgataacta	240
caacgaaaaa	tacattcaga	ccagctccgt	tgatcctatc	cttcataatct	gcttctacgg	300
catggcttcc	tcttaccttg	tcgctctccc	taatgagcgt	cgccatcttg	agcatcagca	360
gcatgctaag	gagcacggtg	gtcattgata	tcgtgggaat	cgtttcgata	tcgagatgat	420
tttagggggg	ttgctgtgaa	atctttctct	gcttgatggt	gacgacgact	caagaattgt	480
gtcttattgt	ttcgttttct	tgaattttcc	tggataatgt	tgacctaaag	gaaaaccttt	540
ctttcgaatt	acactccatg	atagtcaata	attgaagcat	catgatgc		

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 1021564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser	Ser	Glu	Ser	Leu	Ile	Ser	Arg	Ser	Pro	Ile	Arg	Gly	Leu	Gly	Leu
1				5					10					15	
Lys	Glu	Pro	Phe	Leu	Phe	Ser	Ser	Arg	Asn	Asn	Lys	Ser	Arg	Ser	Lys
			20					25					30		
Lys	Glu	Glu	Glu	Ile	Glu	Met	Ala	Leu	Arg	Arg	Val	Tyr	Ser	Glu	Ile
			35				40					45			
Arg	Gly	Lys	Lys	Val	Thr	Glu	Leu	Pro	Gly	Tyr	Ile	Lys	Ser	Thr	Phe
			50				55				60				
Ser	Met	Glu	Thr	Val	Lys	Thr	Ser	Val	Lys	Arg	Gly	Leu	Asp	Asn	Tyr
				70					75					80	
Asn	Glu	Lys	Tyr	Ile	Gln	Thr	Ser	Ser	Val	Asp	Pro	Ile	Leu	His	Ile
				85					90					95	
Cys	Phe	Tyr	Gly	Met	Ala	Phe	Ser	Tyr	Leu	Val	Ala	Leu	Pro	Asn	Glu
			100					105					110		
Arg	Arg	His	Leu	Glu	His	Gln	Gln	His	Ala	Lys	Glu	His	Gly	Gly	His
			115				120						125		

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..90

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(D) OTHER INFORMATION: / Ceres Seq. ID 1021565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Ala Leu Arg Arg Val Tyr Ser Glu Ile Arg Gly Lys Lys Val Thr
 1 5 10 15
 5 Glu Leu Pro Gly Tyr Ile Lys Ser Thr Phe Ser Met Glu Thr Val Lys
 20 25 30
 Thr Ser Val Lys Arg Gly Leu Asp Asn Tyr Asn Glu Lys Tyr Ile Gln
 35 40 45
 Thr Ser Ser Val Asp Pro Ile Leu His Ile Cys Phe Tyr Gly Met Ala
 10 50 55 60
 Phe Ser Tyr Leu Val Ala Leu Pro Asn Glu Arg Arg His Leu Glu His
 65 70 75 80
 Gln Gln His Ala Lys Glu His Gly Gly His
 85 90

15 (2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 586 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..586

25 (D) OTHER INFORMATION: / Ceres Seq. ID 1021576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

ttgcctaaat cattttaaaag actgtataga ggaaaacaaa actgcaaaaa caaaaataaa 60
 aaaaacatcg cacaagaaaa taaaagattt gtagaatcaa ctaagaaaaat ggctagcact 120
 atgatgacta cattgcctca gttcaatggt cttcgagcca ccaaaatctc tgcagctcct 180
 30 gtacaaggcc tggcaagtgt tcagcccatg agacgcaagg gaaatggagc tttgggtgca 240
 aagtgtgact tcatcggttc atcaacaaat ctgataatgg taacgtcgac gaccctgatg 300
 ttgttcgcgg ggagattcgg acttgcgcca tcagccaata ggaaggcgac agctggactt 360
 aggttgagg cagctgactc aggtctacaa acgggtgacc cggccgggtt cacgcttgcg 420
 gacactttgg cttgtggcac cgttgggtcat atcatcggtg taggagttgt ccttggcctt 480
 35 aaaaacattg gtgctatttg aagttcctaa agctctttta tttgtatttg taaaatttgt 540
 agatttttat aacaatattc tcatgcacct gaacgagatc taatgc

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: .

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 1021577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Ala Ser Thr Met Met Thr Thr Leu Pro Gln Phe Asn Gly Leu Arg
 1 5 10 15
 50 Ala Thr Lys Ile Ser Ala Ala Pro Val Gln Gly Leu Ala Ser Val Gln
 20 25 30
 Pro Met Arg Arg Lys Gly Asn Gly Ala Leu Gly Ala Lys Cys Asp Phe
 35 40 45
 55 Ile Gly Ser Ser Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Met
 50 55 60
 Leu Phe Ala Gly Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala
 65 70 75 80
 Thr Ala Gly Leu Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly
 85 90 95
 60 Asp Pro Ala Gly Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val
 100 105 110

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Gly His Ile Ile Gly Val Gly Val Val Leu Gly Leu Lys Asn Ile Gly
 115 120 125

Ala Ile
 130

5 (2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

15

(D) OTHER INFORMATION: / Ceres Seq. ID 1021578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Met Thr Thr Leu Pro Gln Phe Asn Gly Leu Arg Ala Thr Lys Ile
 1 5 10 15

20

Ser Ala Ala Pro Val Gln Gly Leu Ala Ser Val Gln Pro Met Arg Arg
 20 25 30

Lys Gly Asn Gly Ala Leu Gly Ala Lys Cys Asp Phe Ile Gly Ser Ser
 35 40 45

Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Met Leu Phe Ala Gly
 50 55 60

25

Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu
 65 70 75 80

Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly
 85 90 95

30

Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val Gly His Ile Ile
 100 105 110

Gly Val Gly Val Val Leu Gly Leu Lys Asn Ile Gly Ala Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

40

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1021579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

45

Met Thr Thr Leu Pro Gln Phe Asn Gly Leu Arg Ala Thr Lys Ile Ser
 1 5 10 15

Ala Ala Pro Val Gln Gly Leu Ala Ser Val Gln Pro Met Arg Arg Lys
 20 25 30

50

Gly Asn Gly Ala Leu Gly Ala Lys Cys Asp Phe Ile Gly Ser Ser Thr
 35 40 45

Asn Leu Ile Met Val Thr Ser Thr Thr Thr Leu Met Leu Phe Ala Gly Arg
 50 55 60

Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu Arg
 65 70 75 80

55

Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly Phe
 85 90 95

Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val Gly His Ile Ile Gly
 100 105 110

60

Val Gly Val Val Val Leu Gly Leu Lys Asn Ile Gly Ala Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 801 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..801

(D) OTHER INFORMATION: / Ceres Seq. ID 1021927

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

atttttctct	cagaatccat	aaaaagagag	agagataaat	aaagagaaaa	ctgaagaagc	60
tagaagatgg	agaaaagtaa	tgatcatgac	aaggctagcc	acggcggtc	cggtggtggt	120
gccacggaga	agtgggagga	gactagcctc	ggaatccgaa	ctgccgagac	aatgctccgg	180
ttagctccgg	tgggtctttg	tgttgcagcg	cttgttgtca	tgcttaagga	ctctgagact	240
aatgagttcg	gttcaatttc	ttactccaat	ctcacagcct	ttaggtactt	ggtgcacgca	300
aatggaatat	gtgcaggcta	ctctcttcta	tcagcagcca	ttgcagcgat	gcctcgtttc	360
tcttcgacaa	tgccctggtg	ttggaccttc	ttttgtctcg	accagcttct	gacctacctg	420
gttcttgctg	ctggagctgt	atcagctgag	gttctatact	tggcttacia	tggagactca	480
gccattactt	ggagcgatgc	atgtagctcc	tacggcggtt	tctgtcatag	agccactgct	540
tctgttataa	tcacattctt	tgtggtttgt	ttctacatcg	ttctctctct	aatctcctct	600
tataagctct	ttactcgctt	tgatcctcct	tccattgttg	actccgccaa	gaatctcgaa	660
gtcgtgtct	tcggaagtta	gatcctccat	ttgctcttca	agtacatcta	gtttgtcatg	720
tttcaaattg	tgtgtgtttt	taactttggt	caagagaaag	aatgcttatg	tatttctctc	780
tgtttcattg	cttttcttcc	t				

25 (2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 1021928

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Met 1	Glu	Lys	Ser	Asn 5	Asp	His	Asp	Lys	Ala 10	Ser	His	Gly	Gly	Ser 15	Gly
Gly	Gly	Ala	Thr 20	Glu	Lys	Trp	Glu	Glu 25	Thr	Ser	Leu	Gly	Ile 30	Arg	Thr
Ala	Glu	Thr 35	Met	Leu	Arg	Leu	Ala 40	Pro	Val	Gly	Leu	Cys 45	Val	Ala	Ala
Leu	Val 50	Val	Met	Leu	Lys	Asp 55	Ser	Glu	Thr	Asn 60	Glu	Phe	Gly	Ser	Ile
Ser 65	Tyr	Ser	Asn	Leu 70	Thr	Ala	Phe	Arg	Tyr	Leu 75	Val	His	Ala	Asn 80	Gly
Ile	Cys	Ala	Gly 85	Tyr	Ser	Leu	Leu	Ser	Ala 90	Ala	Ile	Ala	Ala 95	Met	Pro
Arg	Ser	Ser	Ser 100	Thr	Met	Pro	Arg	Val 105	Trp	Thr	Phe	Phe	Cys 110	Leu	Asp
Gln	Leu	Leu 115	Thr	Tyr	Leu	Val	Leu 120	Ala	Ala	Gly	Ala	Val 125	Ser	Ala	Glu
Val	Leu 130	Tyr	Leu	Ala	Tyr	Asn 135	Gly	Asp	Ser	Ala 140	Ile	Thr	Trp	Ser	Asp
Ala 145	Cys	Ser	Ser	Tyr	Gly 150	Gly	Phe	Cys	His	Arg 155	Ala	Thr	Ala	Ser 160	Val
Ile	Ile	Thr	Phe 165	Phe	Val	Val	Cys	Phe	Tyr 170	Ile	Val	Leu	Ser 175	Leu	Ile
Ser	Ser	Tyr 180	Lys	Leu	Phe	Thr	Arg	Phe 185	Asp	Pro	Pro	Ser 190	Ile	Val	Asp
Ser	Ala	Lys 195	Asn	Leu	Glu	Val	Ala 200	Val	Phe	Gly	Ser				

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(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1021929

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met	Leu	Arg	Leu	Ala	Pro	Val	Gly	Leu	Cys	Val	Ala	Ala	Leu	Val	Val
1				5					10					15	
Met	Leu	Lys	Asp	Ser	Glu	Thr	Asn	Glu	Phe	Gly	Ser	Ile	Ser	Tyr	Ser
			20					25					30		
Asn	Leu	Thr	Ala	Phe	Arg	Tyr	Leu	Val	His	Ala	Asn	Gly	Ile	Cys	Ala
		35					40					45			
Gly	Tyr	Ser	Leu	Leu	Ser	Ala	Ala	Ile	Ala	Ala	Met	Pro	Arg	Ser	Ser
	50					55					60				
Ser	Thr	Met	Pro	Arg	Val	Trp	Thr	Phe	Phe	Cys	Leu	Asp	Gln	Leu	Leu
65					70					75				80	
Thr	Tyr	Leu	Val	Leu	Ala	Ala	Gly	Ala	Val	Ser	Ala	Glu	Val	Leu	Tyr
			85					90					95		
Leu	Ala	Tyr	Asn	Gly	Asp	Ser	Ala	Ile	Thr	Trp	Ser	Asp	Ala	Cys	Ser
			100					105					110		
Ser	Tyr	Gly	Gly	Phe	Cys	His	Arg	Ala	Thr	Ala	Ser	Val	Ile	Ile	Thr
		115					120					125			
Phe	Phe	Val	Val	Cys	Phe	Tyr	Ile	Val	Leu	Ser	Leu	Ile	Ser	Ser	Tyr
	130					135					140				
Lys	Leu	Phe	Thr	Arg	Phe	Asp	Pro	Pro	Ser	Ile	Val	Asp	Ser	Ala	Lys
145					150					155				160	
Asn	Leu	Glu	Val	Ala	Val	Phe	Gly	Ser							
					165										

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1021930

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Met	Leu	Lys	Asp	Ser	Glu	Thr	Asn	Glu	Phe	Gly	Ser	Ile	Ser	Tyr	Ser
1				5					10					15	
Asn	Leu	Thr	Ala	Phe	Arg	Tyr	Leu	Val	His	Ala	Asn	Gly	Ile	Cys	Ala
			20					25					30		
Gly	Tyr	Ser	Leu	Leu	Ser	Ala	Ala	Ile	Ala	Ala	Met	Pro	Arg	Ser	Ser
		35				40					45				
Ser	Thr	Met	Pro	Arg	Val	Trp	Thr	Phe	Phe	Cys	Leu	Asp	Gln	Leu	Leu
	50					55					60				
Thr	Tyr	Leu	Val	Leu	Ala	Gly	Ala	Val	Ser	Ala	Glu	Val	Leu	Tyr	
65					70				75				80		
Leu	Ala	Tyr	Asn	Gly	Asp	Ser	Ala	Ile	Thr	Trp	Ser	Asp	Ala	Cys	Ser
			85					90					95		
Ser	Tyr	Gly	Gly	Phe	Cys	His	Arg	Ala	Thr	Ala	Ser	Val	Ile	Ile	Thr
		100					105					110			
Phe	Phe	Val	Val	Cys	Phe	Tyr	Ile	Val	Leu	Ser	Leu	Ile	Ser	Ser	Tyr
		115					120					125			

375

Lys Leu Phe Thr Arg Phe Asp Pro Pro Ser Ile Val Asp Ser Ala Lys
 130 135 140
 Asn Leu Glu Val Ala Val Phe Gly Ser
 145 150

5 (2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..602

15 (D) OTHER INFORMATION: / Ceres Seq. ID 1021945

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

atcgagcgat ggatttggca gaactgtggg cgattttcgg acccgattc tccggcgccg 60
 ttttcggaac cgggtggtgg ggtcgacgcc gtcgtttgca gttccatcca agttcccttc 120
 gtccattacc ttcccggcat attcgcttct ctcgagcgtt tgatgttcaa ttgcgtcaga 180
 20 aaagaagaca ttgattactc tccttacgac gaaggcaggt ggagattgaa gctgtggcct 240
 ttcatagcgt atgtcgtagc atttgtttcc ttagctgctt ctgttggcct gctgattcaa 300
 gattcgggtg tgaagactgg gccttcaact tggactgggt tggctggtgt ctttcaatgt 360
 gtatttgtat tgataagtgg gctaattgat tggacatcgc actcagagta gcgcacaggc 420
 acatacttca tctccgactc agattcatat tgtgacaact tacaagttcc tctcgtttct 480
 25 ctactatgta aattcctgtg tcttgtcttg tcaccttggc attgtgtgcg agattcctct 540
 gttgcatcag tgtgtgtttc tgtaaaaact ttgtgtgaat gttattgaaa atactccaaa 600
 cc

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

35 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..136

(D) OTHER INFORMATION: / Ceres Seq. ID 1021946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

40 Ile Glu Arg Trp Ile Trp Gln Asn Cys Gly Arg Phe Ser Asp Pro Asp
 1 5 10 15
 Ser Pro Ala Pro Phe Ser Glu Pro Gly Gly Gly Val Asp Ala Val Val
 20 25 30
 45 Cys Ser Ser Ile Gln Val Pro Phe Val His Tyr Leu Pro Gly Ile Phe
 35 40 45
 Ala Ser Leu Gly Ala Leu Met Phe Asn Cys Val Arg Lys Glu Asp Ile
 50 55 60
 Asp Tyr Ser Pro Tyr Asp Glu Gly Glu Trp Arg Leu Lys Leu Trp Leu
 65 70 75 80
 50 Phe Ile Ala Tyr Val Val Ala Phe Val Ser Leu Ala Ala Ser Val Gly
 85 90 95
 Leu Leu Ile Gln Asp Ser Val Val Lys Thr Gly Pro Ser Thr Trp Thr
 100 105 110
 Gly Val Ala Gly Val Phe Gln Cys Val Phe Val Leu Ile Ser Gly Leu
 55 115 120 125
 Met Tyr Trp Thr Ser His Ser Glu
 130 135

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

60

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(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..82
(D) OTHER INFORMATION: / Ceres Seq. ID 1021947
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Met	Phe	Asn	Cys	Val	Arg	Lys	Glu	Asp	Ile	Asp	Tyr	Ser	Pro	Tyr	Asp
1			5						10					15	
Glu	Gly	Glu	Trp	Arg	Leu	Lys	Leu	Trp	Leu	Phe	Ile	Ala	Tyr	Val	Val
			20					25					30		
Ala	Phe	Val	Ser	Leu	Ala	Ala	Ser	Val	Gly	Leu	Leu	Ile	Gln	Asp	Ser
		35					40					45			
Val	Val	Lys	Thr	Gly	Pro	Ser	Thr	Trp	Thr	Gly	Val	Ala	Gly	Val	Phe
		50				55					60				
Gln	Cys	Val	Phe	Val	Leu	Ile	Ser	Gly	Leu	Met	Tyr	Trp	Thr	Ser	His
65					70					75				80	
Ser	Glu														

(2) INFORMATION FOR SEQ ID NO:110:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 693 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
(A) NAME/KEY: -
(B) LOCATION: 1..693
(D) OTHER INFORMATION: / Ceres Seq. ID 1022170
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

gagtcgctct	tctttccttc	cgccattttt	ttcttttctag	gttgcagagt	taaaggagaa	60
ggtttttcaat	tagggttttg	tagagagaaa	gatgagccga	ag ttgggaa	taccggtgaa	120
gcttcttcac	gaggcctcag	gtcatatcgt	gacggtggag	ctaaagagcg	gcgagcttta	180
cagaggaagt	atgattgagt	gtgaggataa	ctggaactgt	cagctcgagg	atattactta	240
taccgccaag	gatggtaaag	tatcacagct	tgagcatgtc	ttcattcgag	gcagtaaagt	300
caggtttatg	gtcataccag	acattctcaa	acatgctcca	atgttcaagc	ggttagatgc	360
tagaatcaag	ggaaagagct	catcactggg	tgttggcaga	ggtagagctg	caatgcgagg	420
gaaaccggct	gccggggccc	ggcgtggaac	tggaggaagg	ggagcggtag	cacctgtgag	480
gagatgattg	attttacgct	caacatgtaa	gctttgatgc	tgggatagtc	tttctgtgat	540
atccaggtga	aagccgcctt	tcttggttct	gtcattaatg	ctttagagaa	cactgtaaaa	600
ccaaacaaga	gagagatata	tccagatgca	ctagtagttc	tgtattttgg	gttaccaaga	660
tgtttgaatc	attgacaagt	tttcgttggtg	atc			

(2) INFORMATION FOR SEQ ID NO:111:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
(A) NAME/KEY: peptide
(B) LOCATION: 1..131
(D) OTHER INFORMATION: / Ceres Seq. ID 1022171
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Met	Ser	Arg	Ser	Leu	Gly	Ile	Pro	Val	Lys	Leu	Leu	His	Glu	Ala	Ser
1				5					10					15	
Gly	His	Ile	Val	Thr	Val	Glu	Leu	Lys	Ser	Gly	Glu	Leu	Tyr	Arg	Gly
			20					25					30		
Ser	Met	Ile	Glu	Cys	Glu	Asp	Asn	Trp	Asn	Cys	Gln	Leu	Glu	Asp	Ile
		35					40				45				
Thr	Tyr	Thr	Ala	Lys	Asp	Gly	Lys	Val	Ser	Gln	Leu	Glu	His	Val	Phe

377

50 55 60
 Ile Arg Gly Ser Lys Val Arg Phe Met Val Ile Pro Asp Ile Leu Lys
 65 70 75 80
 5 His Ala Pro Met Phe Lys Arg Leu Asp Ala Arg Ile Lys Gly Lys Ser
 85 90 95
 Ser Ser Leu Gly Val Gly Arg Gly Arg Ala Ala Met Arg Gly Lys Pro
 100 105 110
 Ala Ala Gly Pro Gly Arg Gly Thr Gly Gly Arg Gly Ala Val Pro Pro
 115 120 125
 10 Val Arg Arg
 130

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1022172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

25 Met Ile Glu Cys Glu Asp Asn Trp Asn Cys Gln Leu Glu Asp Ile Thr
 1 5 10 15
 Tyr Thr Ala Lys Asp Gly Lys Val Ser Gln Leu Glu His Val Phe Ile
 20 25 30
 Arg Gly Ser Lys Val Arg Phe Met Val Ile Pro Asp Ile Leu Lys His
 35 40 45
 30 Ala Pro Met Phe Lys Arg Leu Asp Ala Arg Ile Lys Gly Lys Ser Ser
 50 55 60
 Ser Leu Gly Val Gly Arg Gly Arg Ala Ala Met Arg Gly Lys Pro Ala
 65 70 75 80
 35 Ala Gly Pro Gly Arg Gly Thr Gly Gly Arg Gly Ala Val Pro Pro Val
 85 90 95
 Arg Arg

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1022173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

50 Glu Ser Leu Phe Phe Pro Ser Ala Ile Phe Phe Phe Leu Gly Cys Arg
 1 5 10 15
 Val Lys Gly Glu Gly Phe Gln Leu Gly Phe Cys Arg Glu Lys Asp Glu
 20 25 30
 Pro Lys Phe Gly Asn Thr Gly Glu Ala Ser Ser Arg Gly Leu Arg Ser
 35 40 45
 55 Tyr Arg Asp Gly Gly Ala Lys Glu Arg Arg Ala Leu Gln Arg Lys Tyr
 50 55 60
 Asp
 65

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 706 base pairs

378

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

5 (ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..706
- (D) OTHER INFORMATION: / Ceres Seq. ID 1022554

(xi) SEQUFNCE DESCRIPTION: SEQ ID NO:114:

```

10 agacccaaaa agcggttggt gtaagatccc aaactcacag attcccaaat aatagtaata      60
   ctcttcctct tctcaactct caccagtcac cagcagatca tcggagatgg gcggagacgg      120
   aaaagttttc accttggtccg aggttcttca gcacagtagc gccaaaggatt gttggatcgt      180
   catcgacggc aagggtttatg atgtgacaaa gttcttggat gatcatcctg gtggtgatga      240
   gggtatcttg acttctacag ggaaagatgc gaccgatgat ttcgaggatg tgggacatag      300
15 ttcgactgcg aaagccatgc tagatgagta ctatgtgggt gatattgaca cagctactgt      360
   gccggttaaa gctaagtttg tgctcctac gtcgacgaaa gccgtggcta ctcaggataa      420
   gagctcggat tttgttatta agctccttca gttccttggt ccacttctaa tcttaggctt      480
   ggctttcggc attcgggtact acactaagac caaggctcct tcttcttgaa agattgaatt      540
   gtggcctaag tgaattgctt gtgtacgacg tgggttaaact ctgtctctac ctctgtttgt      600
20 cttgtaagac atcattatat tctctattgc aatcaactga tagaccttg atttttaagc      660
   catctacctt tggtgtctta tatcaatcaa atccatttac aatata

```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..140
- (D) OTHER INFORMATION: / Ceres Seq. ID 1022555

(xi) SEQUENCE DESCRIPTION. SEQ ID NO:115:

```

35 Met Gly Gly Asp Gly Lys Val Phe Thr Leu Ser Glu Val Ser Gln His
   1      5      10      15
   Ser Ser Ala Lys Asp Cys Trp Ile Val Ile Asp Gly Lys Val Tyr Asp
      20      25      30
   Val Thr Lys Phe Leu Asp Asp His Pro Gly Gly Asp Glu Val Ile Leu
      35      40      45
40 Thr Ser Thr Gly Lys Asp Ala Thr Asp Asp Phe Glu Asp Val Gly His
   50      55      60
   Ser Ser Thr Ala Lys Ala Met Leu Asp Glu Tyr Tyr Val Gly Asp Ile
   65      70      75      80
   Asp Thr Ala Thr Val Pro Val Lys Ala Lys Phe Val Pro Pro Thr Ser
45      85      90      95
   Thr Lys Ala Val Ala Thr Gln Asp Lys Ser Ser Asp Phe Val Ile Lys
      100      105      110
   Leu Leu Gln Phe Leu Val Pro Leu Leu Ile Leu Gly Leu Ala Phe Gly
      115      120      125
50 Ile Arg Tyr Tyr Thr Lys Thr Lys Ala Pro Ser Ser
   130      135      140

```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..70
- (D) OTHER INFORMATION: / Ceres Seq. ID 1022556

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Met Leu Asp Glu Tyr Tyr Val Gly Asp Ile Asp Thr Ala Thr Val Pro
 1 5 10 15
 Val Lys Ala Lys Phe Val Pro Pro Thr Ser Thr Lys Ala Val Ala Thr
 5 20 25 30
 Gln Asp Lys Ser Ser Asp Phe Val Ile Lys Leu Leu Gln Phe Leu Val
 35 40 45
 Pro Leu Leu Ile Leu Gly Leu Ala Phe Gly Ile Arg Tyr Tyr Thr Lys
 50 55 60
 10 Thr Lys Ala Pro Ser Ser
 65 70

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

20 (A) NAME/KEY: -
 (B) LOCATION: 1..722
 (D) OTHER INFORMATION: / Ceres Seq. ID 1022594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

aacgtcatca ttctgacttt tctcaaagaa gagaaatcaa atcaccaagt catcggagcg 60
 25 atcacagaga agaagaaaac catggcggaa gaagagaaaa gcgtgatgaa gcaagtgatg 120
 gtggcgattg atgaaagcga atgtagtaaa cgcgctcttc aatggacgct cgtgtatctc 180
 aaagatagcc tcgccgattc cgacatcatc ctcttcaactg ctcaacctca tcttgatctc 240
 agctgcgtct atgcttcttc ttatggcgcc gctccgattg agcttataaa ctcattgcaa 300
 gagagtcata agaacgctgg attgaatcgt cttgatgaag gaacccaaat ttgtgctgag 360
 30 actgggggta ctccaagaaa ggtgttggaa tttggaaatc ctaaagaagc gatatgtgaa 420
 gctgctgaga agcttggtgt tgatattgctt gtggttggaa gccatggtaa aggagcatta 480
 caaaggactt tccttggaag tgtagcaat tactgtgtta acaatgctaa gtgccagtt 540
 cttgtggtga gaacaaaagc ttgaagacct ctctcatga aagagttcga caaccctggc 600
 ttgatgtgtg tgtgttggaa acatattgat aataatgctc tgcttggtta ctattgtttg 660
 35 aagaaacttt gtgagtaaac ataatttatt ttgtttgata atgaaagagc attgccgtgt 720
 tc

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 187 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

45 (A) NAME/KEY: peptide
 (B) LOCATION: 1..187
 (D) OTHER INFORMATION: / Ceres Seq. ID 1022595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Asn Val Ile Ile Leu Thr Phe Leu Lys Glu Glu Lys Ser Asn His Gln
 50 1 5 10 15
 Val Ile Gly Ala Ile Thr Glu Lys Lys Lys Thr Met Ala Glu Glu Glu
 20 25 30
 Lys Ser Val Met Lys Gln Val Met Val Ala Ile Asp Glu Ser Glu Cys
 35 40 45
 55 Ser Lys Arg Ala Leu Gln Trp Thr Leu Val Tyr Leu Lys Asp Ser Leu
 50 55 60
 Ala Asp Ser Asp Ile Ile Leu Phe Thr Ala Gln Pro His Leu Asp Leu
 65 70 75 80
 Ser Cys Val Tyr Ala Ser Ser Tyr Gly Ala Ala Pro Ile Glu Leu Ile
 85 90 95
 60 Asn Ser Leu Gln Glu Ser His Lys Asn Ala Gly Leu Asn Arg Leu Asp
 100 105 110

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Glu Gly Thr Lys Ile Cys Ala Glu Thr Gly Val Thr Pro Arg Lys Val
 115 120 125
 Leu Glu Phe Gly Asn Pro Lys Glu Ala Ile Cys Glu Ala Ala Glu Lys
 130 135 140
 5 Leu Gly Val Asp Met Leu Val Val Gly Ser His Gly Lys Gly Ala Leu
 145 150 155 160
 Gln Arg Thr Phe Leu Gly Ser Val Ser Asn Tyr Cys Val Asn Asn Ala
 165 170 175
 Lys Cys Pro Val Leu Val Val Arg Thr Lys Ala
 180 185

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1022596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met Ala Glu Glu Glu Lys Ser Val Met Lys Gln Val Met Val Ala Ile
 1 5 10 15
 25 Asp Glu Ser Glu Cys Ser Lys Arg Ala Leu Gln Trp Thr Leu Val Tyr
 20 25 30
 Leu Lys Asp Ser Leu Ala Asp Ser Asp Ile Ile Leu Phe Thr Ala Gln
 35 40 45
 30 Pro His Leu Asp Leu Ser Cys Val Tyr Ala Ser Ser Tyr Gly Ala Ala
 50 55 60
 Pro Ile Glu Leu Ile Asn Ser Leu Gln Glu Ser His Lys Asn Ala Gly
 65 70 75 80
 Leu Asn Arg Leu Asp Glu Gly Thr Lys Ile Cys Ala Glu Thr Gly Val
 85 90 95
 35 Thr Pro Arg Lys Val Leu Glu Phe Gly Asn Pro Lys Glu Ala Ile Cys
 100 105 110
 Glu Ala Ala Glu Lys Leu Gly Val Asp Met Leu Val Val Gly Ser His
 115 120 125
 40 Gly Lys Gly Ala Leu Gln Arg Thr Phe Leu Gly Ser Val Ser Asn Tyr
 130 135 140
 Cys Val Asn Asn Ala Lys Cys Pro Val Leu Val Val Arg Thr Lys Ala
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..152

(D) OTHER INFORMATION: / Ceres Seq. ID 1022597

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Met Lys Gln Val Met Val Ala Ile Asp Glu Ser Glu Cys Ser Lys Arg
 1 5 10 15
 Ala Leu Gln Trp Thr Leu Val Tyr Leu Lys Asp Ser Leu Ala Asp Ser
 20 25 30
 Asp Ile Ile Leu Phe Thr Ala Gln Pro His Leu Asp Leu Ser Cys Val
 35 40 45
 60 Tyr Ala Ser Ser Tyr Gly Ala Ala Pro Ile Glu Leu Ile Asn Ser Leu
 50 55 60

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Gln Glu Ser His Lys Asn Ala Gly Leu Asn Arg Leu Asp Glu Gly Thr
 65 70 75 80
 Lys Ile Cys Ala Glu Thr Gly Val Thr Pro Arg Lys Val Leu Glu Phe
 85 90 95
 5 Gly Asn Pro Lys Glu Ala Ile Cys Glu Ala Ala Glu Lys Leu Gly Val
 100 105 110
 Asp Met Leu Val Val Gly Ser His Gly Lys Gly Ala Leu Gln Arg Thr
 115 120 125
 10 Phe Leu Gly Ser Val Ser Asn Tyr Cys Val Asn Asn Ala Lys Cys Pro
 130 135 140
 Val Leu Val Val Arg Thr Lys Ala
 145 150
 (2) INFORMATION FOR SEQ ID NO:121:
 (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 20 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..610
 (D) OTHER INFORMATION: / Ceres Seq. ID 1022621
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:
 25 aattttgtgt ggtaattaac tggtagagaga gttcaacatc caatctttct ctctctctct 60
 atcttttatc tctcacactc ttaaaatgct tcttctatct ccgatctctg cctctcttcc 120
 accgtcgttt caccggggta atttgatccg gcgatcaatt aagccgtagt gtaggggtgt 180
 tgcaaaggcc aaggacaaca ccgacactgg tggatttctg gagacggcag ctatagccgg 240
 tggtttagtg tcgacgccgg ttattggatg gtcactctac actttgaaga ccacgggatg 300
 30 tggcttacct cccggaccgg ccggtttaat cggagcgttg gaaggtgtga gctacttggt 360
 ggtggttggc atcgtgggct ggtctttgta cactaaaaca aaaactgggt caggtctgcc 420
 aaatgggcca tttggtttgt tgggtgcggt cgagggttta tcgtatctgt cggttctagc 480
 cattcttggtg gtgtttggta ttcagttctt ggataatggg tcggttccag gtccacttcc 540
 tagtgaccag tgttttggtt aaccacgtgt aatgtcgtat aaataaagtg tcaaattaat 600
 35 aattgctttc
 (2) INFORMATION FOR SEQ ID NO:122:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 40 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 45 (B) LOCATION: 1..158
 (D) OTHER INFORMATION: / Ceres Seq. ID 1022622
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:
 Met Leu Leu Leu Ser Pro Ile Ser Ala Ser Leu Pro Pro Ser Phe His
 1 5 10 15
 50 Arg Gly Asn Leu Ile Arg Arg Ser Ile Lys Pro Leu Gly Arg Val Val
 20 25 30
 Ala Lys Ala Lys Asp Asn Thr Asp Thr Gly Gly Phe Leu Glu Thr Ala
 35 40 45
 55 Ala Ile Ala Gly Gly Leu Val Ser Thr Pro Val Ile Gly Trp Ser Leu
 50 55 60
 Tyr Thr Leu Lys Thr Thr Gly Cys Gly Leu Pro Pro Gly Pro Ala Gly
 65 70 75 80
 Leu Ile Gly Ala Leu Glu Gly Val Ser Tyr Leu Val Val Val Gly Ile
 85 90 95
 60 Val Gly Trp Ser Leu Tyr Thr Lys Thr Lys Thr Gly Ser Gly Leu Pro
 100 105 110
 Asn Gly Pro Phe Gly Leu Leu Gly Ala Val Glu Gly Leu Ser Tyr Leu

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115 120 125
 Ser Val Leu Ala Ile Leu Val Val Phe Gly Ile Gln Phe Leu Asp Asn
 130 135 140
 Gly Ser Val Pro Gly Pro Leu Pro Ser Asp Gln Cys Phe Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 872 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..872

(D) OTHER INFORMATION: / Ceres Seq. ID 1024375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

atcgaacatt aaaacctgat tttactgaaa ctgtgctgcg aaggagaagc cgcaaaccat 60
 tttttgtcaa tctagggttc ttcttcgtac ttgcagattt cgcctccggt ttactacga 120
 tctgtgaaga tgttctccgc tcagaacaag atcaataagg acaagaatgc tgagccaaca 180
 gaatgcyagg agcaagttgc tcaggctttg tttgatttgg agaactactaa ccaggagttg 240
 aaaagcgagt tgaaagatct ctacatcaac caagctgttc acatggatat ctctggaaac 300
 cgcaaagctg ttgtgattta cgttccattc agattgagga aagctttccg caagattcat 360
 ccccgctctg tcagagagct tgagaagaag ttcagtggaa aggatgttat ctttgttacc 420
 acaagaagga tcatgctgcc cccaagaag ggtgctgctg ttcagaggcc acgtaacaga 480
 actcttacct cagttcatga agctatgctt gaagatgttg ctttccccgc tgagattgtt 540
 ggaaagcgta ctcgctaccg tcttgatggg tccaagatca tgaaggtcct tttggatgcc 600
 aaggaaaaga acaacacaga gtacaagctc gagactatgg tcggtgtgta ccgtaaaactt 660
 actggcaaag atgttgtttt tgagtaccga gtcgaagctt gaaagaagat gatgaagaac 720
 catcaggata gtgaaagaga gcttttgttt atgttttgtg gtatttagga tgaaggaaac 780
 tctcttgatt cagttccttg ttcacaatct ttaatgttct atttacaatg actacttttt 840
 gtgtttttca attttgaaac ctctatgatt tc

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..190

(D) OTHER INFORMATION: / Ceres Seq. ID 1024376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Met Phe Ser Ala Gln Asn Lys Ile Asn Lys Asp Lys Asn Ala Glu Pro
 1 5 10 15
 Thr Glu Cys Glu Glu Gln Val Ala Gln Ala Leu Phe Asp Leu Glu Asn
 20 25 30
 Thr Asn Gln Glu Leu Lys Ser Glu Leu Lys Asp Leu Tyr Ile Asn Gln
 35 40 45
 Ala Val His Met Asp Ile Ser Gly Asn Arg Lys Ala Val Val Ile Tyr
 50 55 60
 Val Pro Phe Arg Leu Arg Lys Ala Phe Arg Lys Ile His Pro Arg Leu
 65 70 75 80
 Val Arg Glu Leu Glu Lys Lys Phe Ser Gly Lys Asp Val Ile Phe Val
 85 90 95
 Thr Thr Arg Arg Ile Met Arg Pro Pro Lys Lys Gly Ala Ala Val Gln
 100 105 110
 Arg Pro Arg Asn Arg Thr Leu Thr Ser Val His Glu Ala Met Leu Glu
 115 120 125
 Asp Val Ala Phe Pro Ala Glu Ile Val Gly Lys Arg Thr Arg Tyr Arg
 130 135 140

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Leu Asp Gly Ser Lys Ile Met Lys Val Phe Leu Asp Ala Lys Glu Lys
 145 150 155 160
 Asn Asn Thr Glu Tyr Lys Leu Glu Thr Met Val Gly Val Tyr Arg Lys
 165 170 175
 5 Leu Thr Gly Lys Asp Val Val Phe Glu Tyr Pro Val Glu Ala
 180 185 190

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 15 (A) NAME/KEY: peptide
 (B) LOCATION: 1..139
 (D) OTHER INFORMATION: / Ceres Seq. ID 1024377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

20 Met Asp Ile Ser Gly Asn Arg Lys Ala Val Val Ile Tyr Val Pro Phe
 1 5 10 15
 Arg Leu Arg Lys Ala Phe Arg Lys Ile His Pro Arg Leu Val Arg Glu
 20 25 30
 Leu Glu Lys Lys Phe Ser Gly Lys Asp Val Ile Phe Val Thr Thr Arg
 35 40 45
 25 Arg Ile Met Arg Pro Pro Lys Lys Gly Ala Ala Val Gln Arg Pro Arg
 50 55 60
 Asn Arg Thr Leu Thr Ser Val His Glu Ala Met Leu Glu Asp Val Ala
 65 70 75 80
 Phe Pro Ala Glu Ile Val Gly Lys Arg Thr Arg Tyr Arg Leu Asp Gly
 30 85 90 95
 Ser Lys Ile Met Lys Val Phe Leu Asp Ala Lys Glu Lys Asn Asn Thr
 100 105 110
 Glu Tyr Lys Leu Glu Thr Met Val Gly Val Tyr Arg Lys Leu Thr Gly
 115 120 125
 35 Lys Asp Val Val Phe Glu Tyr Pro Val Glu Ala
 130 135

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 545 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- 45 (A) NAME/KEY: -
 (B) LOCATION: 1..545
 (D) OTHER INFORMATION: / Ceres Seq. ID 1024535

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

50 aaaaattgtt aagttcgtgt ccgcgagatc agagtttgtg tccggttata cgattcgtcg 60
 gtacaaaaac cctccgagaa gtgtttcagg tgggaaggta tctctgtcta cagcatgtcc 120
 ggcgaggaag aagccaccgt gagggagcca ctagatctga ttaggctgag tctcgacgag 180
 agaatctatg tcaagctccg gtcagaccgc gaacttcgcg gcaagcttca cgcgtttgat 240
 cagcatttga atatgattct gggtgatgtt gaagaaacta tcactacagt agaaatcgat 300
 gacgagacat atgaagagat tgttcggact acaaagcgga cgattgagtt tctattcgtg 360
 55 agaggagatg gagtgatatt ggtgtctcca ccgctgagga cagcagcctg agttcaaact 420
 caaatctttt gtgtcctctt ttcgtaaggg gaatttgtga ctattcttgt atttagtcac 480
 ttcttgtctt aactaaaaca agcttgaaga agctagtgtt cttaaatttc caatgctttt 540
 cagac

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid

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      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

```

5 (A) NAME/KEY: peptide
(B) LOCATION: 1..98
(D) OTHER INFORMATION: / Ceres Seq. ID 1024536
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

[illegible]

(2) INFORMATION FOR SEO ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 53 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```

30      (ii) MOLECULE TYPE: peptide
      (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..53
          (D) OTHER INFORMATION: / Ceres Seq. ID 1024537

```

```

35      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:
      Lys Leu Leu Ser Ser Cys Pro Arg Asp Gln Ser Leu Cys Pro Val Ile
      1          5          10          15
      Arg Phe Val Gly Thr Lys Thr Leu Arg Glu Val Phe Gln Val Gly Arg
      20          25          30
      Tyr Leu Cys Leu His Asp Val Arg Arg Gly Arg Ser His Arg Glu Gly
      35          40          45
      Ala Thr Arg Ser Asp
      50

```

(2) INFORMATION FOR SEQ ID NO:129:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

```

50      (ii) MOLECULE TYPE: peptide
      (ix) FEATURE:
          (A) NAME/KEY: peptide
          (B) LOCATION: 1..52
          (D) OTHER INFORMATION: / Ceres Seq. ID 1024538

```

```

55      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:
      Met Ile Leu Gly Asp Val Glu Glu Thr Ile Thr Thr Val Glu Ile Asp
      1             5             10             15
      Asp Glu Thr Tyr Glu Glu Ile Val Arg Thr Thr Lys Arg Thr Ile Glu
      20             25             30
      Phe Leu Phe Val Arg Gly Asp Gly Val Ile Leu Val Ser Pro Pro Leu
      35             40             45
      Arg Thr Ala Ala
      50

```


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(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 797 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..797

(D) OTHER INFORMATION: / Ceres Seq. ID 1025683

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

```

aacccttaaa ctccgttacc ctaaacctca agccgctcgtc tccaaagttc cccctcagag      60
acgaaaaaat gaagaccatt ttgtcctcgg agactatgga catccccgac ggcgtcgcca      120
ttaaggtaaa cgccaaggtg attgaggtcg aaggtccacg aggtaaactc actcgtgact      180
tcaagcatct gaatctcgat ttccagttga ttaaagacca agtcactgga aaacgtcagc      240
ttaagattga ttcttggttt ggttctcgta agacaagtgc ttcgattaga actgctttaa      300
gccatggtga taatctcatt gctggtgtta ctcaaggttt tctttataga atgagatttg      360
tgtatgctca ttttcctatc aatgcttcta ttgatggtaa caataagagt attgagattc      420
gtaacttcct tggtgagaag aaggtgagga aggttgagat gttggatggt gtttaagattg      480
ttcgatctga gaaggttaag gatgagatta ttcttgaggg aaatgatatt gagcttggtt      540
cacggtcttg tgctttgatc aatcagaaat gtcatgtgaa gaagaaggat atcaggaagt      600
ttcttgatgg tatctatgtg agcgagaaag gcaagatcgc agtcgaggaa tgaagttcgc      660
tattgaaagt tctatattag attttatatg gtgaagcagt gatattatcg tagctttttg      720
ttttacatct ttcttatgga tttgtagttt tgtttttcct tttgaatcat tgatgaatgc      780
aaattcatta tccgttc

```

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..216

(D) OTHER INFORMATION: / Ceres Seq. ID 1025684

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

```

Pro Leu Asn Ser Val Thr Leu Asn Leu Lys Pro Ser Ser Pro Lys Phe
1      5      10      15
Pro Leu Arg Asp Glu Lys Met Lys Thr Ile Leu Ser Ser Glu Thr Met
20     25     30
Asp Ile Pro Asp Gly Val Ala Ile Lys Val Asn Ala Lys Val Ile Glu
35     40     45
Val Glu Gly Pro Arg Gly Lys Leu Thr Arg Asp Phe Lys His Leu Asn
50     55     60
Leu Asp Phe Gln Leu Ile Lys Asp Gln Val Thr Gly Lys Arg Gln Leu
65     70     75     80
Lys Ile Asp Ser Trp Phe Gly Ser Arg Lys Thr Ser Ala Ser Ile Arg
85     90     95
Thr Ala Leu Ser His Val Asp Asn Leu Ile Ala Gly Val Thr Gln Gly
100    105    110
Phe Leu Tyr Arg Met Arg Phe Val Tyr Ala His Phe Pro Ile Asn Ala
115    120    125
Ser Ile Asp Gly Asn Asn Lys Ser Ile Glu Ile Arg Asn Phe Leu Gly
130    135    140
Glu Lys Lys Val Arg Lys Val Glu Met Leu Asp Gly Val Lys Ile Val
145    150    155    160
Arg Ser Glu Lys Val Lys Asp Glu Ile Ile Leu Glu Gly Asn Asp Ile
165    170    175
Glu Leu Val Ser Arg Ser Cys Ala Leu Ile Asn Gln Lys Cys His Val
180    185    190

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Lys Lys Lys Asp Ile Arg Lys Phe Leu Asp Gly Ile Tyr Val Ser Glu
 195 200 205

Lys Gly Lys Ile Ala Val Glu Glu
 210 215

5 (2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

15 (D) OTHER INFORMATION: / Ceres Seq. ID 1025685

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Met Lys Thr Ile Leu Ser Ser Glu Thr Met Asp Ile Pro Asp Gly Val
 1 5 10 15
 Ala Ile Lys Val Asn Ala Lys Val Ile Glu Val Glu Gly Pro Arg Gly
 20 20 25 30
 Lys Leu Thr Arg Asp Phe Lys His Leu Asn Leu Asp Phe Gln Leu Ile
 35 40 45
 Lys Asp Gln Val Thr Gly Lys Arg Gln Leu Lys Ile Asp Ser Trp Phe
 50 55 60
 25 Gly Ser Arg Lys Thr Ser Ala Ser Ile Arg Thr Ala Leu Ser His Val
 65 70 75 80
 Asp Asn Leu Ile Ala Gly Val Thr Gln Gly Phe Leu Tyr Arg Met Arg
 85 90 95
 Phe Val Tyr Ala His Phe Pro Ile Asn Ala Ser Ile Asp Gly Asn Asn
 30 100 105 110
 Lys Ser Ile Glu Ile Arg Asn Phe Leu Gly Glu Lys Lys Val Arg Lys
 115 120 125
 Val Glu Met Leu Asp Gly Val Lys Ile Val Arg Ser Glu Lys Val Lys
 130 135 140
 35 Asp Glu Ile Ile Leu Glu Gly Asn Asp Ile Glu Leu Val Ser Arg Ser
 145 150 155 160
 Cys Ala Leu Ile Asn Gln Lys Cys His Val Lys Lys Lys Asp Ile Arg
 165 170 175
 Lys Phe Leu Asp Gly Ile Tyr Val Ser Glu Lys Gly Lys Ile Ala Val
 40 180 185 190
 Glu Glu

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

(D) OTHER INFORMATION: / Ceres Seq. ID 1025686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Met Asp Ile Pro Asp Gly Val Ala Ile Lys Val Asn Ala Lys Val Ile
 1 5 10 15
 Glu Val Glu Gly Pro Arg Gly Lys Leu Thr Arg Asp Phe Lys His Leu
 20 25 30
 Asn Leu Asp Phe Gln Leu Ile Lys Asp Gln Val Thr Gly Lys Arg Gln
 35 40 45
 60 Leu Lys Ile Asp Ser Trp Phe Gly Ser Arg Lys Thr Ser Ala Ser Ile
 50 55 60

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Arg Thr Ala Leu Ser His Val Asp Asn Leu Ile Ala Gly Val Thr Gln
 65 70 75 80
 Gly Phe Leu Tyr Arg Met Arg Phe Val Tyr Ala His Phe Pro Ile Asn
 85 90 95
 5 Ala Ser Ile Asp Gly Asn Asn Lys Ser Ile Glu Ile Arg Asn Phe Leu
 100 105 110
 Gly Glu Lys Lys Val Arg Lys Val Glu Met Leu Asp Gly Val Lys Ile
 115 120 125
 Val Arg Ser Glu Lys Val Lys Asp Glu Ile Ile Leu Glu Gly Asn Asp
 10 130 135 140
 Ile Glu Leu Val Ser Arg Ser Cys Ala Leu Ile Asn Gln Lys Cys His
 145 150 155 160
 Val Lys Lys Lys Asp Ile Arg Lys Phe Leu Asp Gly Ile Tyr Val Ser
 165 170 175
 15 Glu Lys Gly Lys Ile Ala Val Glu Glu
 180 185
 (2) INFORMATION FOR SEQ ID NO:134:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 555 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 25 (A) NAME/KEY: -
 (B) LOCATION: 1..555
 (D) OTHER INFORMATION: / Ceres Seq. ID 1027152
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:
 30 ggttttgtca tcgtgctcct cttctcctcc accgcacaga tccaagacat ttgattaca 60
 ctccatcgcc ggcgaaaatg gtgacggaaa agaaaacgaa gaagtctcat gagggtatca 120
 acagtaggtt ggctcttggt atgaagagt gtaaatacac tcttggttac aagtctgttc 180
 tcaaatccct ccgtggctcc aaagggaac tgattcta atctccaccaat tgcccaccgt 240
 tgagaagatc agagattgag tactacgcaa tgctcgctaa agttggtgtc caccattaca 300
 atggaaataa cgttgatttg ggaacagctt gcggaaagta cttccgtgtt tcttgtctga 360
 35 gcattgttga tcctggtgat tctgacatta tcaagtcaat tcctggtgac cagtgatata 420
 attttcagat tttatttttc ccagactttt taccggtcct tgtattcgag tctctcaaaa 480
 ttttatgagc aatagacatt gtgtttcttc tttgtcaagt tttcttatat tgaggaccgg 540
 aaaagaaatt tcttt
 (2) INFORMATION FOR SEQ ID NO:135:
 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..137
 (D) OTHER INFORMATION: / Ceres Seq. ID 1027153
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:
 Phe Cys His Arg Ala Pro Leu Leu Leu His Arg Thr Asp Pro Arg His
 1 5 10 15
 Phe Asp Tyr Thr Pro Ser Pro Ala Lys Met Val Thr Glu Lys Lys Thr
 20 25 30
 55 Lys Lys Ser His Glu Gly Ile Asn Ser Arg Leu Ala Leu Val Met Lys
 35 40 45
 Ser Gly Lys Tyr Thr Leu Gly Tyr Lys Ser Val Leu Lys Ser Leu Arg
 50 55 60
 Gly Ser Lys Gly Lys Leu Ile Leu Ile Ser Thr Asn Cys Pro Pro Leu
 60 65 70 75 80
 Arg Arg Ser Glu Ile Glu Tyr Tyr Ala Met Leu Ala Lys Val Gly Val
 85 90 95

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His His Tyr Asn Gly Asn Asn Val Asp Leu Gly Thr Ala Cys Gly Lys
 100 105 110
 Tyr Phe Arg Val Ser Cys Leu Ser Ile Val Asp Pro Gly Asp Ser Asp
 115 120 125

5 Ile Ile Lys Ser Ile Pro Gly Asp Gln
 130 135

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

15 (A) NAME/KEY: peptide
 (B) LOCATION: 1..112

(D) OTHER INFORMATION: / Ceres Seq. ID 1027154

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

20 Met Val Thr Glu Lys Lys Thr Lys Lys Ser His Glu Gly Ile Asn Ser
 1 5 10 15
 Arg Leu Ala Leu Val Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys
 20 25 30
 Ser Val Leu Lys Ser Leu Arg Gly Ser Lys Gly Lys Leu Ile Leu Ile
 35 40 45
 25 Ser Thr Asn Cys Pro Pro Leu Arg Arg Ser Glu Ile Glu Tyr Tyr Ala
 50 55 60
 Met Leu Ala Lys Val Gly Val His His Tyr Asn Gly Asn Asn Val Asp
 65 70 75 80
 30 Leu Gly Thr Ala Cys Gly Lys Tyr Phe Arg Val Ser Cys Leu Ser Ile
 85 90 95
 Val Asp Pro Gly Asp Ser Asp Ile Ile Lys Ser Ile Pro Gly Asp Gln
 100 105 110

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..91

(D) OTHER INFORMATION: / Ceres Seq. ID 1027155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

45 Met Lys Ser Gly Lys Tyr Thr Leu Gly Tyr Lys Ser Val Leu Lys Ser
 1 5 10 15
 Leu Arg Gly Ser Lys Gly Lys Leu Ile Leu Ile Ser Thr Asn Cys Pro
 20 25 30
 50 Pro Leu Arg Arg Ser Glu Ile Glu Tyr Tyr Ala Met Leu Ala Lys Val
 35 40 45
 Gly Val His His Tyr Asn Gly Asn Asn Val Asp Leu Gly Thr Ala Cys
 50 55 60
 Gly Lys Tyr Phe Arg Val Ser Cys Leu Ser Ile Val Asp Pro Gly Asp
 65 70 75 80
 55 Ser Asp Ile Ile Lys Ser Ile Pro Gly Asp Gln
 85 90

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 653 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

389

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..653

(D) OTHER INFORMATION: / Ceres Seq. ID 1028095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

aaataaagtt tttatttattc tatctatcca attggagacg aatcatatcg agcgatggat      60
ttggcagaac tgtgggcatg tttcggaccc ggattctccg gcgccgtttt cggaaccggg      120
tggtgggttt gggtcgacgc cgtcgtttgc agttccatcc aagttccctt cgtccattac      180
cttcccggca tattcgcttc tctcggagct ttgatgttca attgcgtcag aaaagaagac      240
attgattact ctcccttacga cgaaggcgag tggagattga agctgtggct tttcatagcg      300
tatgtcgtag catttggttc cttagctgct tctgttggct tgctgattca agattcgggt      360
gtgaagactg ggccttcaac ttggactggt gtggctggtg tctttcaatg tgtatttgta      420
ttgataagtg ggctaagtga ttggacatcg cactcagagt agcgcacagg cacatacttc      480
atctccgact cagattcata ctgtgacaac ttacaagttc ctctcgtttc tctactatgt      540
aaattcctgt gtcttgtctt gtcaccttgg cattgtgtgc gagattcctc tgttgcacatca      600
gtgtgtgttt ctgttaaaac tttgtgtgaa tgttattgaa aataactccaa atc

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1028096

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

Met Asp Leu Ala Glu Leu Trp Ala Ile Phe Gly Pro Gly Phe Ser Gly
1      5      10      15
Ala Val Phe Gly Thr Gly Trp Trp Phe Trp Val Asp Ala Val Val Cys
20     25     30
Ser Ser Ile Gln Val Pro Phe Val His Tyr Leu Pro Gly Ile Phe Ala
35     40     45
Ser Leu Gly Ala Leu Met Phe Asn Cys Val Arg Lys Glu Asp Ile Asp
50     55     60
Tyr Ser Pro Tyr Asp Glu Gly Glu Trp Arg Leu Lys Leu Trp Leu Phe
65     70     75     80
Ile Ala Tyr Val Val Ala Phe Val Ser Leu Ala Ala Ser Val Gly Leu
85     90     95
Leu Ile Gln Asp Ser Val Val Lys Thr Gly Pro Ser Thr Trp Thr Gly
100    105    110
Val Ala Gly Val Phe Gln Cys Val Phe Val Leu Ile Ser Gly Leu Met
115    120    125
Tyr Trp Thr Ser His Ser Glu
130    135

```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1028097

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

Met Phe Asn Cys Val Arg Lys Glu Asp Ile Asp Tyr Ser Pro Tyr Asp
1      5      10      15
Glu Gly Glu Trp Arg Leu Lys Leu Trp Leu Phe Ile Ala Tyr Val Val

```

390

20 25 30
 Ala Phe Val Ser Leu Ala Ala Ser Val Gly Leu Leu Ile Gln Asp Ser
 35 40 45
 Val Val Lys Thr Gly Pro Ser Thr Trp Thr Gly Val Ala Gly Val Phe
 5 50 55 60
 Gln Cys Val Phe Val Leu Ile Ser Gly Leu Met Tyr Trp Thr Ser His
 65 70 75 80
 Ser Glu

10 (2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..80

(D) OTHER INFORMATION: / Ceres Seq. ID 1028098

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Ile Lys Phe Leu Phe Ile Tyr Leu Ser Asn Trp Arg Arg Ile Ile Ser
 1 5 10 15
 Ser Asp Gly Phe Gly Arg Thr Val Gly Asp Phe Arg Thr Arg Ile Leu
 20 25 30
 Arg Arg Arg Phe Arg Asn Arg Val Val Val Leu Gly Arg Arg Arg Arg
 35 40 45
 Leu Gln Phe His Pro Ser Ser Leu Arg Pro Leu Pro Ser Arg His Ile
 50 55 60
 Arg Phe Ser Arg Ser Phe Asp Val Gln Leu Arg Gln Lys Arg Arg His
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 779 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..779

(D) OTHER INFORMATION: / Ceres Seq. ID 1028608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

gtctaaactc taaactctaa agactttgtc atttcgtgaa ccgtcgatcat aactgatacct 60
 45 tccaaagaat ctccaaaatc cctaaacttc gaaaatggca gaaaccgccg agacaatcaa 120
 caccacgata tcatcgccgc caccggaatc cgaaagctcc accactatct ctgcaatgac 180
 agatccaaca tctcaagaag cagcctcaaa agacacagat ctgacgaaag aagccgaatc 240
 agagaagaaa ccaggaggaa tctctctccg aatctggcca ccgactcaga aaactcgaga 300
 cgccgttctg aatcgccctga tctgagacctt atccaccgaa tcaatcctct ctaagagata 360
 50 cggtactctt aaatctgacg atgcaaccac cgctcgcaaaa cttatcgaag aagaggctta 420
 tgggtgttgct tcgaatgctg tgtcgagtga tgatgatggg attaagattc ttgagcttta 480
 ttctaaagag attagtaaga ggatgcttga atctgttaag gctagatcta atgctagtgt 540
 tggaaatgga agtgtggagg atgctaatac tgatgctagt gaggtttcta aagatgatgc 600
 tggctcctgt tcagaggagg agaagagtga ggcttgagaa atttggtttt acttccttat 660
 55 tataatctgt tgtctcttag ggttttgctg ttcttgtaat gatgatgatg acttggtgat 720
 ttggtattat gcatatttga agatgtttct tcttccttaa tatgagtgc aagtgtcttc

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

391

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

5 (D) OTHER INFORMATION: / Ceres Seq. ID 1028609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

Met Ala Glu Thr Ala Glu Thr Ile Asn Thr Thr Ile Ser Ser Pro Pro
 1 5 10 15
 Pro Glu Ser Glu Ser Ser Thr Thr Ile Ser Ala Met Thr Asp Pro Thr
 10 20 25 30
 Ser Gln Glu Ala Ala Ser Lys Asp Thr Asp Leu Thr Lys Glu Ala Glu
 35 40 45
 Ser Glu Lys Lys Pro Gly Gly Ile Ser Leu Arg Ile Trp Pro Pro Thr
 50 55 60
 15 Gln Lys Thr Arg Asp Ala Val Leu Asn Arg Leu Ile Glu Thr Leu Ser
 65 70 75 80
 Thr Glu Ser Ile Leu Ser Lys Arg Tyr Gly Thr Leu Lys Ser Asp Asp
 85 90 95
 Ala Thr Thr Val Ala Lys Leu Ile Glu Glu Ala Tyr Gly Val Ala
 100 105 110
 20 Ser Asn Ala Val Ser Ser Asp Asp Gly Ile Lys Ile Leu Glu Leu
 115 120 125
 Tyr Ser Lys Glu Ile Ser Lys Arg Met Leu Glu Ser Val Lys Ala Arg
 130 135 140
 25 Ser Asn Ala Ser Val Gly Asn Gly Ser Val Glu Asp Ala Asn Thr Asp
 145 150 155 160
 Ala Ser Glu Val Ser Lys Asp Asp Ala Gly Pro Gly Ser Glu Glu Glu
 165 170 175
 30 Lys Ser Glu Ala
 180

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

35 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

40 (B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1028610

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Met Thr Asp Pro Thr Ser Gln Glu Ala Ala Ser Lys Asp Thr Asp Leu
 1 5 10 15
 45 Thr Lys Glu Ala Glu Ser Glu Lys Lys Pro Gly Gly Ile Ser Leu Arg
 20 25 30
 Ile Trp Pro Pro Thr Gln Lys Thr Arg Asp Ala Val Leu Asn Arg Leu
 35 40 45
 Ile Glu Thr Leu Ser Thr Glu Ser Ile Leu Ser Lys Arg Tyr Gly Thr
 50 55 60
 Leu Lys Ser Asp Asp Ala Thr Thr Val Ala Lys Leu Ile Glu Glu Glu
 65 70 75 80
 Ala Tyr Gly Val Ala Ser Asn Ala Val Ser Ser Asp Asp Asp Gly Ile
 85 90 95
 55 Lys Ile Leu Glu Leu Tyr Ser Lys Glu Ile Ser Lys Arg Met Leu Glu
 100 105 110
 Ser Val Lys Ala Arg Ser Asn Ala Ser Val Gly Asn Gly Ser Val Glu
 115 120 125
 Asp Ala Asn Thr Asp Ala Ser Glu Val Ser Lys Asp Asp Ala Gly Pro
 130 135 140
 60 Gly Ser Glu Glu Glu Lys Ser Glu Ala
 145 150

392

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1028611

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

Met Gln Pro Pro Ser Arg Asn Leu Ser Lys Lys Arg Leu Met Val Leu
1          5          10          15
Leu Arg Met Leu Cys Arg Val Met Met Met Gly Leu Arg Phe Leu Ser
15        20        25        30
Phe Ile Leu Lys Arg Leu Val Arg Gly Cys Leu Asn Leu Leu Arg Leu
35        40        45
Asp Leu Met Leu Val Leu Glu Met Glu Val Trp Arg Met Leu Ile Leu
20        50        55        60
Met Leu Val Arg Phe Leu Lys Met Met Leu Val Leu Val Gln Arg Arg
65        70        75        80
Arg Arg Val Arg Leu Glu Lys Phe Gly Phe Thr Ser Leu Leu
85        90

```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 673 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..673

(D) OTHER INFORMATION: / Ceres Seq. ID 1030069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

atccaaaaaa aacaaaacaa aaaattatat tcaagagaaa aaggaaaaaa tgaatttcat      60
ctccgatcag gtaaagaaac tctcaagctc aacaccagag gagccagacc acaacaagcc      120
agtcgaagga accgaaacag ctacaagacc agctaccaac gccgagctca tggcaagtgc      180
caaggttgta gctgaagctg ctcaagccgc agctcgtaac gaatcagaca aactcgacaa      240
gggtaaagtc gccggagcct ctgctgatat cttagacgct tccgagaaat acggtaagtt      300
cgatgaaaag agtagcactg gtcactacct cgacaaggct gagaagtatc tcaacgacta      360
cgagtcgtca cactccaccg gtgctggttg tcctcctcct ccgacgagtc aggctgagcc      420
agcaagtcag cctgagccgg cggctaagaa agacgatgaa gagtctggtg gtgggcttgg      480
aggttatgcc aagatggctc aaggtttcct gaagtgattt gatctttaat tggtgttcat      540
cattttcgta ataataaatt aaataactag tatcgtttgt gactagttaa tggtgttctg      600
tttatgttta tggggagtga cgagtgagtg taataacttc tggatgatcat gaatctaata      660
catctttgtt gtg

```

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1030070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```

Ser Lys Lys Asn Lys Thr Lys Asn Tyr Ile Gln Glu Lys Lys Glu Lys
1          5          10          15

```


393

Met Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro
 20 25 30
 Glu Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala Thr
 35 40 45
 5 Arg Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val Ala
 50 55 60
 Glu Ala Ala Gln Ala Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp Lys
 65 70 75 80
 10 Gly Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ser Glu Lys
 85 90 95
 Tyr Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly His Tyr Leu Asp Lys
 100 105 110
 Ala Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly Ala
 115 120 125
 15 Gly Gly Pro Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln Pro
 130 135 140
 Glu Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Gly Leu Gly
 145 150 155 160
 20 Gly Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1030071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro
 1 5 10 15
 35 Glu Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala Thr
 20 25 30
 Arg Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val Ala
 35 40 45
 40 Glu Ala Ala Gln Ala Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp Lys
 50 55 60
 Gly Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ser Glu Lys
 65 70 75 80
 Tyr Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly His Tyr Leu Asp Lys
 85 90 95
 45 Ala Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly Ala
 100 105 110
 Gly Gly Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln Pro
 115 120 125
 50 Glu Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Gly Leu Gly
 130 135 140
 Gly Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys
 145 150 155

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

394

(D) OTHER INFORMATION: / Ceres Seq. ID 1030072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```

Met Ala Ser Ala Lys Val Val Ala Glu Ala Ala Gln Ala Ala Ala Arg
1      5      10      15
5  Asn Glu Ser Asp Lys Leu Asp Lys Gly Lys Val Ala Gly Ala Ser Ala
    20      25      30
    Asp Ile Leu Asp Ala Ser Glu Lys Tyr Gly Lys Phe Asp Glu Lys Ser
    35      40      45
10 Ser Thr Gly His Tyr Leu Asp Lys Ala Glu Lys Tyr Leu Asn Asp Tyr
    50      55      60
    Glu Ser Ser His Ser Thr Gly Ala Gly Gly Pro Pro Pro Thr Ser
    65      70      75      80
    Gln Ala Glu Pro Ala Ser Gln Pro Glu Pro Ala Ala Lys Lys Asp Asp
    85      90      95
15 Glu Glu Ser Gly Gly Gly Leu Gly Gly Tyr Ala Lys Met Ala Gln Gly
    100      105      110
    Phe Leu Lys
    115

```

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 944 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..944

(D) OTHER INFORMATION: / Ceres Seq. ID 1032069

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

attgcgaatt ttaattgatc actctctctc tctatctctg ttcaaacatc tctcccaaag      60
taggtagaag aagatgggga cgacgttaga tgtatcaaga gcagagctag cacttggtgt      120
aatgtatttg aacaaagcag aggcaagaga taagttagtc agagctatac agtatgggtc      180
caagttcttg agtgggtggac aacctgggtac tgctcaaaat gttgacaaat ctactagctt      240
35 agcaagaaaa gtcttccgtc ttttcaagtt tgtgaatgac ttgcatggtc ttatcagtc      300
    tgtgcctaaa ggaactcctc ttcctcttgt tttacttgga aagtcgaaga acgcactttt      360
    atctacattc ttgttccttg atcaaattgt ctggcttggg agatcaggaa tatataagaa      420
    caaagaacga gctgagttac ttggacgtat atctctcttc tgctggatgg gatcttctgt      480
    ctgcacaact ttagtcgagg ttggtgagat gggaaggctt tcttcaccaa tgaagaagat      540
40 cgaaaaggga ctcaagaatg gaaacaagta tcaggatgag gattatcgtg ctaagctaaa      600
    aaaatcaaac gagaggtcac ttgctttgat caaatcagct atggacattg ttgtagcagc      660
    tggctcttctt cagttagctc caacgaagat cactcctcgt gtcaccggag cttttggatt      720
    catcacctcc atcatttctt gttaccagtt gcttccgaca cgccccaaga tcaaaacacc      780
    ctgaagtcaa tcgaggaagc tgggtgttaag gagaaagtca tttcagaaag tttctgttct      840
45 tcttattatt aaggaaattc actgctgtta taaaacatcg tataaaatac ttatttgcag      900
    gaattacggt tattataaat ttatgcctca gattcttgat acgc

```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..236

(D) OTHER INFORMATION: / Ceres Seq. ID 1032070

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

Met Gly Thr Thr Leu Asp Val Ser Arg Ala Glu Leu Ala Leu Val Val
60 1      5      10      15
    Met Tyr Leu Asn Lys Ala Glu Ala Arg Asp Lys Leu Cys Arg Ala Ile
    20      25      30

```

395

Gln Tyr Gly Ser Lys Phe Leu Ser Gly Gly Gln Pro Gly Thr Ala Gln
 35 40 45
 Asn Val Asp Lys Ser Thr Ser Leu Ala Arg Lys Val Phe Arg Leu Phe
 50 55 60
 5 Lys Phe Val Asn Asp Leu His Gly Leu Ile Ser Pro Val Pro Lys Gly
 65 70 75 80
 Thr Pro Leu Pro Leu Val Leu Leu Gly Lys Ser Lys Asn Ala Leu Leu
 85 90 95
 10 Ser Thr Phe Leu Phe Leu Asp Gln Ile Val Trp Leu Gly Arg Ser Gly
 100 105 110
 Ile Tyr Lys Asn Lys Glu Arg Ala Glu Leu Leu Gly Arg Ile Ser Leu
 115 120 125
 Phe Cys Trp Met Gly Ser Ser Val Cys Thr Thr Leu Val Glu Val Gly
 130 135 140
 15 Glu Met Gly Arg Leu Ser Ser Ser Met Lys Lys Ile Glu Lys Gly Leu
 145 150 155 160
 Lys Asn Gly Asn Lys Tyr Gln Asp Glu Asp Tyr Arg Ala Lys Leu Lys
 165 170 175
 20 Lys Ser Asn Glu Arg Ser Leu Ala Leu Ile Lys Ser Ala Met Asp Ile
 180 185 190
 Val Val Ala Ala Gly Leu Leu Gln Leu Ala Pro Thr Lys Ile Thr Pro
 195 200 205
 Arg Val Thr Gly Ala Phe Gly Phe Ile Thr Ser Ile Ile Ser Cys Tyr
 210 215 220
 25 Gln Leu Leu Pro Thr Arg Pro Lys Ile Lys Thr Pro
 225 230 235
 (2) INFORMATION FOR SEQ ID NO:152:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 220 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..220
 (D) OTHER INFORMATION: / Ceres Seq. ID 1032071
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:
 40 Met Tyr Leu Asn Lys Ala Glu Ala Arg Asp Lys Leu Cys Arg Ala Ile
 1 5 10 15
 Gln Tyr Gly Ser Lys Phe Leu Ser Gly Gly Gln Pro Gly Thr Ala Gln
 20 25 30
 Asn Val Asp Lys Ser Thr Ser Leu Ala Arg Lys Val Phe Arg Leu Phe
 35 40 45
 45 Lys Phe Val Asn Asp Leu His Gly Leu Ile Ser Pro Val Pro Lys Gly
 50 55 60
 Thr Pro Leu Pro Leu Val Leu Leu Gly Lys Ser Lys Asn Ala Leu Leu
 65 70 75 80
 Ser Thr Phe Leu Phe Leu Asp Gln Ile Val Trp Leu Gly Arg Ser Gly
 85 90 95
 50 Ile Tyr Lys Asn Lys Glu Arg Ala Glu Leu Leu Gly Arg Ile Ser Leu
 100 105 110
 Phe Cys Trp Met Gly Ser Ser Val Cys Thr Thr Leu Val Glu Val Gly
 115 120 125
 55 Glu Met Gly Arg Leu Ser Ser Ser Met Lys Lys Ile Glu Lys Gly Leu
 130 135 140
 Lys Asn Gly Asn Lys Tyr Gln Asp Glu Asp Tyr Arg Ala Lys Leu Lys
 145 150 155 160
 Lys Ser Asn Glu Arg Ser Leu Ala Leu Ile Lys Ser Ala Met Asp Ile
 165 170 175
 60 Val Val Ala Ala Gly Leu Leu Gln Leu Ala Pro Thr Lys Ile Thr Pro
 180 185 190

396

Arg Val Thr Gly Ala Phe Gly Phe Ile Thr Ser Ile Ile Ser Cys Tyr
 195 200 205
 Gln Leu Leu Pro Thr Arg Pro Lys Ile Lys Thr Pro
 210 215 220

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 769 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..769
 (D) OTHER INFORMATION: / Ceres Seq. ID 1033557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

ggtatcgtcc gtagacgata gaggttccac actatgtaaa ggagaccgga gaaacaaagg      60
aactgggttt ggagataaga agtgggaact tgaatggctt ccttatccac ttccgttgta      120
gcttcggctt cgtcgcgttt atggaatcct gctgcctcca acggcaagat ttgcgttcct      180
tctgcttcgc tttctctgcg tacgggttgt agacggagtt cgtcctctct cacttcttcc      240
gcttcttcgc aattgcttca ttgctcgttt ctctcgtcgc ctgtttccct agcgtctcca      300
ttttctgggt tgtccattgc gtttgatctc agcagtcaaa ctagtggact gaatggccag      360
agacgcagag gccttgtggt tagagctgga aaagctgctc tgtgtcaaac taagagaagc      420
agatcaagaa aatctctagc taggactcat ggtttccgta gaaggatgag gaccactagc      480
ggtagagcaa ccataaagcg tcgacgtgcc aagggacgtt ggaacctctg tcccaagtcc      540
aaccctagca gcggcaaacg ggcttgaagt ttgtttctct cttcactcta tctgtaatct      600
tgtttcatgt gctttttttc caccagaaga tacaatgaga aacatgggtc gttgagctct      660
tttctgcgtt ttaactctct tgcacacctg attcgtttat aaatcaatgt tcttgaatt      720
catcacatgt actactatac tacttgcttc attgaatttg ttactactc

```

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..157
 (D) OTHER INFORMATION: / Ceres Seq. ID 1033558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```

Met Ala Ser Leu Ser Thr Ser Val Val Ala Ser Ala Ser Ser Arg Leu
1      5      10      15
Trp Asn Pro Ala Ala Ser Asn Gly Lys Ile Cys Val Pro Ser Ala Ser
20      25      30
Leu Ser Leu Arg Thr Gly Cys Arg Arg Ser Ser Ser Ser Leu Thr Ser
35      40      45
Ser Ala Ser Ser Gln Leu Leu His Cys Ser Phe Leu Ser Ser Pro Val
50      55      60
Ser Leu Ala Ser Pro Phe Ser Gly Leu Ser Ile Ala Phe Asp Leu Ser
65      70      75      80
Ser Gln Thr Ser Gly Leu Asn Gly Gln Arg Arg Arg Gly Leu Val Val
85      90      95
Arg Ala Gly Lys Ala Ala Leu Cys Gln Thr Lys Arg Ser Arg Ser Arg
100      105      110
Lys Ser Leu Ala Arg Thr His Gly Phe Arg Arg Arg Met Arg Thr Thr
115      120      125
Ser Gly Arg Ala Thr Ile Lys Arg Arg Arg Ala Lys Gly Arg Trp Asn
130      135      140
Leu Cys Pro Lys Ser Asn Pro Ser Ser Gly Lys Arg Ala
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:155:

397

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..679

(D) OTHER INFORMATION: / Ceres Seq. ID 1034688

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

aaaaaaaaaac  aaaaacaaaaa  attatatattca  agagaaaaaag  gaaaaaatga  atttcatctc      60
cgatcaggta  aagaaactct  caagctcaac  accagaggag  ccagaccaca  acaagccagt     120
cgaaggaacc  gaaacagcta  caagaccagc  taccaacgcc  gagctcatgg  caagtgccaa     180
15  gggtgtagct  gaagctgctc  aagccgcagc  tcgtaacgaa  tcagacaaac  tcgacaaggg     240
taaagtcgcc  ggagcctctg  ctgatatctt  agacgctgcc  gagaaatacg  gtaagttcga     300
tgaaaagagt  agcactggtc  agtacctcga  caaggctgag  aagtatctca  acgactacga     360
gtcgtcacac  tccaccggtg  ctggtgggtc  tcctcctcca  acgagtcagg  ctgagccagc     420
aagtcagcct  gagccggcgg  ctaagaaaga  cgatgaagag  tctggtggtg  ggcttgagg     480
20  ttatgccaa  atggctcaag  gtttcttgaa  gtgatttgat  ctttaattgt  tggtcatcat     540
tttcgtaata  ataaattaa  taactagtat  cgtttgtagc  tagtttatgt  tgcttcggtt     600
atgtttatgg  ggagtgacga  gtgagtgtaa  taacttctgg  tgatcatgaa  tctaattccat     660
ctttgttggtg  attatgctc

```

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..170

(D) OTHER INFORMATION: / Ceres Seq. ID 1034689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

```

Lys Lys Asn Lys Thr Lys Asn Tyr Ile Gln Glu Lys Lys Glu Lys Met
1      5      10      15
Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro Glu
20      25      30
40  Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala Thr Arg
35      40      45
Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val Ala Glu
50      55      60
Ala Ala Gln Ala Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp Lys Gly
45  65      70      75      80
Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ala Glu Lys Tyr
85      90      95
Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly Gln Tyr Leu Asp Lys Ala
100      105      110
50  Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly Ala Gly
115      120      125
Gly Pro Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln Pro Glu
130      135      140
Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Gly Leu Gly Gly
55  145      150      155      160
Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys
165      170

```

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

398

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1034690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```

Met Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro
1      5      10      15
10  Glu Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala Thr
      20      25      30
    Arg Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val Ala
      35      40      45
15  Glu Ala Ala Gln Ala Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp Lys
      50      55      60
    Gly Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ala Glu Lys
      65      70      75      80
    Tyr Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly Gln Tyr Leu Asp Lys
      85      90      95
20  Ala Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly Ala
      100     105     110
    Gly Gly Pro Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln Pro
      115     120     125
25  Glu Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Gly Leu Gly
      130     135     140
    Gly Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys
      145     150     155

```

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1034691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```

Met Ala Ser Ala Lys Val Val Ala Glu Ala Ala Gln Ala Ala Ala Arg
1      5      10      15
40  Asn Glu Ser Asp Lys Leu Asp Lys Gly Lys Val Ala Gly Ala Ser Ala
      20      25      30
    Asp Ile Leu Asp Ala Ala Glu Lys Tyr Gly Lys Phe Asp Glu Lys Ser
      35      40      45
45  Ser Thr Gly Gln Tyr Leu Asp Lys Ala Glu Lys Tyr Leu Asn Asp Tyr
      50      55      60
    Glu Ser Ser His Ser Thr Gly Ala Gly Gly Pro Pro Pro Thr Ser
      65      70      75      80
50  Gln Ala Glu Pro Ala Ser Gln Pro Glu Pro Ala Ala Lys Lys Asp Asp
      85      90      95
    Glu Glu Ser Gly Gly Gly Leu Gly Gly Tyr Ala Lys Met Ala Gln Gly
      100     105     110
    Phe Leu Lys
      115

```

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

399

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..471

(D) OTHER INFORMATION: / Ceres Seq. ID 1035033

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```

atataaaaaa aaaacttatt ttgttcattc ttttaagttt aaaaacagtc aattcattta      60
tatcatctat gatgaagaaa ctcatccaag tctcgttcac tggtatgatt atcttcacca      120
ttcttggtgct aggagtgggtg gcaaatgagg ggctaggaaa accaaaaaaa caatgtaatg      180
agattctaaa gcaatccaac tgtgttgctg cagagtgtga ctctatgtgt gtgaagaaga      240
gggggaaagg agccggttac tgctctcctt ctaaaaagtgt ttactgctat tatcattgcc      300
cttaacgatt ttattattta caataataag agatttatga taaagtagta aaataatgaa      360
tcgggtgttt atagcctaac gattgatata gttgtctcta tcaaataaac tatatagact      420
aaaagtaata ataataatga caatcataac tcagaagttt ttgtttagtc c

```

(2) INFORMATION FOR SEQ ID NO:160:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1035034

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

Ile Lys Lys Lys Leu Ile Leu Phe Ile Leu Leu Ser Leu Lys Thr Val
1      5      10      15
Asn Ser Phe Ile Ser Ser Met Met Lys Lys Leu Ile Gln Val Ser Phe
      20      25      30
Thr Val Met Ile Ile Phe Thr Ile Leu Val Leu Gly Val Val Ala Asn
      35      40      45
Glu Gly Leu Gly Lys Pro Lys Lys Gln Cys Asn Glu Ile Leu Lys Gln
      50      55      60
Ser Asn Cys Val Ala Ala Glu Cys Asp Ser Met Cys Val Lys Lys Arg
35      65      70      75      80
Gly Lys Gly Ala Gly Tyr Cys Ser Pro Ser Lys Lys Cys Tyr Cys Tyr
      85      90      95
Tyr His Cys Pro
      100

```

40 (2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

50 (D) OTHER INFORMATION: / Ceres Seq. ID 1035035

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

Met Met Lys Lys Leu Ile Gln Val Ser Phe Thr Val Met Ile Ile Phe
1      5      10      15
Thr Ile Leu Val Leu Gly Val Val Ala Asn Glu Gly Leu Gly Lys Pro
55      20      25      30
Lys Lys Gln Cys Asn Glu Ile Leu Lys Gln Ser Asn Cys Val Ala Ala
      35      40      45
Glu Cys Asp Ser Met Cys Val Lys Lys Arg Gly Lys Gly Ala Gly Tyr
      50      55      60
Cys Ser Pro Ser Lys Lys Cys Tyr Cys Tyr Tyr His Cys Pro
60      65      70      75

```

(2) INFORMATION FOR SEQ ID NO:162:

400

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 1035036

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```

Met Lys Lys Leu Ile Gln Val Ser Phe Thr Val Met Ile Ile Phe Thr
 1           5           10           15
Ile Leu Val Leu Gly Val Val Ala Asn Glu Gly Leu Gly Lys Pro Lys
15           20           25           30
Lys Gln Cys Asn Glu Ile Leu Lys Gln Ser Asn Cys Val Ala Ala Glu
           35           40           45
Cys Asp Ser Met Cys Val Lys Lys Arg Gly Lys Gly Ala Gly Tyr Cys
           50           55           60
20 Ser Pro Ser Lys Lys Cys Tyr Cys Tyr Tyr His Cys Pro
           65           70           75

```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 985 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..985

(D) OTHER INFORMATION: / Ceres Seq. ID 1035071

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

```

taacgcactc tcttctccga atctagggtt tttgtctcta gcctcctcaa gctttgcaaa      60
35 caatcatggc gacccagatc agcaagaaga gaaagttcgt agccgatggg gtgttttacg      120
ctgaactcaa tgaggttcta accagagagc ttgctgagga tggttactct ggtgttgagg      180
ttcgcgtcac tccatgctgc actgagatca tcattagagc cactcgtact caaacggttc      240
tcggtgagaa gggaaggagg attagggaat tgacatctct tgtacaaaag agattcaaat      300
ttcctcagga cagtgttgag ctttatgctg agaagggttg taacagaggt ctttgtgcta      360
40 ttgctcaggc tgagtctctt cgttacaagc ttcttggttg tcttgctgtt cgtagggcgt      420
gctatggtgt tttaagggtt gttatggaga gtggagctaa aggatgcgaa gtcattgtga      480
gtggaaaact ccgtgctgca cgtgctaagt agatgaagtt caaggatggt tacatgggtt      540
cctcagggtc gccaaccaag gaatacattg atgctgcagt taggcatggt cttcttagac      600
agggtgtgct tgggtctcaag gtgaagatca tgcttgactg ggaccccaag ggcaacaag      660
45 gaccgatgac accattgcct gatgttgtga tcatccatac accgaaagaa gatgatgtat      720
acattgcacc tgctcagggt gttactcaag ctgcttttgt accggaagct ccattaacca      780
ccacagatta tccagcaatg ccagttgctt agagagcctt ttcgttttct ggtttaaaac      840
ccaatgggga tggttctttt tttgggacag tactagtttt ctcatgttat tctaagttaa      900
50 tacttaaagt tctggagggt gaattacatc aaggatatga atgtatgttt ttcgttatct      960
tttgtttaaa ttttatttat ctatt

```

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1035072

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

401

Met Ala Thr Gln Ile Ser Lys Lys Arg Lys Phe Val Ala Asp Gly Val
 1 5 10 15
 Phe Tyr Ala Glu Leu Asn Glu Val Leu Thr Arg Glu Leu Ala Glu Asp
 20 25 30
 5 Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Met Arg Thr Glu Ile
 35 40 45
 Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu Gly Glu Lys Gly Arg
 50 55 60
 Arg Ile Arg Glu Leu Thr Ser Leu Val Gln Lys Arg Phe Lys Phe Pro
 10 65 70 75 80
 Gln Asp Ser Val Glu Leu Tyr Ala Glu Lys Val Ala Asn Arg Gly Leu
 85 90 95
 Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly
 100 105 110
 15 Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu Arg Phe Val Met Glu
 115 120 125
 Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser Gly Lys Leu Arg Ala
 130 135 140
 Ala Arg Ala Lys
 145
 20

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..105

(D) OTHER INFORMATION: / Ceres Seq. ID 1035073

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu
 1 5 10 15
 35 Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser Leu Val Gln Lys
 20 25 30
 Arg Phe Lys Phe Pro Gln Asp Ser Val Glu Leu Tyr Ala Glu Lys Val
 35 40 45
 40 Ala Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr
 50 55 60
 Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu
 65 70 75 80
 Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser
 85 90 95
 45 Gly Lys Leu Arg Ala Ala Arg Ala Lys
 100 105

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1035074

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Met Lys Phe Lys Asp Gly Tyr Met Val Ser Ser Gly Gln Pro Thr Lys
 1 5 10 15
 60 Glu Tyr Ile Asp Ala Ala Val Arg His Val Leu Leu Arg Gln Gly Val
 20 25 30

402

Leu Gly Leu Lys Val Lys Ile Met Leu Asp Trp Asp Pro Lys Gly Lys
 35 40 45
 Gln Gly Pro Met Thr Pro Leu Pro Asp Val Val Ile Ile His Thr Pro
 50 55 60
 5 Lys Glu Asp Asp Val Tyr Ile Ala Pro Ala Gln Val Val Thr Gln Ala
 65 70 75 80
 Ala Phe Val Pro Glu Ala Pro Leu Thr Thr Thr Asp Tyr Pro Ala Met
 85 90 95
 Pro Val Ala

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 759 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..759

(D) OTHER INFORMATION: / Ceres Seq. ID 1376587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

atccgcagaa	aaccctattg	ctcccctttg	ctcaagctca	gtgcctcttt	gcagcgaaag	60
ctcaaccaac	aagacgatga	ttatctcaga	gaacaatcgc	agagagatct	gcaaataacct	120
tttcaaagag	ggagtatgct	ttgctaagaa	ggatttcaat	ctcccaaagc	atccgttgat	180
tgatgtacca	aacctgcaag	tgattaagct	catgcagagt	ttcaagtcca	aggagtacgt	240
tagggagaca	tttgcggtgga	tgcattatta	ttggtttctg	actaatgaag	gaattgagtt	300
cttgagaact	tatcttaacc	ttccttcoga	tggtgtccct	gctactttga	agaagtctgc	360
taagcccggg	ggtcgtccct	ttgggtggccc	acctggtgat	cgccaaagag	gaccacctcg	420
ctctgatgga	gaccgtccca	gatttgggtga	ccgtgatgga	taccgtggag	gcccacgagg	480
tggtgatgag	aagagtggag	ctccagctga	tttccagccg	tctttccaag	gaggtggtgg	540
taggcctggt	tttggccgtg	gtgcaggcgg	ttacagtga	gcagcaccat	ctggttcagg	600
gttcccttga	aaaatttttt	gtcatattgc	gacgatggaa	ggacagtttt	gttttttggt	660
ctagtctctg	ttgtgtaatg	caaatctgga	atctataatc	tatctattac	cttcaccttg	720
gtttaaacga	acaaatcctg	tagtttcagg	attagtgcc			

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..202

(D) OTHER INFORMATION: / Ceres Seq. ID 1376588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

Ser	Ala	Glu	Asn	Pro	Ile	Ala	Pro	Leu	Cys	Ser	Ser	Ser	Val	Pro	Leu	
1				5				10					15			
50	Cys	Ser	Glu	Ser	Ser	Thr	Asn	Lys	Thr	Met	Ile	Ile	Ser	Glu	Asn	Asn
				20				25					30			
	Arg	Arg	Glu	Ile	Cys	Lys	Tyr	Leu	Phe	Lys	Glu	Gly	Val	Cys	Phe	Ala
				35				40					45			
55	Lys	Lys	Asp	Phe	Asn	Leu	Pro	Lys	His	Pro	Leu	Ile	Asp	Val	Pro	Asn
				50				55					60			
	Leu	Gln	Val	Ile	Lys	Leu	Met	Gln	Ser	Phe	Lys	Ser	Lys	Glu	Tyr	Val
				65				70					75			80
	Arg	Glu	Thr	Phe	Ala	Trp	Met	His	Tyr	Tyr	Trp	Phe	Leu	Thr	Asn	Glu
				85									90			95
60	Gly	Ile	Glu	Phe	Leu	Arg	Thr	Tyr	Leu	Asn	Leu	Pro	Ser	Asp	Val	Val
				100									105			110
	Pro	Ala	Thr	Leu	Lys	Lys	Ser	Ala	Lys	Pro	Gly	Gly	Arg	Pro	Phe	Gly

403

115 120 125
 Gly Pro Pro Gly Asp Arg Gln Arg Gly Pro Pro Arg Ser Asp Gly Asp
 130 135 140
 5 Arg Pro Arg Phe Gly Asp Arg Asp Gly Tyr Arg Gly Gly Pro Arg Gly
 145 150 155 160
 Gly Asp Glu Lys Ser Gly Ala Pro Ala Asp Phe Gln Pro Ser Phe Gln
 165 170 175
 Gly Gly Gly Gly Arg Pro Gly Phe Gly Arg Gly Ala Gly Gly Tyr Ser
 180 185 190
 10 Ala Ala Ala Pro Ser Gly Ser Gly Phe Pro
 195 200

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20 (A) NAME/KEY: peptide
 (B) LOCATION: 1..177
 (D) OTHER INFORMATION: / Ceres Seq. ID 1376589

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

25 Met Ile Ile Ser Glu Asn Asn Arg Arg Glu Ile Cys Lys Tyr Leu Phe
 1 5 10 15
 Lys Glu Gly Val Cys Phe Ala Lys Lys Asp Phe Asn Leu Pro Lys His
 20 25 30
 Pro Leu Ile Asp Val Pro Asn Leu Gln Val Ile Lys Leu Met Gln Ser
 35 40 45
 30 Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Phe Ala Trp Met His Tyr
 50 55 60
 Tyr Trp Phe Leu Thr Asn Glu Gly Ile Glu Phe Leu Arg Thr Tyr Leu
 65 70 75 80
 Asn Leu Pro Ser Asp Val Val Pro Ala Thr Leu Lys Lys Ser Ala Lys
 35 85 90 95
 Pro Gly Gly Arg Pro Phe Gly Gly Pro Pro Gly Asp Arg Gln Arg Gly
 100 105 110
 Pro Pro Arg Ser Asp Gly Asp Arg Pro Arg Phe Gly Asp Arg Asp Gly
 115 120 125
 40 Tyr Arg Gly Gly Pro Arg Gly Gly Asp Glu Lys Ser Gly Ala Pro Ala
 130 135 140
 Asp Phe Gln Pro Ser Phe Gln Gly Gly Gly Gly Arg Pro Gly Phe Gly
 145 150 155 160
 Arg Gly Ala Gly Gly Tyr Ser Ala Ala Ala Pro Ser Gly Ser Gly Phe
 45 165 170 175
 Pro

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

55 (A) NAME/KEY: peptide
 (B) LOCATION: 1..132
 (D) OTHER INFORMATION: / Ceres Seq. ID 1376590

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

60 Met Gln Ser Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Phe Ala Trp
 1 5 10 15
 Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Glu Phe Leu Arg

404

20 25 30
 Thr Tyr Leu Asn Leu Pro Ser Asp Val Val Pro Ala Thr Leu Lys Lys
 35 40 45
 5 Ser Ala Lys Pro Gly Gly Arg Pro Phe Gly Gly Pro Pro Gly Asp Arg
 50 55 60
 Gln Arg Gly Pro Pro Arg Ser Asp Gly Asp Arg Pro Arg Phe Gly Asp
 65 70 75 80
 Arg Asp Gly Tyr Arg Gly Gly Pro Arg Gly Gly Asp Glu Lys Ser Gly
 85 90 95
 10 Ala Pro Ala Asp Phe Gln Pro Ser Phe Gln Gly Gly Gly Gly Arg Pro
 100 105 110
 Gly Phe Gly Arg Gly Ala Gly Gly Tyr Ser Ala Ala Ala Pro Ser Gly
 115 120 125
 Ser Gly Phe Pro
 15 130
 (2) INFORMATION FOR SEQ ID NO:171:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 645 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 25 (B) LOCATION: 1..645
 (D) OTHER INFORMATION: / Ceres Seq. ID 1378581
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:
 gatttcccat tttggttgca gcgatcgag agctctgacg gcaccagcca cctctgcggc 60
 ttcgcaaatac caaataagct gtggatgaaa cgaagaatcc tagatttctg aatggcgaca 120
 30 ccatttatag cgggggttgc agtagctgca acagcacttg ctggtagata tggaaatccaa 180
 gcatggcaag cattcaaggc aaggccacca aggcccaaaa ttaagaaatt ttatgagggc 240
 ggtttccagc ctacgatgac gaaaagggaa gctgctctca tcttggtcgt caggagaggt 300
 gtagcggcgg aaaaggtgaa ggaagcacac aggaaggtaa tggagcaaa ccatccagat 360
 gcaggtggta gccatttcct agcctctaag atcaatgaag cttaaagacgt gatgctaggc 420
 35 aaaactaaaa acagcggatc cgcttttttga tgcaaatttc aatcaaaaaga cttccttatg 480
 aatcatctta tgttatagga ctgtaatgtc aaaatgcaga ttttatgtta atttataagc 540
 ttgtggtctg tttgtgacac ataaagactc gaatcttttc tttcacttgt tgctgctgaa 600
 aagaacacaa aaataaaaac gcaaagcaga agggcgttct agtcg
 (2) INFORMATION FOR SEQ ID NO:172:
 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 45 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..112
 (D) OTHER INFORMATION: / Ceres Seq. ID 1378582
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:
 Met Ala Thr Pro Phe Ile Ala Gly Val Ala Val Ala Ala Thr Ala Leu
 1 5 10 15
 Ala Gly Arg Tyr Gly Ile Gln Ala Trp Gln Ala Phe Lys Ala Arg Pro
 20 25 30
 55 Pro Arg Pro Lys Ile Lys Lys Phe Tyr Glu Gly Gly Phe Gln Pro Thr
 35 40 45
 Met Thr Lys Arg Glu Ala Ala Leu Ile Leu Gly Val Arg Glu Ser Val
 50 55 60
 Ala Ala Glu Lys Val Lys Glu Ala His Arg Lys Val Met Val Ala Asn
 60 65 70 75 80
 His Pro Asp Ala Gly Ser His Phe Leu Ala Ser Lys Ile Asn Glu
 85 90 95

405

Ala Lys Asp Val Met Leu Gly Lys Thr Lys Asn Ser Gly Ser Ala Phe
 100 105 110

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..64
 (D) OTHER INFORMATION: / Ceres Seq. ID 1378583

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

Met Thr Lys Arg Glu Ala Ala Leu Ile Leu Gly Val Arg Glu Ser Val
 1 5 10 15
 Ala Ala Glu Lys Val Lys Glu Ala His Arg Lys Val Met Val Ala Asn
 20 25 30
 His Pro Asp Ala Gly Gly Ser His Phe Leu Ala Ser Lys Ile Asn Glu
 35 40 45
 Ala Lys Asp Val Met Leu Gly Lys Thr Lys Asn Ser Gly Ser Ala Phe
 50 55 60

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..803
 (D) OTHER INFORMATION: / Ceres Seq. ID 1383462

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

aggacacggt tctatctaga gagaacacaa cacatcgaac catggagaaa tcaacaagaa 60
 ccctattcat aaccatcgtg ataacctcca tggttgctagg gtttggaac tctgatcttg 120
 ctcaggacag agaggagtgt acgaaccagc tcatagaact atccacgtgt attccgtacg 180
 ttggaggaga cgccaaggct ccaacaaaag attggtgtgc agggtttggc caagttataa 240
 gaaagagtga gaagtgtggt tgcataattg tccagagacaa agatgatcct caacttggtg 300
 tcaagattaa cgcaacccta gccgctcatc ttccctccgc ttgtcatatc acggctccta 360
 acatcactga ctgtatttcg attctgcatc tacctcgtaa ctcaacattg gctaaagagt 420
 ttgagaactt aggaaggatt gaagacaact acaactccac atctcctaca caaattcata 480
 aagatgggac aggaggagga aaagccgaac cagtgaagag taatggatgg aaggagaaga 540
 gttggttggg tggttgagctt ttaatatatt tgctagtttc tctcatcttc ttttaattac 600
 ttcctttctt taatgttcct ttgctttatt attacaataa cttataagat atctatttat 660
 atatgagaca catgcatgtg tttgcgatct atatgcatgt aaatgagtca ctggttaatt 720
 tttaatcacg aagcgtacat tttaatttcg ttgttgccaa ttgatcttgt acgttagtga 780
 attttatgga ttatcgactt act

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..197
 (D) OTHER INFORMATION: / Ceres Seq. ID 1383463

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Asp Thr Phe Leu Ser Arg Glu Asn Thr Thr His Arg Thr Met Glu Lys
 1 5 10 15

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Ser Thr Arg Thr Leu Phe Ile Thr Ile Val Ile Thr Ser Met Leu Leu
 20 25 30
 Gly Phe Gly Asn Ser Asp Leu Ala Gln Asp Arg Glu Glu Cys Thr Asn
 35 40 45
 5 Gln Leu Ile Glu Leu Ser Thr Cys Ile Pro Tyr Val Gly Gly Asp Ala
 50 55 60
 Lys Ala Pro Thr Lys Asp Cys Cys Ala Gly Phe Gly Gln Val Ile Arg
 65 70 75 80
 10 Lys Ser Glu Lys Cys Val Cys Ile Leu Val Arg Asp Lys Asp Asp Pro
 85 90 95
 Gln Leu Gly Ile Lys Ile Asn Ala Thr Leu Ala Ala His Leu Pro Ser
 100 105 110
 Ala Cys His Ile Thr Ala Pro Asn Ile Thr Asp Cys Ile Ser Ile Leu
 115 120 125
 15 His Leu Pro Arg Asn Ser Thr Leu Ala Lys Glu Phe Glu Asn Leu Gly
 130 135 140
 Arg Ile Glu Asp Asn Tyr Asn Ser Thr Ser Pro Thr Gln Ile His Lys
 145 150 155 160
 20 Asp Gly Thr Gly Gly Lys Ala Glu Pro Val Lys Ser Asn Gly Trp
 165 170 175
 Lys Glu Lys Ser Trp Leu Gly Val Glu Leu Leu Ile Tyr Leu Leu Val
 180 185 190
 Ser Leu Ile Phe Phe
 195

25 (2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..184

35 (D) OTHER INFORMATION: / Ceres Seq. ID 1383464

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met Glu Lys Ser Thr Arg Thr Leu Phe Ile Thr Ile Val Ile Thr Ser
 1 5 10 15
 Met Leu Leu Gly Phe Gly Asn Ser Asp Leu Ala Gln Asp Arg Glu Glu
 20 25 30
 40 Cys Thr Asn Gln Leu Ile Glu Leu Ser Thr Cys Ile Pro Tyr Val Gly
 35 40 45
 Gly Asp Ala Lys Ala Pro Thr Lys Asp Cys Cys Ala Gly Phe Gly Gln
 50 55 60
 45 Val Ile Arg Lys Ser Glu Lys Cys Val Cys Ile Leu Val Arg Asp Lys
 65 70 75 80
 Asp Asp Pro Gln Leu Gly Ile Lys Ile Asn Ala Thr Leu Ala Ala His
 85 90 95
 50 Leu Pro Ser Ala Cys His Ile Thr Ala Pro Asn Ile Thr Asp Cys Ile
 100 105 110
 Ser Ile Leu His Leu Pro Arg Asn Ser Thr Leu Ala Lys Glu Phe Glu
 115 120 125
 Asn Leu Gly Arg Ile Glu Asp Asn Tyr Asn Ser Thr Ser Pro Thr Gln
 130 135 140
 55 Ile His Lys Asp Gly Thr Gly Gly Gly Lys Ala Glu Pro Val Lys Ser
 145 150 155 160
 Asn Gly Trp Lys Glu Lys Ser Trp Leu Gly Val Glu Leu Leu Ile Tyr
 165 170 175
 Leu Leu Val Ser Leu Ile Phe Phe
 180

60 (2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..180

10

(D) OTHER INFORMATION: / Ceres Seq. ID 1386216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

Arg	Gly	Lys	Gln	Asn	Cys	Lys	Asn	Lys	Lys	Asn	Ile	Ala	Gln
1				5				10				15	
Glu	Asn	Lys	Arg	Phe	Val	Glu	Ser	Thr	Lys	Lys	Met	Ala	Ser
			20					25				30	Thr
Met	Thr	Thr	Leu	Pro	Gln	Phe	Asn	Gly	Leu	Arg	Ala	Thr	Lys
			35				40					45	Ile
Ala	Ala	Pro	Val	Gln	Gly	Leu	Ala	Ser	Val	Gln	Pro	Met	Arg
			50			55				60			Arg
Gly	Asn	Gly	Ala	Leu	Gly	Ala	Lys	Cys	Asp	Phe	Ile	Gly	Ser
				70					75				80
Asn	Leu	Ile	Met	Val	Thr	Ser	Thr	Thr	Leu	Met	Leu	Phe	Ala
			85					90					95
Phe	Gly	Leu	Ala	Pro	Ser	Ala	Asn	Arg	Lys	Ala	Thr	Ala	Gly
			100					105				110	Leu
Leu	Glu	Ala	Arg	Asp	Ser	Gly	Leu	Gln	Thr	Gly	Asp	Pro	Ala
			115				120					125	Gly
Thr	Leu	Ala	Asp	Thr	Leu	Ala	Cys	Ala	Ser	Asn	Leu	Thr	Pro
			130				135				140		Ile
Pro	Ser	Ser	Pro	Asn	Leu	Glu	Ser	Met	Lys	Thr	Ser	Pro	Met
				150					155				Lys
Leu	Ser	Leu	Arg	Asn	Arg	Gln	Trp	Leu	Leu	Ser	Gln	Leu	Glu
			165					170					Ile
													175
Arg	Trp	Leu	Ile										
			180										

35

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

45

(D) OTHER INFORMATION: / Ceres Seq. ID 1386217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

Met	Ala	Ser	Thr	Met	Met	Thr	Thr	Leu	Pro	Gln	Phe	Asn	Gly
1				5				10					15
Ala	Thr	Lys	Ile	Ser	Ala	Ala	Pro	Val	Gln	Gly	Leu	Ala	Ser
			20					25				30	Val
Pro	Met	Arg	Arg	Lys	Gly	Asn	Gly	Ala	Leu	Gly	Ala	Lys	Cys
			35				40					45	Asp
Ile	Gly	Ser	Ser	Thr	Asn	Leu	Ile	Met	Val	Thr	Ser	Thr	Leu
			50			55				60			Met
Leu	Phe	Ala	Gly	Arg	Phe	Gly	Leu	Ala	Pro	Ser	Ala	Asn	Arg
				70					75				Lys
Thr	Ala	Gly	Leu	Arg	Leu	Glu	Ala	Arg	Asp	Ser	Gly	Leu	Gln
			85					90				95	Thr
Asp	Pro	Ala	Gly	Phe	Thr	Leu	Ala	Asp	Thr	Leu	Ala	Cys	Ala
			100					105				110	Ser
Leu	Thr	Pro	Ile	Ser	Pro	Ser	Ser	Pro	Asn	Leu	Glu	Ser	Met
													Lys

60

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115 120 125
 Ser Pro Met Lys Arg Leu Ser Leu Arg Asn Arg Gln Trp Leu Leu Ser
 130 135 140
 Gln Leu Glu Ile Ser Arg Trp Leu Ile
 145 150

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..149

(D) OTHER INFORMATION: / Ceres Seq. ID 1386218

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Met Met Thr Thr Leu Pro Gln Phe Asn Gly Leu Arg Ala Thr Lys Ile
 1 5 10 15
 Ser Ala Ala Pro Val Gln Gly Leu Ala Ser Val Gln Pro Met Arg Arg
 20 25 30
 Lys Gly Asn Gly Ala Leu Gly Ala Lys Cys Asp Phe Ile Gly Ser Ser
 35 40 45
 Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Met Leu Phe Ala Gly
 50 55 60
 Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu
 65 70 75 80
 Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly
 85 90 95
 Phe Thr Leu Ala Asp Thr Leu Ala Cys Ala Ser Asn Leu Thr Pro Ile
 100 105 110
 Ser Pro Ser Ser Pro Asn Leu Glu Ser Met Lys Thr Ser Pro Met Lys
 115 120 125
 Arg Leu Ser Leu Arg Asn Arg Gln Trp Leu Leu Ser Gln Leu Glu Ile
 130 135 140
 Ser Arg Trp Leu Ile
 145

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 2025156

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Met Ala Leu Val Ala Ala Gly Asn Ile Ser Val Ala Asn Met Asn Lys
 1 5 10 15
 Ala Val Ala Leu Leu Lys Glu Glu Ala Leu Lys Lys Ile Ile Ala Ala
 20 25 30
 Lys Thr Ala Lys Leu Arg Ala Lys Gly Ala Leu Thr Asn Leu Gln Asp
 35 40 45
 Ile Val Ile Arg Gln Ser Lys Val Thr Gly Lys Arg Lys Glu Asp Glu
 50 55 60
 Arg
 65

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 770 base pairs

410

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 5 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..770
 (D) OTHER INFORMATION: / Ceres Seq. ID 1388499
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

10	aaaaaactca	ttctcataac	aattccctta	actctatctc	taggtgactt	aagagtaaaa	60
	aatggtagag	gcagagggtg	aagtagatgt	ggaaatcaaa	tctacggctg	ataagttttt	120
	catgttctct	agaagatcac	aacatgcctc	caaagccact	cgctatgtac	agggatgtga	180
	tctgctcgaa	ggcgagtggg	gcgaagtggg	aagcatactc	ttgtggaaat	taactgttga	240
	tggagagcca	aaagtgtcaa	aggatatgat	tgaggcgatt	gatatgaaga	tgaatatgat	300
15	ccagtggagg	gtgttagagg	gacctctgaa	ggaagagtac	aatattttct	cgaaaacgat	360
	gaaagtaagc	cctaagcaag	gaggggtctg	aagtgtgggtg	aagtgggaact	tgaagtatga	420
	gagaattgat	gaaaagggtg	ctcacctaga	gaggctcctt	cagttcttcg	tcgaatgtgt	480
	taacgagatt	gaccaatacc	tattgtctga	gggttagggg	acttttctcc	ctggcttatg	540
	tgtgggagag	ttattgtatg	cgtacgtgta	aggactcttc	ttgtgtttta	tatgtctttc	600
20	tcaataatgt	gatatcttga	gatttagaag	agaggtatcc	aagtgtgcta	tacctcatgt	660
	cttcaagtgtg	gaagttgtat	aacattttaa	gttgcttatg	agtttctcat	atatgtagtg	720
	tgtttggttg	ttgaaaaatc	atattataat	gcaacgatac	catgtttttt		

(2) INFORMATION FOR SEQ ID NO:184:
 (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 30 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..151
 (D) OTHER INFORMATION: / Ceres Seq. ID 1388500
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

35	Met	Val	Glu	Ala	Glu	Val	Glu	Val	Asp	Val	Glu	Ile	Lys	Ser	Thr	Ala
	1				5					10					15	
	Asp	Lys	Phe	Phe	Met	Phe	Ser	Arg	Arg	Ser	Gln	His	Ala	Ser	Lys	Ala
				20					25					30		
	Thr	Arg	Tyr	Val	Gln	Gly	Cys	Asp	Leu	Leu	Glu	Gly	Glu	Trp	Gly	Glu
40				35				40					45			
	Val	Gly	Ser	Ile	Leu	Leu	Trp	Lys	Leu	Thr	Val	Asp	Gly	Glu	Pro	Lys
		50					55					60				
	Val	Ser	Lys	Asp	Met	Ile	Glu	Ala	Ile	Asp	Met	Lys	Met	Asn	Met	Ile
				65		70				75				80		
45	Gln	Trp	Arg	Val	Leu	Glu	Gly	Pro	Leu	Lys	Glu	Glu	Tyr	Asn	Ile	Phe
				85					90					95		
	Ser	Lys	Thr	Met	Lys	Val	Ser	Pro	Lys	Gln	Gly	Gly	Ser	Gly	Ser	Val
				100					105					110		
	Val	Lys	Trp	Asn	Leu	Lys	Tyr	Glu	Arg	Ile	Asp	Glu	Lys	Val	Ala	His
50				115				120					125			
	Leu	Glu	Arg	Leu	Leu	Gln	Phe	Phe	Val	Glu	Cys	Val	Asn	Glu	Ile	Asp
		130					135						140			
	Gln	Tyr	Leu	Leu	Ser	Glu	Gly									
		145				150										

(2) INFORMATION FOR SEQ ID NO:185:
 (i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 60 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

411

(A) NAME/KEY: peptide

(B) LOCATION: 1..131

(D) OTHER INFORMATION: / Ceres Seq. ID 1388501

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

5 Met Phe Ser Arg Arg Ser Gln His Ala Ser Lys Ala Thr Arg Tyr Val
 1 5 10 15
 Gln Gly Cys Asp Leu Leu Glu Gly Glu Trp Gly Glu Val Gly Ser Ile
 20 25 30
 10 Leu Leu Trp Lys Leu Thr Val Asp Gly Glu Pro Lys Val Ser Lys Asp
 35 40 45
 Met Ile Glu Ala Ile Asp Met Lys Met Asn Met Ile Gln Trp Arg Val
 50 55 60
 Leu Glu Gly Pro Leu Lys Glu Glu Tyr Asn Ile Phe Ser Lys Thr Met
 65 70 75 80
 15 Lys Val Ser Pro Lys Gln Gly Gly Ser Gly Ser Val Val Lys Trp Asn
 85 90 95
 Leu Lys Tyr Glu Arg Ile Asp Glu Lys Val Ala His Leu Glu Arg Leu
 100 105 110
 20 Leu Gln Phe Phe Val Glu Cys Val Asn Glu Ile Asp Gln Tyr Leu Leu
 115 120 125
 Ser Glu Gly
 130

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

30 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1388502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

35 Met Ile Glu Ala Ile Asp Met Lys Met Asn Met Ile Gln Trp Arg Val
 1 5 10 15
 Leu Glu Gly Pro Leu Lys Glu Glu Tyr Asn Ile Phe Ser Lys Thr Met
 20 25 30
 40 Lys Val Ser Pro Lys Gln Gly Gly Ser Gly Ser Val Val Lys Trp Asn
 35 40 45
 Leu Lys Tyr Glu Arg Ile Asp Glu Lys Val Ala His Leu Glu Arg Leu
 50 55 60
 Leu Gln Phe Phe Val Glu Cys Val Asn Glu Ile Asp Gln Tyr Leu Leu
 65 70 75 80
 45 Ser Glu Gly

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 752 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

55 (A) NAME/KEY: -

(B) LOCATION: 1..752

(D) OTHER INFORMATION: / Ceres Seq. ID 1388519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

60 aatctcacgc gctttcatca tcttcttctt agattcgctc ctccactatt cgaaaaaatg 60
 gcgaaactgg tgatgttggt ggttctctgt atcttaccgg cgatagccat ggcggaagg 120
 aggggaaata ttggaaagaa tacaatggtg gttcaaggta gcacctactg tgacatttgc 180
 aaattcggct tcgagactcc tgaatcctcc tacttcatcc ccggtgcaac ggtgaagcta 240

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tcatgcaaag acaggaagac aatggaagag gtttacacag acaaagctgt atcagacaaa 300
 gaaggaaagt ataagttcat tgtccacgac gatcacagag accagatgtg cgatgttttg 360
 cttgtgaaaa gctcggataa aacctgctct aaaatctccg ttggacgtga gaagtctcgt 420
 gtgatcttga accattacag tggcattgcc tcgcagatca gacatgctaa caacatggga 480
 5 tttgagaaag aagtgaagtga tgtgttctgc tctgctttgt ttcagaagta tatggttgat 540
 gaagatgagg atgatattaa aaaccatctc taatctctct gtttaattct atgatctgct 600
 gttttcttca ttaatgagtt tccagttatg gaagagatat atttgtattt gtttgattac 660
 ttatttggtg tctttagaga tgttgactct ggtgatcggg taactatctg tttgtgtaag 720
 cttcttatat attgatgtgt catttccttg cc

10 (2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..190

20 (D) OTHER INFORMATION: / Ceres Seq. ID 1388520

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Asn Leu Thr Arg Phe His His Leu Leu Pro Arg Phe Ala Pro Pro Leu
 1 5 10 15
 Phe Glu Lys Met Ala Lys Leu Val Met Leu Leu Val Leu Cys Ile Leu
 25 20 25 30
 Pro Ala Ile Ala Met Ala Ala Arg Arg Gly Asn Ile Gly Lys Asn Thr
 35 40 45
 Met Val Val Gln Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe
 50 55 60
 30 Glu Thr Pro Glu Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu
 65 70 75 80
 Ser Cys Lys Asp Arg Lys Thr Met Glu Glu Val Tyr Thr Asp Lys Ala
 85 90 95
 Val Ser Asp Lys Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His
 35 100 105 110
 Arg Asp Gln Met Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr
 115 120 125
 Cys Ser Lys Ile Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn
 130 135 140
 40 His Tyr Ser Gly Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly
 145 150 155 160
 Phe Glu Lys Glu Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys
 165 170 175
 Tyr Met Val Asp Glu Asp Glu Asp Asp Ile Lys Asn His Leu
 45 180 185 190

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

50 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

55 (B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1388521

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Met Ala Lys Leu Val Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile
 1 5 10 15
 60 Ala Met Ala Ala Arg Arg Gly Asn Ile Gly Lys Asn Thr Met Val Val
 20 25 30
 Gln Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro

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35 40 45
 Glu Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys
 50 55 60
 Asp Arg Lys Thr Met Glu Val Tyr Thr Asp Lys Ala Val Ser Asp
 5 65 70 75 80
 Lys Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln
 85 90 95
 Met Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys
 100 105 110
 10 Ile Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser
 115 120 125
 Gly Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys
 130 135 140
 Glu Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val
 15 145 150 155 160
 Asp Glu Asp Glu Asp Asp Ile Lys Asn His Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1388522

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

30 Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile Ala Met Ala Ala Arg
 1 5 10 15
 Arg Gly Asn Ile Gly Lys Asn Thr Met Val Val Gln Gly Ser Thr Tyr
 20 25 30
 Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu Ser Ser Tyr Phe
 35 35 40 45
 Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp Arg Lys Thr Met
 50 55 60
 Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys Glu Gly Lys Tyr
 65 70 75 80
 40 Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met Cys Asp Val Leu
 85 90 95
 Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile Ser Val Gly Arg
 100 105 110
 Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly Ile Ala Ser Gln
 45 115 120 125
 Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu Val Ser Asp Val
 130 135 140
 Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp Glu Asp Glu Asp
 145 150 155 160
 50 Asp Ile Lys Asn His Leu
 165

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 658 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

60 (A) NAME/KEY: -

(B) LOCATION: 1..658

(D) OTHER INFORMATION: / Ceres Seq. ID 1388563

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

aagaagtttt ctctacatcc acaaaagaaa aaaagtttcc caaaaaacaa aaacttacac 60
 aagtttagat atggatcttg aattactaca agatttggtcc aaattcaatt tcccaacacc 120
 catcaagatc cgatccaaaa cctcaaaaga caaagaagga cgaagggtgat gacgacgaag 180
 5 atgacctcag ctgcagcaca cccacatccc aagaacacaa gattcccgcc gtcatagact 240
 ctccacctcc tccgccgaga aaaccccggc caccaccgtc agcaccgtcg gctacggcgg 300
 ctctgatgat cagatcgtgc aagaggaagc ttttagtggtc gacttggtgag ataatcatga 360
 atcgggaaga gattgaccgt ttcttctcct ccgtctacaa tgagacgtcg actacggcta 420
 aacggcggag aagttaccct tattgttctc gaagatgagg cttaattcaa tatttacatt 480
 10 tttttacagt ttactggaa atattgtgaa attaattatc tgttggtggt cggttttaaa 540
 tatttttaat ttagttatga atatggatgg ataattttct gcaaccgcgc atattaattt 600
 cgcattggagg ggtcgtatgtt gtaaattgag taataaatga aatttaattc caattgcc

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1388564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

25 Arg Ser Phe Leu Tyr Ile His Lys Arg Lys Lys Val Ser Gln Lys Thr
 1 5 10 15
 Lys Thr Tyr Thr Ser Leu Asp Met Asp Leu Glu Leu Leu Gln Asp Leu
 20 25 30
 Ser Lys Phe Asn Phe Pro Thr Pro Ile Lys Ile Arg Ser Lys Thr Ser
 30 35 40 45
 Lys Asp Lys Glu Gly Arg Arg
 50 55

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 50 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 1388565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

45 Met Ile Arg Ser Cys Lys Arg Lys Leu Leu Val Ser Thr Cys Glu Ile
 1 5 10 15
 Ile Met Asn Arg Glu Glu Ile Asp Arg Phe Phe Ser Ser Val Tyr Asn
 20 25 30
 Glu Thr Ser Thr Thr Ala Lys Arg Arg Arg Ser Tyr Pro Tyr Cys Ser
 50 35 40 45
 Arg Arg
 50

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..39

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(D) OTHER INFORMATION: / Ceres Seq. ID 1388566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Met Arg Leu Asn Ser Ile Phe Thr Phe Phe Tyr Ser Phe Thr Gly Asn
 1 5 10 15
 5 Ile Val Lys Leu Ile Ile Cys Trp Cys Ser Val Leu Asn Ile Phe Asn
 20 25 30
 Leu Val Met Asn Met Asp Gly
 35

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 866 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..866

(D) OTHER INFORMATION: / Ceres Seq. ID 1388793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

aacggtgtgg gctaattctca cgcgctttca tcatcttctt cctagattcg ctccctccact 60
 gtcttaaatt tcactatctt cttcttcatt ttccttcctt ctcaacttcaa atccataatc 120
 gctctacttc tctctctctc tagattcgaa aaaatggcga aactggatgat gttgttggtt 180
 ctctgtatct taccggcgat agccatggcg gcaaggaggg gaaatattgg aaagaatata 240
 25 atggtgggtt aaggtagcac ctactgtgac atttgcaaat tcggcttcga gactcctgaa 300
 tcctcctact tcatccccgg tgcaacgggtg aagctatcat gcaaagacag gaagacaatg 360
 gaagagggtt acacagacaa agctgtatca gacaaagaag gaaagtataa gttcattgtc 420
 cacgacgatc acagagacca gatgtgcatg gttttgcttg tgaaaagctc ggataaaaacc 480
 tgctctaaaa tctccgttgg acgtgagaag tctcgtgtga tcttgaacca ttacagtggc 540
 30 attgcctcgc agatcagaca tgctaacaac atgggatttg agaaagaagt gagtgatgtg 600
 ttctgctctg ctttgtttca gaagtatatg gttgatgaag atgaggatga tattaataaac 660
 catctctaatt ctctctgttt aatcttatga tctgctgttt tcttcattaa tgagtttcga 720
 gttatggaag agatatattt gtatttgttt gattacttat ttgttgtctt tagagatgtt 780
 gactctggtg atcggataac tatctgtttg tgtaagcttc ttatatattg atatgtcatt 840
 35 tccttgctta ggaagtgtct tttatt

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1388794

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Met Ala Lys Leu Val Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile
 1 5 10 15
 50 Ala Met Ala Ala Arg Arg Gly Asn Ile Gly Lys Asn Thr Met Val Val
 20 25 30
 Gln Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro
 35 40 45
 55 Glu Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys
 50 55 60
 Asp Arg Lys Thr Met Glu Val Tyr Thr Asp Lys Ala Val Ser Asp
 65 70 75 80
 Lys Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln
 85 90 95
 60 Met Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys
 100 105 110
 Ile Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser

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115 120 125
 Gly Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys
 130 135 140
 Glu Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val
 5 145 150 155 160
 Asp Glu Asp Glu Asp Asp Ile Lys Asn His Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1388795

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

20 Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile Ala Met Ala Ala Arg
 1 5 10 15
 Arg Gly Asn Ile Gly Lys Asn Thr Met Val Val Gln Gly Ser Thr Tyr
 20 25 30
 Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu Ser Ser Tyr Phe
 25 35 40 45
 Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp Arg Lys Thr Met
 50 55 60
 Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys Glu Gly Lys Tyr
 65 70 75 80
 30 Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met Cys Asp Val Leu
 85 90 95
 Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile Ser Val Gly Arg
 100 105 110
 Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly Ile Ala Ser Gln
 35 115 120 125
 Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu Val Ser Asp Val
 130 135 140
 Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp Glu Asp Glu Asp
 145 150 155 160
 40 Asp Ile Lys Asn His Leu
 165

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1388796

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

55 Met Ala Ala Arg Arg Gly Asn Ile Gly Lys Asn Thr Met Val Val Gln
 1 5 10 15
 Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu
 20 25 30
 Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp
 35 40 45
 60 Arg Lys Thr Met Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys
 50 55 60
 Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met


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65              70              75              80
Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile
      85              90              95
5  Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly
      100             105             110
Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu
      115             120             125
Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp
      130             135             140
10 Glu Asp Glu Asp Asp Ile Lys Asn His Leu
     145             150
(2) INFORMATION FOR SEQ ID NO:199:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 533 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: DNA (genomic)
    (ix) FEATURE:
        (A) NAME/KEY: -
        (B) LOCATION: 1..533
        (D) OTHER INFORMATION: / Ceres Seq. ID 1392041
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:
25 aaccataaca caaatacacc aaaaaaaaaa aaacagaaag taacatgaga tctctcttat          60
   tagccgtgtg cctggttctt gctttacact gcggtgaagc agccgtgtct tgcaaacacgg          120
   tgattgcgga tctttaccct tgcttatcct acgtgactca gggcggaagg gtcccaacct          180
   tctgctgcaa cggtctcacac acactcaaga gtcagggtca aacttctgtg gaccgtcagg          240
   ggggtctgtcg ttgcatcaaa tctgctattg gaggactcac tctctctcct agaaccatcc          300
   aaaatgcttt ggaattgcct tctaaatgtg gtgtcgatct cccttaacaag ttcagccctt          360
30 ccactgactg cgacagtatc cagttagaca agcagaaaat cttaaaggaa gctactacaa          420
   gaactataat aacctataaa ttaataaatg agggcatttg tttgctagtt gctaattgat          480
   cagtgatgta ttgtcatttt gaatgttcta atatcagcag gcacttatct ctg
(2) INFORMATION FOR SEQ ID NO:200:
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 113 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: peptide
    (ix) FEATURE:
        (A) NAME/KEY: peptide
        (B) LOCATION: 1..113
        (D) OTHER INFORMATION: / Ceres Seq. ID 1392042
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:
45 Met Arg Ser Leu Leu Leu Ala Val Cys Leu Val Leu Ala Leu His Cys
     1           5           10           15
Gly Glu Ala Ala Val Ser Cys Asn Thr Val Ile Ala Asp Leu Tyr Pro
      20           25           30
50 Cys Leu Ser Tyr Val Thr Gln Gly Gly Pro Val Pro Thr Leu Cys Cys
     35           40           45
Asn Gly Leu Thr Thr Leu Lys Ser Gln Ala Gln Thr Ser Val Asp Arg
     50           55           60
Gln Gly Val Cys Arg Cys Ile Lys Ser Ala Ile Gly Gly Leu Thr Leu
     65           70           75           80
55 Ser Pro Arg Thr Ile Gln Asn Ala Leu Glu Leu Pro Ser Lys Cys Gly
      85           90           95
Val Asp Leu Pro Tyr Lys Phe Ser Pro Ser Thr Asp Cys Asp Ser Ile
      100            105            110
Gln
60
(2) INFORMATION FOR SEQ ID NO:201:
    (i) SEQUENCE CHARACTERISTICS:
```

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(A) LENGTH: 1028 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..1028
 (D) OTHER INFORMATION: / Ceres Seq. ID 1393342

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

```

aatatgtcct taattgctct tatcggagaa ggcttactct gtttttcagg cgaactctgt      60
ttatcttctc cgagctcgta cgagaatatt cgtaaagggt tcttgtagac ttaaaccgatg      120
agtacccttg agaccacaag agctgagctt ggtctggtag ttgtgtattt gaataaagcg      180
gaggcgagag acaagatttg tcgagctatt caatatgggt ccaagttctt gagtgatggc      240
15 caacctggca ctgctcaaaa tgtcgacaag aacaccagct tggctaggaa agttttccgt      300
ctcttcaagt ttgtaaataga tcttcatgct ctcatagacc ctgttcccaa agggactcca      360
ctcccgttg ttctgctcgg aaagtctaaa aacgcgttgc tgtcaacgtt cttgttcccta      420
gatcaaattg tgtggcttgg caggactggg atttacaagg acaaagaacg tgctgagatt      480
cttgagcgta tatcactttt ctggttgatg ggttcttcgg ttgacacatc cttggttgag      540
20 gttggggagc ttggtaggct gtcagcatca attaagaagt tagaaaaaga gatagggaac      600
aaggataaac accagaatga gcaataccgt gcaaaagtag agaaatcaaa cgagagggtca      660
ttggctctga tcaaagcagg gatggatgta gttgttgctt tcggattgct tcaattggct      720
ccaaagaaga tcactccccg agtcacaggt gcttctcgat tcgcctcatc acttatctct      780
tggtatcagc tattgccgct acatcccaag tccaagatgg tctgataaaa gggaacaacg      840
25 gaaaggcgaa ctagtttcat tgtccacatg ttccatatat agtttgtgtc tgttttacta      900
ttacttggtg ttaaatttgt cttgcttgac tactttaatg tttgtgtag attctatggt      960
atataagata atgataaaca ttgcagtctc tgtagaataa taagaacaga taagcattac      1020
gaggtgtc

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(2) INFORMATION FOR SEQ ID NO:202:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide
 (B) LOCATION: 1..235
 (D) OTHER INFORMATION: / Ceres Seq. ID 1393343

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

```

Met Ser Thr Leu Glu Thr Thr Arg Ala Glu Leu Gly Leu Val Val Val
1      5      10      15
Tyr Leu Asn Lys Ala Glu Ala Arg Asp Lys Ile Cys Arg Ala Ile Gln
      20      25      30
45 Tyr Gly Ser Lys Phe Leu Ser Asp Gly Gln Pro Gly Thr Ala Gln Asn
      35      40      45
Val Asp Lys Asn Thr Ser Leu Ala Arg Lys Val Phe Arg Leu Phe Lys
      50      55      60
Phe Val Asn Asp Leu His Ala Leu Ile Ser Pro Val Pro Lys Gly Thr
50 65      70      75      80
Pro Leu Pro Leu Val Leu Leu Gly Lys Ser Lys Asn Ala Leu Leu Ser
      85      90      95
Thr Phe Leu Phe Leu Asp Gln Ile Val Trp Leu Gly Arg Thr Gly Ile
      100     105     110
55 Tyr Lys Asp Lys Glu Arg Ala Glu Ile Leu Gly Arg Ile Ser Leu Phe
      115     120     125
Cys Trp Met Gly Ser Ser Val Cys Thr Ser Leu Val Glu Val Gly Glu
      130     135     140
60 Leu Gly Arg Leu Ser Ala Ser Ile Lys Lys Leu Glu Lys Glu Ile Gly
      145     150     155     160
Asn Lys Asp Lys His Gln Asn Glu Gln Tyr Arg Ala Lys Val Glu Lys
      165     170     175

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Ser Asn Glu Arg Ser Leu Ala Leu Ile Lys Ala Gly Met Asp Val Val
 180 185 190
 Val Ala Phe Gly Leu Leu Gln Leu Ala Pro Lys Lys Val Thr Pro Arg
 195 200 205
 5 Val Thr Gly Ala Phe Gly Phe Ala Ser Ser Leu Ile Ser Cys Tyr Gln
 210 215 220
 Leu Leu Pro Ser His Pro Lys Ser Lys Met Val
 225 230 235

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 653 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..653

(D) OTHER INFORMATION: / Ceres Seq. ID 1393556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

tcttcccaat cccaacagct tcatcggttt atcttccaat caaagcagct caaatcaagc 60
 tcgcaaagat gatgcacatg accttctact gggaatcaa agccacaatt ctcttcgatt 120
 tctggaatac tgactcatgg cttagtata tctcacttt aatcgcttgc ttcgtcttct 180
 ccgctttcta tcaatacctc gagaatcgcc gcatccaatt caaatccctt tcttcctccc 240
 25 gtcgtgctcc tccaccgcct cgctcttctt ccggcgtctc cgcgctctt atccctaaat 300
 ccggtaccag atccgccgct aaagctgctt cgggtcttct ttcggcgctc aacgcagcga 360
 tcggttactt gctgatgctt gcagctatgt ctttcaacgg aggtgttttc atcgcgattg 420
 tcgtcggtt aaccgccgga tacgctgttt ttagatctga tgacggcggt gctgataccg 480
 ccacggatga tccatgtcca tgtgcttgat aatgattgat aataaaatca aaatcgga 540
 30 aatctcaaaa aaggtgtgtt tgataattga tgtttgtatt gttgtttgtt tctgtatgat 600
 tagttgcttt gtaacaaaat aatccaatct aaatgtgttt cttgagtata tgc

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 1393557

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Phe Pro Ile Pro Thr Ala Ser Ser Phe Tyr Leu Pro Ile Lys Ala Ala
 1 5 10 15
 Gln Ile Lys Leu Ala Lys Met Met His Met Thr Phe Tyr Trp Gly Ile
 20 25 30
 Lys Ala Thr Ile Leu Phe Asp Phe Trp Lys Thr Asp Ser Trp Leu Ser
 35 40 45
 50 Tyr Ile Leu Thr Leu Ile Ala Cys Phe Val Phe Ser Ala Phe Tyr Gln
 50 55 60
 Tyr Leu Glu Asn Arg Arg Ile Gln Phe Lys Ser Leu Ser Ser Ser Arg
 65 70 75 80
 Arg Ala Pro Pro Pro Pro Arg Ser Ser Ser Gly Val Ser Ala Pro Leu
 85 90 95
 55 Ile Pro Lys Ser Gly Thr Arg Ser Ala Lys Ala Ala Ser Val Leu
 100 105 110
 Leu Phe Gly Val Asn Ala Ala Ile Gly Tyr Leu Leu Met Leu Ala Ala
 115 120 125
 60 Met Ser Phe Asn Gly Gly Val Phe Ile Ala Ile Val Val Gly Leu Thr
 130 135 140
 Ala Gly Tyr Ala Val Phe Arg Ser Asp Asp Gly Gly Ala Asp Thr Ala

420

145 150 155 160
Thr Asp Asp Pro Cys Pro Cys Ala
 165

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1393558

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Met Met His Met Thr Phe Tyr Trp Gly Ile Lys Ala Thr Ile Leu Phe
1 5 10 15

Asp Phe Trp Lys Thr Asp Ser Trp Leu Ser Tyr Ile Leu Thr Leu Ile
20 25 30

Ala Cys Phe Val Phe Ser Ala Phe Tyr Gln Tyr Leu Glu Asn Arg Arg
35 40 45

Ile Gln Phe Lys Ser Leu Ser Ser Ser Arg Arg Ala Pro Pro Pro Pro
50 55 60

Arg Ser Ser Ser Gly Val Ser Ala Pro Leu Ile Pro Lys Ser Gly Thr
65 70 75 80

Arg Ser Ala Ala Lys Ala Ala Ser Val Leu Leu Phe Gly Val Asn Ala
85 90 95

Ala Ile Gly Tyr Leu Leu Met Leu Ala Ala Met Ser Phe Asn Gly Gly
100 105 110

Val Phe Ile Ala Ile Val Val Gly Leu Thr Ala Gly Tyr Ala Val Phe
115 120 125

Arg Ser Asp Asp Gly Gly Ala Asp Thr Ala Thr Asp Asp Pro Cys Pro
130 135 140

Cys Ala

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 1393559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met His Met Thr Phe Tyr Trp Gly Ile Lys Ala Thr Ile Leu Phe Asp
1 5 10 15

Phe Trp Lys Thr Asp Ser Trp Leu Ser Tyr Ile Leu Thr Leu Ile Ala
20 25 30

Cys Phe Val Phe Ser Ala Phe Tyr Gln Tyr Leu Glu Asn Arg Arg Ile
35 40 45

Gln Phe Lys Ser Leu Ser Ser Ser Arg Arg Ala Pro Pro Pro Pro Arg
50 55 60

Ser Ser Ser Gly Val Ser Ala Pro Leu Ile Pro Lys Ser Gly Thr Arg
65 70 75 80

Ser Ala Ala Lys Ala Ala Ser Val Leu Leu Phe Gly Val Asn Ala Ala
85 90 95

Ile Gly Tyr Leu Leu Met Leu Ala Ala Met Ser Phe Asn Gly Gly Val
100 105 110

Phe Ile Ala Ile Val Val Gly Leu Thr Ala Gly Tyr Ala Val Phe Arg

421

115 120 125
 Ser Asp Asp Gly Gly Ala Asp Thr Ala Thr Asp Asp Pro Cys Pro Cys
 130 135 140

Ala
 145

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 525 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..525

(D) OTHER INFORMATION: / Ceres Seq. ID 1396782

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

atgatttttta cagacgagag gagacggcga caatggcgaa tttgatgatg agattaccaa 60
 ttagcttgag aagcttctct gtttcagctt cttcatccaa cggttcgccg ccggtgatcg 120
 gaggatctag cggcggtgta ggaccgatga ttgtggaatt accggtggag aagatacgaa 180
 gaccgttgat gcgaaccaga tccaacgatc agaacaaagt gaaagagctt atggatagta 240
 tccgtcaaatt cggctcttcaa gttccgattg atgtgattga agttgatgga acttactatg 300
 ggttctcggg atgtcacaga tacgaggcgc atcagaagct aggtcttcca acaatacggt 360
 gcaaaatacg taaaggaaca aaggaaacat taaggcatca tcttcgctga agagagtttt 420
 acttttatgt atattgtttg tatgatagga actcgagtat gtgtatgaaa gttaagaata 480
 agaactttgt acaactttgt gatagattta gtgactggat tctgc

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1396783

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Asp Phe Tyr Arg Arg Glu Glu Thr Ala Thr Met Ala Asn Leu Met Met
 1 5 10 15
 Arg Leu Pro Ile Ser Leu Arg Ser Phe Ser Val Ser Ala Ser Ser Ser
 20 25 30
 Asn Gly Ser Pro Pro Val Ile Gly Gly Ser Ser Gly Gly Val Gly Pro
 35 40 45
 Met Ile Val Glu Leu Pro Leu Glu Lys Ile Arg Arg Pro Leu Met Arg
 50 55 60
 Thr Arg Ser Asn Asp Gln Asn Lys Val Lys Glu Leu Met Asp Ser Ile
 65 70 75 80
 Arg Gln Ile Gly Leu Gln Val Pro Ile Asp Val Ile Glu Val Asp Gly
 85 90 95
 Thr Tyr Tyr Gly Phe Ser Gly Cys His Arg Tyr Glu Ala His Gln Lys
 100 105 110
 Leu Gly Leu Pro Thr Ile Arg Cys Lys Ile Arg Lys Gly Thr Lys Glu
 115 120 125
 Thr Leu Arg His His Leu Arg
 130 135

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

422

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 1396784

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

Met Ala Asn Leu Met Met Arg Leu Pro Ile Ser Leu Arg Ser Phe Ser
 1 5 10 15
 Val Ser Ala Ser Ser Ser Asn Gly Ser Pro Pro Val Ile Gly Gly Ser
 20 25 30
 Ser Gly Gly Val Gly Pro Met Ile Val Glu Leu Pro Leu Glu Lys Ile
 35 40 45
 Arg Arg Pro Leu Met Arg Thr Arg Ser Asn Asp Gln Asn Lys Val Lys
 50 55 60
 Glu Leu Met Asp Ser Ile Arg Gln Ile Gly Leu Gln Val Pro Ile Asp
 65 70 75 80
 Val Ile Glu Val Asp Gly Thr Tyr Tyr Gly Phe Ser Gly Cys His Arg
 85 90 95
 Tyr Glu Ala His Gln Lys Leu Gly Leu Pro Thr Ile Arg Cys Lys Ile
 100 105 110
 Arg Lys Gly Thr Lys Glu Thr Leu Arg His His Leu Arg
 115 120 125

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1396785

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

Met Met Arg Leu Pro Ile Ser Leu Arg Ser Phe Ser Val Ser Ala Ser
 1 5 10 15
 Ser Ser Asn Gly Ser Pro Pro Val Ile Gly Gly Ser Ser Gly Gly Val
 20 25 30
 Gly Pro Met Ile Val Glu Leu Pro Leu Glu Lys Ile Arg Arg Pro Leu
 35 40 45
 Met Arg Thr Arg Ser Asn Asp Gln Asn Lys Val Lys Glu Leu Met Asp
 50 55 60
 Ser Ile Arg Gln Ile Gly Leu Gln Val Pro Ile Asp Val Ile Glu Val
 65 70 75 80
 Asp Gly Thr Tyr Tyr Gly Phe Ser Gly Cys His Arg Tyr Glu Ala His
 85 90 95
 Gln Lys Leu Gly Leu Pro Thr Ile Arg Cys Lys Ile Arg Lys Gly Thr
 100 105 110
 Lys Glu Thr Leu Arg His His Leu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 939 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..939

(D) OTHER INFORMATION: / Ceres Seq. ID 1396802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

423

ataacaaacc agggtcaggg ttttatcttc catattcttt tcccaactgat tcttacaatc 60
 gatctaaggg aatctacgaa ctgtttggta atttctgggtg ggaaaagtct tgatcttgct 120
 gtttgggttg gagtaatggt gaggcttggtg tttgttggtg gctcaccggg gatggactct 180
 tcgagcagtc catgttttatg tctggatgct cacacgacgg gtaccatcag gaggaagaag 240
 5 atccttgcca aagcaagaaa tctggaatta ggaagctctt tcaactggctc acgcattggt 300
 tttaggcttt ctccgaagcg tgtatcgaga attgcgaatc gaaagagcaa aaagctcttg 360
 attgtgaatg aggatgttgc tggtaattac gacgatacct tcggtgatgt acaaaagcaa 420
 attgttaatt attttacata caaagctgtg aggacggttc ttcacagct gtacgaaatg 480
 aatcctcctc aatacacttg gttctataat catatcataa caaacagacc gacggatggc 540
 10 aaacgtttcc tccgtgccct cggcaaggag agtcaggagc ttgcagaaag agtgatgatc 600
 acgcgtcttc acttgatggt caaatggatc aagaaatgcg accatgggaa gatataccag 660
 gaaatatcgg atgaaaactt ggcgttgatg cgtgaacgac tgatggagac cgtgatattg 720
 ccttccgatg acacaaactc aaggtaatag gctgaagaag acagcgacac ccacagcaca 780
 acatttgctt tgtcaatttg cttctcagtt tttaggactt cgagtttttt agtttgatta 840
 15 catattacta tagtgaaaga gcagtgtgta tatgatgtct attcttgcca tgtactatat 900
 gatattaggg gcaaaaaaca acacccttct tgtgctcct

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 248 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25 (A) NAME/KEY: peptide
 (B) LOCATION: 1..248

(D) OTHER INFORMATION: / Ceres Seq. ID 1396803

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

30 Ile Thr Asn Gln Gly Gln Gly Phe Ile Phe His Ile Leu Phe Pro Leu
 1 5 10 15
 Ile Leu Thr Ile Asp Leu Arg Glu Ser Thr Asn Cys Leu Val Ile Ser
 20 25 30
 Gly Gly Lys Ser Leu Asp Leu Ala Val Trp Phe Gly Val Met Val Ser
 35 35 40 45
 Ala Trp Phe Val Val Gly Ser Pro Val Met Asp Ser Ser Ser Ser Pro
 50 55 60
 Cys Leu Cys Leu Asp Ala His Thr Thr Gly Thr Ile Arg Arg Lys Lys
 65 70 75 80
 40 Ile Leu Gly Lys Ala Arg Asn Leu Glu Leu Gly Ser Ser Phe Thr Gly
 85 90 95
 Ser Arg Ile Val Phe Arg Leu Ser Pro Lys Arg Val Ser Arg Ile Ala
 100 105 110
 Asn Arg Lys Ser Lys Lys Leu Leu Ile Val Asn Glu Asp Val Ala Gly
 115 120 125
 45 Asn Tyr Asp Asp Thr Phe Gly Asp Val Gln Lys Gln Ile Val Asn Tyr
 130 135 140
 Phe Thr Tyr Lys Ala Val Arg Thr Val Leu His Gln Leu Tyr Glu Met
 145 150 155 160
 50 Asn Pro Pro Gln Tyr Thr Trp Phe Tyr Asn His Ile Ile Thr Asn Arg
 165 170 175
 Pro Thr Asp Gly Lys Arg Phe Leu Arg Ala Leu Gly Lys Glu Ser Gln
 180 185 190
 Glu Leu Ala Glu Arg Val Met Ile Thr Arg Leu His Leu Tyr Gly Lys
 195 200 205
 55 Trp Ile Lys Lys Cys Asp His Gly Lys Ile Tyr Gln Glu Ile Ser Asp
 210 215 220
 Glu Asn Leu Ala Leu Met Arg Glu Arg Leu Met Glu Thr Val Ile Trp
 225 230 235 240
 Pro Ser Asp Asp Thr Asn Ser Arg
 60 245

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:

424

(A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..203
 (D) OTHER INFORMATION: / Ceres Seq. ID 1396804

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Met	Val	Ser	Ala	Trp	Phe	Val	Val	Gly	Ser	Pro	Val	Met	Asp	Ser	Ser
1				5					10					15	
Ser	Ser	Pro	Cys	Leu	Cys	Leu	Asp	Ala	His	Thr	Thr	Gly	Thr	Ile	Arg
			20					25					30		
15	Arg	Lys	Lys	Ile	Leu	Gly	Lys	Ala	Arg	Asn	Leu	Glu	Leu	Gly	Ser
			35					40					45		
Phe	Thr	Gly	Ser	Arg	Ile	Val	Phe	Arg	Leu	Ser	Pro	Lys	Arg	Val	Ser
			50				55				60				
20	Arg	Ile	Ala	Asn	Arg	Lys	Ser	Lys	Lys	Leu	Leu	Ile	Val	Asn	Glu
						70				75					80
Val	Ala	Gly	Asn	Tyr	Asp	Asp	Thr	Phe	Gly	Asp	Val	Gln	Lys	Gln	Ile
				85				90						95	
Val	Asn	Tyr	Phe	Thr	Tyr	Lys	Ala	Val	Arg	Thr	Val	Leu	His	Gln	Leu
			100					105					110		
25	Tyr	Glu	Met	Asn	Pro	Pro	Gln	Tyr	Thr	Trp	Phe	Tyr	Asn	His	Ile
			115					120					125		
Thr	Asn	Arg	Pro	Thr	Asp	Gly	Lys	Arg	Phe	Leu	Arg	Ala	Leu	Gly	Lys
			130			135				140					
30	Glu	Ser	Gln	Glu	Leu	Ala	Glu	Arg	Val	Met	Ile	Thr	Arg	Leu	His
						150				155					160
Tyr	Gly	Lys	Trp	Ile	Lys	Lys	Cys	Asp	His	Gly	Lys	Ile	Tyr	Gln	Glu
				165				170						175	
Ile	Ser	Asp	Glu	Asn	Leu	Ala	Leu	Met	Arg	Glu	Arg	Leu	Met	Glu	Thr
			180					185					190		
35	Val	Ile	Trp	Pro	Ser	Asp	Asp	Thr	Asn	Ser	Arg				
			195					200							

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..191
 (D) OTHER INFORMATION: / Ceres Seq. ID 1396805

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met	Asp	Ser	Ser	Ser	Ser	Pro	Cys	Leu	Cys	Leu	Asp	Ala	His	Thr	Thr
1					5				10					15	
Gly	Thr	Ile	Arg	Arg	Lys	Lys	Ile	Leu	Gly	Lys	Ala	Arg	Asn	Leu	Glu
			20					25					30		
Leu	Gly	Ser	Ser	Phe	Thr	Gly	Ser	Arg	Ile	Val	Phe	Arg	Leu	Ser	Pro
			35				40					45			
55	Lys	Arg	Val	Ser	Arg	Ile	Ala	Asn	Arg	Lys	Ser	Lys	Lys	Leu	Ile
			50				55					60			
Val	Asn	Glu	Asp	Val	Ala	Gly	Asn	Tyr	Asp	Asp	Thr	Phe	Gly	Asp	Val
			65			70				75					80
Gln	Lys	Gln	Ile	Val	Asn	Tyr	Phe	Thr	Tyr	Lys	Ala	Val	Arg	Thr	Val
				85				90						95	
60	Leu	His	Gln	Leu	Tyr	Glu	Met	Asn	Pro	Pro	Gln	Tyr	Thr	Trp	Phe
				100				105						110	

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Asn His Ile Ile Thr Asn Arg Pro Thr Asp Gly Lys Arg Phe Leu Arg
 115 120 125
 Ala Leu Gly Lys Glu Ser Gln Glu Leu Ala Glu Arg Val Met Ile Thr
 130 135 140
 5 Arg Leu His Leu Tyr Gly Lys Trp Ile Lys Lys Cys Asp His Gly Lys
 145 150 155 160
 Ile Tyr Gln Glu Ile Ser Asp Glu Asn Leu Ala Leu Met Arg Glu Arg
 165 170 175
 10 Leu Met Glu Thr Val Ile Trp Pro Ser Asp Asp Thr Asn Ser Arg
 180 185 190
 (2) INFORMATION FOR SEQ ID NO:215:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 753 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..753
 (D) OTHER INFORMATION: / Ceres Seq. ID 1397130
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:
 aaagatttgg agaaaaagtt tactaaaaaa gaatctgggg aagtaagtga gatgaaggaa 60
 gaggaggaga tcggaaaacc agcgaaacca aaagccaaga aagatgttgc tcctgggagg 120
 25 ttgattgata cctatgctgc acagtgcgat aactgtcaca agtggagggt gattgatagc 180
 caggaggaat atgaagatat cagaagtaaa atgctcgagg atccttttaa ctgtcagaag 240
 aaacagggca tgtcttgtga agagcctgct gatattgact acgattcttc tcggacttgg 300
 gtcattgaca agcctggtct ccccaaaacg cctaaagggt tcaagagaag cttagttctc 360
 agaaaagatt actctaagat ggatacctac tactttactc ctaccgggaa gaagctcagg 420
 30 agtcgcaatg aaatcgctgc cttcggttga gccaatccgg aattcaggaa cgcaccactt 480
 ggagacttca atttcactgt cccaagggtc atggaagata ctgttcccc tgatccgaag 540
 cttggctctc cttttccaag cactactacc actacttcag agaagagcag tgtcaagcag 600
 agccataact aatatgttct cttctccggg cttttttcta ctttctttct gctccctaaa 660
 gcaatgcgtt ttgagtcctt atagatttga tgttctctaa aactgttatg atattaacat 720
 35 ctctaagcaa aaaaatatga tctttgtct ctc
 (2) INFORMATION FOR SEQ ID NO:216:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 40 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..203
 (D) OTHER INFORMATION: / Ceres Seq. ID 1397131
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:
 Lys Asp Leu Glu Lys Lys Phe Thr Lys Lys Glu Ser Gly Glu Val Ser
 1 5 10 15
 50 Glu Met Lys Glu Glu Glu Glu Ile Gly Lys Pro Ala Lys Pro Lys Ala
 20 25 30
 Lys Lys Asp Val Ala Pro Gly Arg Leu Ile Asp Thr Tyr Ala Ala Gln
 35 40 45
 55 Cys Asp Asn Cys His Lys Trp Arg Val Ile Asp Ser Gln Glu Glu Tyr
 50 55 60
 Glu Asp Ile Arg Ser Lys Met Leu Glu Asp Pro Phe Asn Cys Gln Lys
 65 70 75 80
 Lys Gln Gly Met Ser Cys Glu Glu Pro Ala Asp Ile Asp Tyr Asp Ser
 85 90 95
 60 Ser Arg Thr Trp Val Ile Asp Lys Pro Gly Leu Pro Lys Thr Pro Lys
 100 105 110
 Gly Phe Lys Arg Ser Leu Val Leu Arg Lys Asp Tyr Ser Lys Met Asp

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115 120 125
 Thr Tyr Phe Thr Pro Thr Gly Lys Lys Leu Arg Ser Arg Asn Glu
 130 135 140
 5 Ile Ala Ala Phe Val Glu Ala Asn Pro Glu Phe Arg Asn Ala Pro Leu
 145 150 155 160
 Gly Asp Phe Asn Phe Thr Val Pro Lys Val Met Glu Asp Thr Val Pro
 165 170 175
 Pro Asp Pro Lys Leu Gly Ser Pro Phe Pro Ser Thr Thr Thr Thr Thr
 180 185 190
 10 Ser Glu Lys Ser Ser Val Lys Gln Ser His Asn
 195 200

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 186 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20 (A) NAME/KEY: peptide

(B) LOCATION: 1..186

(D) OTHER INFORMATION: / Ceres Seq. ID 1397132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

25 Met Lys Glu Glu Glu Glu Ile Gly Lys Pro Ala Lys Pro Lys Ala Lys
 1 5 10 15
 Lys Asp Val Ala Pro Gly Arg Leu Ile Asp Thr Tyr Ala Ala Gln Cys
 20 25 30
 Asp Asn Cys His Lys Trp Arg Val Ile Asp Ser Gln Glu Tyr Glu
 35 40 45
 30 Asp Ile Arg Ser Lys Met Leu Glu Asp Pro Phe Asn Cys Gln Lys Lys
 50 55 60
 Gln Gly Met Ser Cys Glu Glu Pro Ala Asp Ile Asp Tyr Asp Ser Ser
 65 70 75 80
 Arg Thr Trp Val Ile Asp Lys Pro Gly Leu Pro Lys Thr Pro Lys Gly
 85 90 95
 35 Phe Lys Arg Ser Leu Val Leu Arg Lys Asp Tyr Ser Lys Met Asp Thr
 100 105 110
 Tyr Tyr Phe Thr Pro Thr Gly Lys Lys Leu Arg Ser Arg Asn Glu Ile
 115 120 125
 40 Ala Ala Phe Val Glu Ala Asn Pro Glu Phe Arg Asn Ala Pro Leu Gly
 130 135 140
 Asp Phe Asn Phe Thr Val Pro Lys Val Met Glu Asp Thr Val Pro Pro
 145 150 155 160
 Asp Pro Lys Leu Gly Ser Pro Phe Pro Ser Thr Thr Thr Thr Thr Ser
 165 170 175
 45 Glu Lys Ser Ser Val Lys Gln Ser His Asn
 180 185

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

55 (A) NAME/KEY: peptide

(B) LOCATION: 1..133

(D) OTHER INFORMATION: / Ceres Seq. ID 1397133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

60 Met Leu Glu Asp Pro Phe Asn Cys Gln Lys Lys Gln Gly Met Ser Cys
 1 5 10 15
 Glu Glu Pro Ala Asp Ile Asp Tyr Asp Ser Ser Arg Thr Trp Val Ile

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20 25 30
 Asp Lys Pro Gly Leu Pro Lys Thr Pro Lys Gly Phe Lys Arg Ser Leu
 35 40 45
 Val Leu Arg Lys Asp Tyr Ser Lys Met Asp Thr Tyr Tyr Phe Thr Pro
 50 55 60
 Thr Gly Lys Lys Leu Arg Ser Arg Asn Glu Ile Ala Ala Phe Val Glu
 65 70 75 80
 Ala Asn Pro Glu Phe Arg Asn Ala Pro Leu Gly Asp Phe Asn Phe Thr
 85 90 95
 Val Pro Lys Val Met Glu Asp Thr Val Pro Pro Asp Pro Lys Leu Gly
 100 105 110
 Ser Pro Phe Pro Ser Thr Thr Thr Thr Thr Ser Glu Lys Ser Ser Val
 115 120 125
 Lys Gln Ser His Asn
 130
 (2) INFORMATION FOR SEQ ID NO:219:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 784 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..784
 (D) OTHER INFORMATION: / Ceres Seq. ID 1398004
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:
 actcatcaac caaaacaaaa cataaaaaaa caagtggaag ctttaaaacg agaggggagag 60
 agcaaaaatg gcgacgtcgg gaacgtacgt gacggaagtt ccgctaaaag gatcggccga 120
 gaaatactac aagaggtgga agaacgagaa ccatgtcttc cctgatgcta tcggccacca 180
 catccaaaat gttaccgttc acgaaggcga acatgactct cacgggtcta tcaggagtgtg 240
 gaactacaca tgggatggaa aggaggaggt gttcaaggag agaagagaga tagacgatga 300
 gaccaaaccg ttgacgttaa gaggacttga gggtcacgtg atggagcagc tcaaagtgtg 360
 cgacgtcgtc taccaattca ttcccaaattc tgaggatacc tgcacgga aaatcacttt 420
 aatatgggag aagcgcaacg atgattcccc agaaccaagc ggctacataa aattcgtcaa 480
 gagcttgggt gctgacatgg gaaaccacgt tagcaaaact taatcatcat tcccacagtc 540
 gtcgtgctcg tcatcatcat catcatcatc atcatcatca tcatcatcat catcatcatc 600
 atcatcatca ctatctcgat ttataagtta agatgttttc agtataataa atgggggtctt 660
 gtggatcggt cattttctatg tgtaaacctg ttgggtctgt atgatgcttc gatataattgt 720
 tatgttcgat atcatatgtc gggttcgata taatgattct taagattaat ttactacaca 780
 tttc
 (2) INFORMATION FOR SEQ ID NO:220:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..151
 (D) OTHER INFORMATION: / Ceres Seq. ID 1398005
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:
 Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser
 1 5 10 15
 Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro
 20 25 30
 Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu
 35 40 45
 His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly
 50 55 60
 Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys

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	65		70		75		80
	Thr	Leu	Thr	Leu	Arg	Gly	Leu
					85		
	Val	Tyr	Asp	Val	Val	Tyr	Gln
5					100		
	Ile	Gly	Lys	Ile	Thr	Leu	Ile
					115		
	Glu	Pro	Ser	Gly	Tyr	Ile	Lys
					130		
10	Gly	Asn	His	Val	Ser	Lys	Thr
					145		

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..389

(D) OTHER INFORMATION: / Ceres Seq. ID 1399370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

25	aaaaactttt	tcagagtcg	aggtttcaga	cagagaggaa	gaagatgaag	cggacggtga	60
	tggacaacgc	gattcgatca	tcggtggtgg	tggtgggatc	attggccttt	ggttacttgt	120
	cactggagct	tggttacaag	cctttcccttg	aaaaggctga	acaatacgaa	agatctcttc	180
	agtcttctca	acaacatcaa	caacaagatg	aacaagaaga	agcgagggtg	gacaatagca	240
	atgtcgaggg	gtgggaggag	aaaaggtagt	cttataatcg	gtttcaatac	agacatatca	300
30	aagtgtgtaa	ggaagaagaa	ccttatcaaa	attttcttct	taatcaaccg	taagttcaat	360

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..88

(D) OTHER INFORMATION: / Ceres Seq. ID 1399371

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

	Lys	Leu	Phe	Gln	Ser	Arg	Arg	Phe	Gln	Thr	Glu	Arg	Lys	Lys	Met	Lys
	1				5					10					15	
45	Arg	Thr	Val	Met	Asp	Asn	Ala	Ile	Arg	Ser	Ser	Val	Val	Val	Leu	Gly
				20					25					30		
	Ser	Leu	Ala	Phe	Gly	Tyr	Leu	Ser	Leu	Glu	Leu	Gly	Tyr	Lys	Pro	Phe
			35				40					45				
50	Leu	Glu	Lys	Ala	Glu	Gln	Tyr	Glu	Arg	Ser	Leu	Gln	Ser	Ser	Gln	Gln
		50				55					60					
	His	Gln	Gln	Gln	Asp	Glu	Gln	Glu	Glu	Ala	Arg	Trp	Asp	Asn	Ser	Asn
	65				70				75					80		
	Val	Glu	Gly	Trp	Glu	Lys	Arg									
				85												

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

429

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1399372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

5 Met Lys Arg Thr Val Met Asp Asn Ala Ile Arg Ser Ser Val Val Val
 1 5 10 15
 Leu Gly Ser Leu Ala Phe Gly Tyr Leu Ser Leu Glu Leu Gly Tyr Lys
 20 25 30
 10 Pro Phe Leu Glu Lys Ala Glu Gln Tyr Glu Arg Ser Leu Gln Ser Ser
 35 40 45
 Gln Gln His Gln Gln Gln Asp Glu Gln Glu Glu Ala Arg Trp Asp Asn
 50 55 60
 Ser Asn Val Glu Gly Trp Glu Glu Lys Arg
 65 70

15 (2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

25 (D) OTHER INFORMATION: / Ceres Seq. ID 1399373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Met Asp Asn Ala Ile Arg Ser Ser Val Val Val Leu Gly Ser Leu Ala
 1 5 10 15
 Phe Gly Tyr Leu Ser Leu Glu Leu Gly Tyr Lys Pro Phe Leu Glu Lys
 30 20 25 30
 Ala Glu Gln Tyr Glu Arg Ser Leu Gln Ser Ser Gln Gln His Gln Gln
 35 40 45
 Gln Asp Glu Gln Glu Glu Ala Arg Trp Asp Asn Ser Asn Val Glu Gly
 50 55 60
 35 Trp Glu Glu Lys Arg
 65

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 745 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

45 (A) NAME/KEY: -

(B) LOCATION: 1..745

(D) OTHER INFORMATION: / Ceres Seq. ID 1425147

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

atttcttcgt ctctgtctcc aaaatcgaat caaaatctct aaagtttcaa tttttttgtt 60
 50 ctgttctttt ttttttttta aagaatggct tcaatttctg caactttgcc ttcgccattg 120
 ttactcacac agagaaaatc caatctcaca tcgattcaaa aactccatt ttctctaact 180
 cgaggtacga atgatctttc tccattatct ctactcgaa accctagcag catcagtcgt 240
 atggtgaaat ctagtggaga aagctcagat tcatcgactg atctcgacgt tgtagtacg 300
 attcagaatg tttgggataa gtctgaagat aggttaggtc ttattggttt gggttttgct 360
 55 ggtattgtag ctctttgggc atcattgaat ctcatcacg caattgacaa attgccgtt 420
 atctcgagcg gattcgaact agttggtatc ttgttctcca cgtgggtcac atactgatat 480
 ctcttggtca aaccggacag acaggagctt tcgaaaattg tcaagaaatc agtagcggat 540
 atacttgccc agtgaacctt gtgtgtgtga taatacttca tctttggaag atgatttggt 600
 tgcaagtttg taaaattaca tgacagggtg gttgttggtt ctagtccaat aatgtcatgc 660
 60 atttgaaacc tgtaataact ttattgttgg tttttggttg tgagcaaat caatcttttc 720
 taatttcaaa gattctcttt tatgt

(2) INFORMATION FOR SEQ ID NO:226:

430

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1425148

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

```

Met Ala Ser Ile Ser Ala Thr Leu Pro Ser Pro Leu Leu Leu Thr Gln
1      5      10      15
Arg Lys Ser Asn Leu Thr Ser Ile Gln Lys Leu Pro Phe Ser Leu Thr
15     20     25     30
Arg Gly Thr Asn Asp Leu Ser Pro Leu Ser Leu Thr Arg Asn Pro Ser
35     40     45
Ser Ile Ser Leu Met Val Lys Ser Ser Gly Glu Ser Ser Asp Ser Ser
50     55     60
Thr Asp Leu Asp Val Val Ser Thr Ile Gln Asn Val Trp Asp Lys Ser
20     65     70     75     80
Glu Asp Arg Leu Gly Leu Ile Gly Leu Gly Phe Ala Gly Ile Val Ala
85     90     95
Leu Trp Ala Ser Leu Asn Leu Ile Thr Ala Ile Asp Lys Leu Pro Val
25     100    105    110
Ile Ser Ser Gly Phe Glu Leu Val Gly Ile Leu Phe Ser Thr Trp Phe
115    120    125
Thr Tyr Arg Tyr Leu Leu Phe Lys Pro Asp Arg Gln Glu Leu Ser Lys
130    135    140
Ile Val Lys Lys Ser Val Ala Asp Ile Leu Gly Gln
30     145    150    155

```

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1425149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

```

Met Val Lys Ser Ser Gly Glu Ser Ser Asp Ser Ser Thr Asp Leu Asp
45     5      10      15
Val Val Ser Thr Ile Gln Asn Val Trp Asp Lys Ser Glu Asp Arg Leu
20     25     30
Gly Leu Ile Gly Leu Gly Phe Ala Gly Ile Val Ala Leu Trp Ala Ser
35     40     45
Leu Asn Leu Ile Thr Ala Ile Asp Lys Leu Pro Val Ile Ser Ser Gly
50     55     60
Phe Glu Leu Val Gly Ile Leu Phe Ser Thr Trp Phe Thr Tyr Arg Tyr
65     70     75     80
Leu Leu Phe Lys Pro Asp Arg Gln Glu Leu Ser Lys Ile Val Lys Lys
55     85     90     95
Ser Val Ala Asp Ile Leu Gly Gln
100

```

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 769 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

431

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..769

(D) OTHER INFORMATION: / Ceres Seq. ID 1441102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

ccacaacaca acttcagctt taagacagct aaaactaaat acaaagaaac agagatgggt      60
ttgggttacag aggaggtgag agctaaggca gagatgtaca ccggagatga gatatgtaga      120
gagaagacaa agtggtttcct caaggaaata tctatgccca atgggtttatt accattgaag      180
gatatagaag aggttggtgta tgacagagag tcaggtgttg tatggctgaa gcagaagaag      240
agcatcactc acaagttcac agagatagat aagcttgtct cctatggaac cgaagtcaca      300
gccattgttg agaccgggaa aatcaagaag ctcaactggag tcaaagccaa ggaacttctt      360
atttgggtca ctatcaatga gatctatacc gaggaacccc ctaccaagat cagtttcaag      420
acaccgacca cactgtccag gactttcccg gtcacagctt ttatagtccc agaagaacct      480
gccaaggagg aacctgccaa agaggaacct gccaaggaga agagcagcga agccaccgag      540
gccaaggagg ctgttgcaat caaggaggct gtcgcagtca aagaggcggc ctaatcagct      600
cagcttcagc agataaaaga gacccgaatt tttaagtgtta cttcaagaat ttgaacaaat      660
catggagagt tagtgtttct cactgtctta actatcatgt attatctacc taccacttgt      720
tgctgcttgt tttacctgta ataagatatc aatatcatcc tgttccact

```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

(D) OTHER INFORMATION: / Ceres Seq. ID 1441103

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Pro Gln His Asn Phe Ser Phe Lys Thr Lys Thr Lys T_ ~ Lys Glu
1          5          10          15
35 Thr Glu Met Gly Leu Val Thr Glu Glu Val Arg Ala Lys Ala Glu Met
          20          25          30
Tyr Thr Gly Asp Glu Ile Cys Arg Glu Lys Thr Lys Cys Phe Leu Lys
          35          40          45
Glu Ile Ser Met Pro Asn Gly Leu Leu Pro Leu Lys Asp Ile Glu Glu
40          50          55          60
Val Gly Tyr Asp Arg Glu Ser Gly Val Val Trp Leu Lys Gln Lys Lys
65          70          75          80
Ser Ile Thr His Lys Phe Thr Glu Ile Asp Lys Leu Val Ser Tyr Gly
          85          90          95
45 Thr Glu Val Thr Ala Ile Val Glu Thr Gly Lys Ile Lys Lys Leu Thr
          100          105          110
Gly Val Lys Ala Lys Glu Leu Leu Ile Trp Val Thr Ile Asn Glu Ile
          115          120          125
Tyr Thr Glu Glu Pro Pro Thr Lys Ile Thr Phe Lys Thr Pro Thr Thr
50          130          135          140
Leu Ser Arg Thr Phe Pro Val Thr Ala Phe Ile Val Pro Glu Glu Pro
145          150          155          160
Ala Lys Glu Glu Pro Ala Lys Glu Glu Pro Ala Lys Glu Lys Ser Ser
          165          170          175
55 Glu Ala Thr Glu Ala Lys Glu Ala Val Ala Ile Lys Glu Ala Val Ala
          180          185          190
Val Lys Glu Ala Ala
          195

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

432

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1441104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

5 Met Gly Leu Val Thr Glu Glu Val Arg Ala Lys Ala Glu Met Tyr Thr
 10 1 5 10 15
 Gly Asp Glu Ile Cys Arg Glu Lys Thr Lys Cys Phe Leu Lys Glu Ile
 20 25 30
 Ser Met Pro Asn Gly Leu Leu Pro Leu Lys Asp Ile Glu Val Gly
 35 40 45
 15 Tyr Asp Arg Glu Ser Gly Val Val Trp Leu Lys Gln Lys Lys Ser Ile
 50 55 60
 Thr His Lys Phe Thr Glu Ile Asp Lys Leu Val Ser Tyr Gly Thr Glu
 65 70 75 80
 Val Thr Ala Ile Val Glu Thr Gly Lys Ile Lys Lys Leu Thr Gly Val
 20 85 90 95
 Lys Ala Lys Glu Leu Leu Ile Trp Val Thr Ile Asn Glu Ile Tyr Thr
 100 105 110
 Glu Glu Pro Pro Thr Lys Ile Thr Phe Lys Thr Pro Thr Thr Leu Ser
 115 120 125
 25 Arg Thr Phe Pro Val Thr Ala Phe Ile Val Pro Glu Glu Pro Ala Lys
 130 135 140
 Glu Glu Pro Ala Lys Glu Glu Pro Ala Lys Glu Lys Ser Ser Glu Ala
 145 150 155 160
 Thr Glu Ala Lys Glu Ala Val Ala Ile Lys Glu Ala Val Ala Val Lys
 30 165 170 175
 Glu Ala Ala

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1441105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

45 Met Tyr Thr Gly Asp Glu Ile Cys Arg Glu Lys Thr Lys Cys Phe Leu
 1 5 10 15
 Lys Glu Ile Ser Met Pro Asn Gly Leu Leu Pro Leu Lys Asp Ile Glu
 20 25 30
 Glu Val Gly Tyr Asp Arg Glu Ser Gly Val Val Trp Leu Lys Gln Lys
 35 40 45
 50 Lys Ser Ile Thr His Lys Phe Thr Glu Ile Asp Lys Leu Val Ser Tyr
 50 55 60
 Gly Thr Glu Val Thr Ala Ile Val Glu Thr Gly Lys Ile Lys Lys Leu
 65 70 75 80
 55 Thr Gly Val Lys Ala Lys Glu Leu Leu Ile Trp Val Thr Ile Asn Glu
 85 90 95
 Ile Tyr Thr Glu Glu Pro Pro Thr Lys Ile Thr Phe Lys Thr Pro Thr
 100 105 110
 Thr Leu Ser Arg Thr Phe Pro Val Thr Ala Phe Ile Val Pro Glu Glu
 115 120 125
 60 Pro Ala Lys Glu Glu Pro Ala Lys Glu Glu Pro Ala Lys Glu Lys Ser
 130 135 140

433

Ser Glu Ala Thr Glu Ala Lys Glu Ala Val Ala Ile Lys Glu Ala Val
 145 150 155 160
 Ala Val Lys Glu Ala Ala

165

5 (2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 607 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..607

(D) OTHER INFORMATION: / Ceres Seq. ID 1447480

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

aaaatctcta	aagtttcaat	tttttkgttc	tgttcttttt	ttttttaaag	aatggcttca	60
atttctgcaa	ctttgccttc	gccattgta	ctcacacaga	gaaaatccaa	tctcacatcg	120
attcaaaaac	tccatttttc	tctaactcga	ggtacgaatg	atctttctcc	attatctctt	180
actcgaaacc	ctagcagcat	cagtctgatg	gtgaaagcta	gtggagaaag	ctcagattca	240
tcgactgata	tcgacgttgt	tagtacgatt	cagaatgttg	caattgacaa	attgcccggt	300
atctcgagcg	gattcgaact	agttggtatc	ttgttctcca	cgtgggtcac	atatcgatat	360
ctcttggtta	aaccggacag	acaggagctt	tcgaaaattg	tcaagaaatc	agtagcggat	420
atacttggcc	agtgaacctt	gtgtgtgtga	taatacttca	tctttggaag	atgatttggt	480
tgcaagtttg	taaaattaca	tgacaggggtg	gttgttggtt	ctagtccaat	aatgtcatgc	540
atttgaaacc	tgtaaatact	ttattgttgg	tttttggttg	tgagcaaaat	caatcttttc	600
taatttc						

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

35 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1447481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

Met	Ala	Ser	Ile	Ser	Ala	Thr	Leu	Pro	Ser	Pro	Leu	Leu	Leu	Thr	Gln
1				5					10					15	
Arg	Lys	Ser	Asn	Leu	Thr	Ser	Ile	Gln	Lys	Leu	Pro	Phe	Ser	Leu	Thr
			20					25					30		
Arg	Gly	Thr	Asn	Asp	Leu	Ser	Pro	Leu	Ser	Leu	Thr	Arg	Asn	Pro	Ser
		35					40					45			
Ser	Ile	Ser	Leu	Met	Val	Lys	Ala	Ser	Gly	Glu	Ser	Ser	Asp	Ser	Ser
		50				55				60					
Thr	Asp	Leu	Asp	Val	Val	Ser	Thr	Ile	Gln	Asn	Val	Ala	Ile	Asp	Lys
		65			70				75					80	
Leu	Pro	Val	Ile	Ser	Ser	Gly	Phe	Glu	Leu	Val	Gly	Ile	Leu	Phe	Ser
			85					90					95		
Thr	Trp	Phe	Thr	Tyr	Arg	Tyr	Leu	Leu	Phe	Lys	Pro	Asp	Arg	Gln	Glu
			100				105						110		
Leu	Ser	Lys	Ile	Val	Lys	Lys	Ser	Val	Ala	Asp	Ile	Leu	Gly	Gln	
		115				120						125			

55 (2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: peptide

434

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1447482

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

Met Val Lys Ala Ser Gly Glu Ser Ser Asp Ser Ser Thr Asp Leu Asp
 1 5 10 15
 Val Val Ser Thr Ile Gln Asn Val Ala Ile Asp Lys Leu Pro Val Ile
 20 25 30
 Ser Ser Gly Phe Glu Leu Val Gly Ile Leu Phe Ser Thr Trp Phe Thr
 35 40 45
 Tyr Arg Tyr Leu Leu Phe Lys Pro Asp Arg Gln Glu Leu Ser Lys Ile
 50 55 60
 Val Lys Lys Ser Val Ala Asp Ile Leu Gly Gln
 65 70 75

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 668 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..668

(D) OTHER INFORMATION: / Ceres Seq. ID 1447577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

aaaaaaaaac aaaacaaaaa attatattca agagaaaaag gaaaaaatga atttcattctc 60
 cgatcaggta aagaaactct caagctcaac accagaggcc agaccacaac aagccagtcg 120
 aaggaaccga aacagctaca agaccagcta ccaacgccga gctcatggca agtgccaagg 180
 ttgtagctga agctgctcaa gccgcagctc gtaacgaatc agacaaactc gacaagggta 240
 aagtcgccgg agcctctgct gatattct*ag acgctgccga gaaatacggg aagttcagtg 300
 aaaagagtag cactggctcag tacctcgaca aggttgagaa gtattctcaac gactacgagt 360
 cgtcacactc caccgggtgc ggtggctctc ctctccgac gagtcaggct gagccagcaa 420
 gtcagcctga gccggcggct aagaaagacg atgaagagtc tgggtggtggg cttggagggtt 480
 atgccaagat ggctcaagggt ttcttgaagt gatttgatct ttaattgttg ttcatcattt 540
 tcgtaataat aaattaaata actagtatcg tttgtgacta gtttatgttg cttcgtttat 600
 gtttatgggg agtgacgagt gagtgtaata acttctggtg atcatgaatc taatccatct 660
 ttgttgctc

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1447578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Lys Lys Asn Lys Thr Lys Asn Tyr Ile Gln Glu Lys Lys Glu Lys Met
 1 5 10 15
 Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro Glu
 20 25 30
 Ala Arg Pro Gln Gln Ala Ser Arg Arg Asn Arg Asn Ser Tyr Lys Thr
 35 40 45
 Ser Tyr Gln Arg Arg Ala His Gly Lys Cys Gln Gly Cys Ser
 50 55 60

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

435

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..115
 (D) OTHER INFORMATION: / Ceres Seq. ID 1447579
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

10 Met Ala Ser Ala Lys Val Val Ala Glu Ala Ala Gln Ala Ala Ala Arg
 1 5 10 15
 Asn Glu Ser Asp Lys Leu Asp Lys Gly Lys Val Ala Gly Ala Ser Ala
 20 25 30
 15 Asp Ile Leu Asp Ala Ala Glu Lys Tyr Gly Lys Phe Asp Glu Lys Ser
 35 40 45
 Ser Thr Gly Gln Tyr Leu Asp Lys Ala Glu Lys Tyr Leu Asn Asp Tyr
 50 55 60
 Glu Ser Ser His Ser Thr Gly Ala Gly Gly Pro Pro Pro Pro Thr Ser
 65 70 75 80
 20 Gln Ala Glu Pro Ala Ser Gln Pro Glu Pro Ala Ala Lys Lys Asp Asp
 85 90 95
 Glu Glu Ser Gly Gly Gly Leu Gly Gly Tyr Ala Lys Met Ala Gln Gly
 100 105 110
 Phe Leu Lys
 115

(2) INFORMATION FOR SEQ ID NO:238:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 amino acids
 (B) TYPE: amino acid
 30 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 35 (B) LOCATION: 1..69
 (D) OTHER INFORMATION: / Ceres Seq. ID 1447580
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Met Lys Arg Val Ala Leu Val Ser Thr Ser Thr Arg Leu Arg Ser Ile
 1 5 10 15
 40 Ser Thr Thr Thr Ser Arg His Thr Pro Pro Val Leu Val Val Leu Leu
 20 25 30
 Leu Arg Arg Val Arg Leu Ser Gln Val Ser Leu Ser Arg Arg Leu
 35 40 45
 45 Arg Lys Thr Met Lys Ser Leu Val Val Gly Leu Glu Val Met Pro Arg
 50 55 60
 Trp Leu Lys Val Ser
 65

(2) INFORMATION FOR SEQ ID NO:239:
 (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 55 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..717
 (D) OTHER INFORMATION: / Ceres Seq. ID 1447922
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

60 cttcgtctct gtctccaaaa tcgaatcaaa atctctaaag tttcaatttt tttgttctgt 60
 tctttttttt ttttttaaaga atggcttcaa tttctgcaac tttgccttcg ccattgttac 120
 tcacacagag aaaatccaat ctcacatcga ttcaaaaact cccattttct ctaactcgag 180

436

```

gtacgaatga tctttctcca ttatctctta ctcgaaaccc tagcagcatc agtctgatgg 240
tgaaagctag tggagaaagc tcagattcat cgactgatct cgacgttggt agtacgattc 300
agaatgtttg ggataagtct gaagataggt taggtcttat tggtttgggt tttgctggta 360
5  ttgtagctct ttgggcatca ttgaatctca tcacggcaat tgacaaattg cccgttatct 420
cgagcggatt cgaactagtt ggtatcttgt tctccacgtg gttcacatat cgatatctct 480
tggtcaaacc ggacagacag gagctttcga aaattgtcaa gaaatcagta gcggatatac 540
ttggccagtg aaccttggtg gtgtgataat acttcacatt tggagatga tttgtttgca 600
agtttgtaaa attacatgac aggggtggtt ttgtttctag tccaataatg tcatgcattt 660
gaaacctgta aatactttat tgttggtttt tggttgtgag caaaatcaat cttttct

```

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..156

(D) OTHER INFORMATION: / Ceres Seq. ID 1447923

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

Met Ala Ser Ile Ser Ala Thr Leu Pro Ser Pro Leu Leu Leu Thr Gln
1      5      10      15
Arg Lys Ser Asn Leu Thr Ser Ile Gln Lys Leu Pro Phe Ser Leu Thr
25     20     25     30
Arg Gly Thr Asn Asp Leu Ser Pro Leu Ser Leu Thr Arg Asn Pro Ser
35     35     40     45
Ser Ile Ser Leu Met Val Lys Ala Ser Gly Glu Ser Ser Asp Ser Ser
50     55     60
Thr Asp Leu Asp Val Val Ser Thr Ile Gln Asn Val Trp Asp Lys Ser
30     65     70     75     80
Glu Asp Arg Leu Gly Leu Ile Gly Leu Gly Phe Ala Gly Ile Val Ala
85     90     95
Leu Trp Ala Ser Leu Asn Leu Ile Thr Ala Ile Asp Lys Leu Pro Val
35     100    105    110
Ile Ser Ser Gly Phe Glu Leu Val Gly Ile Leu Phe Ser Thr Trp Phe
115    120    125
Thr Tyr Arg Tyr Leu Leu Phe Lys Pro Asp Arg Gln Glu Leu Ser Lys
40     130    135    140
Ile Val Lys Lys Ser Val Ala Asp Ile Leu Gly Gln
145    150    155

```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1447924

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

Met Val Lys Ala Ser Gly Glu Ser Ser Asp Ser Ser Thr Asp Leu Asp
55 1      5      10      15
Val Val Ser Thr Ile Gln Asn Val Trp Asp Lys Ser Glu Asp Arg Leu
20     25     30
Gly Leu Ile Gly Leu Gly Phe Ala Gly Ile Val Ala Leu Trp Ala Ser
35     40     45
Leu Asn Leu Ile Thr Ala Ile Asp Lys Leu Pro Val Ile Ser Ser Gly
60 50     55     60
Phe Glu Leu Val Gly Ile Leu Phe Ser Thr Trp Phe Thr Tyr Arg Tyr

```

```

65          70          75          80
Leu Leu Phe Lys Pro Asp Arg Gln Glu Leu Ser Lys Ile Val Lys Lys
          85          90          95
Ser Val Ala Asp Ile Leu Gly Gln
          100

```

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 656 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..656

(D) OTHER INFORMATION: / Ceres Seq. ID 1448012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

ggaattttctc	actctctcta	tctctcttag	ccagctctga	ccatttccgat	ttttttccgg	60
tgaaaaggga	gcagaaacat	ggttgtagct	atcagattat	cgagatttgg	atgcaaaaat	120
cggccatttt	ttagggttat	ggctgctgat	agcagatctc	caagagacgg	gaagcatctt	180
gaggtccttag	gttacttcaa	tcttttgcca	ggccaggacg	gtggttaagag	gatgggtctc	240
aagttcgcac	gaattaagta	ctggttatct	gttggtgctc	agccatcaga	cccggttcaa	300
cgccttcttt	tcagatccgg	tttacttcct	cctcctccaa	tggtggctat	gggacgtaaa	360
ggtggagcac	gagacacacg	cccagttgat	ccaatgactg	gtcgcctatgt	ggatgcagag	420
aataaaacag	ttaatgccaa	tgataaccag	cctaaggaag	aggattcaga	agacaagatt	480
gcattgattca	ttagccttct	gtcgtcgtag	cttttcaagt	tcactttgta	gtcgcattata	540
tttgtataatg	cagcatttaga	caactgcact	gtttcctttg	tttggcgata	aacggcaagg	600
tgtttgcac	tttttgcaga	aacggcacat	attttgcatt	gggatatttt	aatttt	

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 1448013

(xi) SEQUENCE DESCRIPTION: SEO ID NO:243:

Met	Val	Val	Arg	Ile	Arg	Leu	Ser	Arg	Phe	Gly	Cys	Lys	Asn	Arg	Pro
1				5					10					15	
Phe	Phe	Arg	Val	Met	Ala	Ala	Asp	Ser	Arg	Ser	Pro	Arg	Asp	Gly	Lys
			20				25						30		
His	Leu	Glu	Val	Leu	Gly	Tyr	Phe	Asn	Pro	Leu	Pro	Gly	Gln	Asp	Gly
		35				40						45			
Gly	Lys	Arg	Met	Gly	Leu	Lys	Phe	Asp	Arg	Ile	Lys	Tyr	Trp	Leu	Ser
	50				55						60				
Val	Gly	Ala	Gln	Pro	Ser	Asp	Pro	Val	Gln	Arg	Leu	Leu	Phe	Arg	Ser
65					70					75					80
Gly	Leu	Leu	Pro	Pro	Pro	Pro	Met	Val	Ala	Met	Gly	Arg	Lys	Gly	Gly
				85					90					95	
Ala	Arg	Asp	Thr	Arg	Pro	Val	Asp	Pro	Met	Thr	Gly	Arg	Tyr	Val	Asp
			100				105						110		
Ala	Glu	Asn	Lys	Thr	Val	Asn	Ala	Asn	Asp	Asn	Gln	Pro	Lys	Glu	Glu
		115				120						125			
Asp	Ser	Glu	Asp	Lys	Ile	Ala									
	130					135									

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

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- (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..115
 (D) OTHER INFORMATION: / Ceres Seq. ID 1448014
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly Lys His Leu Glu Val
 1 5 10 15
 Leu Gly Tyr Phe Asn Pro Leu Pro Gly Gln Asp Gly Gly Lys Arg Met
 20 25 30
 Gly Leu Lys Phe Asp Arg Ile Lys Tyr Trp Leu Ser Val Gly Ala Gln
 35 40 45
 Pro Ser Asp Pro Val Gln Arg Leu Leu Phe Arg Ser Gly Leu Leu Pro
 50 55 60
 Pro Pro Pro Met Val Ala Met Gly Arg Lys Gly Gly Ala Arg Asp Thr
 65 70 75 80
 Arg Pro Val Asp Pro Met Thr Gly Arg Tyr Val Asp Ala Glu Asn Lys
 85 90 95
 Thr Val Asn Ala Asn Asp Asn Gln Pro Lys Glu Glu Asp Ser Glu Asp
 100 105 110
 Lys Ile Ala
 115

- (2) INFORMATION FOR SEQ ID NO:245:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..84
 (D) OTHER INFORMATION: / Ceres Seq. ID 1448015

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:
 Met Gly Leu Lys Phe Asp Arg Ile Lys Tyr Trp Leu Ser Val Gly Ala
 1 5 10 15
 Gln Pro Ser Asp Pro Val Gln Arg Leu Leu Phe Arg Ser Gly Leu Leu
 20 25 30
 Pro Pro Pro Pro Met Val Ala Met Gly Arg Lys Gly Gly Ala Arg Asp
 35 40 45
 Thr Arg Pro Val Asp Pro Met Thr Gly Arg Tyr Val Asp Ala Glu Asn
 50 55 60
 Lys Thr Val Asn Ala Asn Asp Asn Gln Pro Lys Glu Glu Asp Ser Glu
 65 70 75 80
 Asp Lys Ile Ala

- (2) INFORMATION FOR SEQ ID NO:246:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..458
 (D) OTHER INFORMATION: / Ceres Seq. ID 1448135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:
 aattttctag ggttttgaag agtgtctctc gtcgccgttg taattcctct gtttagcaaat 60
 cgacaaaatg ggtcactcta atgtatggaa ctctcatccg aagaagtacg gtcctggatc 120

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tcgtttatgc cgtgtgtgcg ggaactcgca cgggctgac cggaagtatg gtttgaactg 180
 ctgcagacag tgtttccgta gcaacgctaa ggagattgga ttcattaagt accgttaatc 240
 aagcaccaac ttcattgattg atgcttaatg atataaacat gaaggcgctcg atggggttgg 300
 cttttaagct tttgtagttt ttgaaatttt tacttttgag aaccattggt attttggggag 360
 5 ttaattaagt tgttgaacct ctcattaagc atgtcttatt ttggattaat gatgttttgg 420
 ctattctcg atttttgttt tatcagtcaa atttgact

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 1448136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

20 Phe Ser Arg Val Leu Lys Ser Val Ser Arg Arg Arg Cys Asn Ser Ser
 1 5 10 15
 Val Ser Lys Ser Thr Lys Trp Val Thr Leu Met Tyr Gly Thr Leu Ile
 20 25 30
 Arg Arg Ser Thr Val Leu Asp Leu Val Tyr Ala Val Cys Ala Gly Thr
 35 40 45
 25 Arg Thr Gly
 50

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

(D) OTHER INFORMATION: / Ceres Seq. ID 1448137

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

40 Met Gly His Ser Asn Val Trp Asn Ser His Pro Lys Lys Tyr Gly Pro
 1 5 10 15
 Gly Ser Arg Leu Cys Arg Val Cys Gly Asn Ser His Gly Leu Ile Arg
 20 25 30
 Lys Tyr Gly Leu Asn Cys Cys Arg Gln Cys Phe Arg Ser Asn Ala Lys
 35 40 45
 45 Glu Ile Gly Phe Ile Lys Tyr Arg
 50 55

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1448138

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

60 Met Glu Leu Ser Ser Glu Glu Val Arg Ser Trp Ile Ser Phe Met Pro
 1 5 10 15
 Cys Val Arg Glu Leu Ala Arg Ala Asp Pro Glu Val Trp Phe Glu Leu
 20 25 30

440

Leu Gln Thr Val Phe Pro

35

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 603 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..603

(D) OTHER INFORMATION: / Ceres Seq. ID 1448185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

15 gaagaagaga gtatcgttgt gaggtttggg gatcgcgaaa atggagggttc caggttcacg      60
   gaagaagatg atcgcaacgc aagaagagat gtctgcagct aaaatagcac ttggatctag      120
   agatatgtgc gctcatctct tgattccgct caacaaatgt cgtcaggctg agttttacct      180
   tccatggaaa tgtgaagacg agcgtcacgt ttatgagaag tgtgaatacg agcttgttat      240
   ggagagaatg cttgcgatga agaagatccg tgaagaagaa gctttggcta aacagaataa      300
20 actacaagga aacgctgctg ttcctcttat ccctaaaact gctaattgctt aggattcgat      360
   tccttctcca atttgccgat tccagattcc gggattctct ggaactgtga agatgggtggg      420
   ggctctgctt ttcaatcttt ttcttcttgc tagtgatgaa aaattggtgc tacattttca      480
   gatgtgaatg ttcaagattc tctatctttt tttttttttt gaactctttt taacttggag      540
   tggtttccca aaaaataaga tgcaaaaactc atctttttgt tggttttcta tctttaatct      600
   gtg

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..103

(D) OTHER INFORMATION: / Ceres Seq. ID 1448186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

Met Glu Val Pro Gly Ser Ser Lys Lys Met Ile Ala Thr Gln Glu Glu
1      5      10      15
40 Met Ser Ala Ala Lys Ile Ala Leu Gly Ser Arg Asp Met Cys Ala His
   20      25      30
   Leu Leu Ile Pro Leu Asn Lys Cys Arg Gln Ala Glu Phe Tyr Leu Pro
   35      40      45
45 Trp Lys Cys Glu Asp Glu Arg His Val Tyr Glu Lys Cys Glu Tyr Glu
   50      55      60
   Leu Val Met Glu Arg Met Leu Ala Met Lys Lys Ile Arg Glu Glu Glu
   65      70      75      80
   Ala Leu Ala Lys Gln Asn Lys Leu Gln Gly Asn Ala Ala Val Pro Leu
   85      90      95
50 Ile Pro Lys Thr Ala Asn Ala
   100

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1448187

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

Met Ile Ala Thr Gln Glu Glu Met Ser Ala Ala Lys Ile Ala Leu Gly
 1 5 10 15
 5 Ser Arg Asp Met Cys Ala His Leu Leu Ile Pro Leu Asn Lys Cys Arg
 20 25 30
 Gln Ala Glu Phe Tyr Leu Pro Trp Lys Cys Glu Asp Glu Arg His Val
 35 40 45
 Tyr Glu Lys Cys Glu Tyr Glu Leu Val Met Glu Arg Met Leu Ala Met
 50 55 60
 10 Lys Lys Ile Arg Glu Glu Glu Ala Leu Ala Lys Gln Asn Lys Leu Gln
 65 70 75 80
 Gly Asn Ala Ala Val Pro Leu Ile Pro Lys Thr Ala Asn Ala
 85 90

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1448188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Met Ser Ala Ala Lys Ile Ala Leu Gly Ser Arg Asp Met Cys Ala His
 1 5 10 15
 Leu Leu Ile Pro Leu Asn Lys Cys Arg Gln Ala Glu Phe Tyr Leu Pro
 20 25 30
 30 Trp Lys Cys Glu Asp Glu Arg His Val Tyr Glu Lys Cys Glu Tyr Glu
 35 40 45
 Leu Val Met Glu Arg Met Leu Ala Met Lys Lys Ile Arg Glu Glu Glu
 50 55 60
 Ala Leu Ala Lys Gln Asn Lys Leu Gln Gly Asn Ala Ala Val Pro Leu
 65 70 75 80
 35 Ile Pro Lys Thr Ala Asn Ala
 85

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2034 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2034

(D) OTHER INFORMATION: / Ceres Seq. ID 1450875

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

50 tttatcaaaa tcgatggctg cttctagatt gtgttccgcg gcggcgatag ctgctgcctt 60
 cacttcaatg tcaatgtctc agaaccgtgc ttacgccgat tcttctcgat tccggtttcc 120
 tttcttttct tcttctcctt ctctcctcc gtcagattct ccggcgatc aatcttctac 180
 aaactctagt aagtctaaag cagagcctga tgagcctaaa ggatcgggtt ttgatcctga 240
 ggctcttgag agagctgcta aagctcttag agatatcaat agctctcccc attccaaaca 300
 55 ggtgtttgat ctcattgagga agcaggagaa aactcgggta gctgaattag cggcagagac 360
 ttctcattac gaagctattc aagcacacaa tgatattggc agacagcaga aattggctga 420
 ggaccagaga aatcttttgc agacacaggc gcaaaccaaa gcgcaaaatc tgcgatatga 480
 ggatgaattg gccagaaaga gacagcagac agatcatgaa gctcagaggc atcataatgt 540
 ggaattgggt aagatgcaag aggcgtcttc tatcaggaaa gagaaggcaa aaatcgccac 600
 60 agaagaacag atccaagctc agcatcgcca aactgagaaa gagagagctg aacttgagcg 660
 agagacgatt cgtgtcaagg ccatggctga agctgaaggc cgggctcatg aagccaaact 720
 tactgaagag caaaacagaa gattgcttat ggaaaggatt aatggtgaaa gagagaagtg 780

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gcttgctgca atcaacacaa tgttcagtca catcgaaggg ggattcagga ccttattaac 840
 tgatcgaaat aagctgatta tgactgttgg aggagctact gcattagctg caggggttta 900
 tacaactcgt gaaggagcta gagttacatg gggttatatt aataggatgc ttggacaacc 960
 5 gtcacttatt cgagaatctt ccatgcgtag atttccatgg acaggctcag tgtctcaatt 1020
 taagaacagg atctcagggg ctgcagcagc ttctgcagca gaaggcaaaa agccgcttga 1080
 taatgtaatt ctccatactt ctttgaagaa acgaatcgag cgtctcgcta gagctacagc 1140
 aaacacacaaa tcccatacaag caccattccg caacatgatg ttttatggac ctctgtgtac 1200
 cggtaaaaact atggtggcaa gggaaatagc tcggaaatcg ggtctggatt atgctatgat 1260
 gacaggaggt gatgttgctc ccttgggatac acaagctgtt actaaaatcc atcagatatt 1320
 10 tgattgggct aagaaatcga acagaggctt actccttttc attgatgaag ccgatgcttt 1380
 tctatgcgag cgtaacagca cttacatgag tgaggctcaa cgtagtgctc tgaacgcttt 1440
 gctcttccga actggtgatc aatctcggga cattgttctt gtcttggcta caaacagacc 1500
 tggagatctc gatagtgcgg ttacagacag gattgatgaa gtcattgagt tcccacttcc 1560
 aggggaagaa gaacgtttca agcttctcaa tctctatctc aacaaatatac taaagatggg 1620
 15 tgataacaac gaagacacaa aaccgaaatg gagtcatttg tttaagaagc tgtcacagaa 1680
 gattaccgtt gaagaagact taactgataa agtgatttct gaggtgcaa agaagacaga 1740
 aggattctct ggccgtgaga ttgcaaagct tgtggctgga gtacaagctg gactgtacgg 1800
 acgagcggat tgtgttttgg attcacagct ttttaaagag attgttgaat ataaggttga 1860
 agaacatcac cgaaggcata tgcttgcttc tgaaggtttt cagccattac tcttctctta 1920
 20 gtcatttgga ttttgattat acatgtcatt tacttgatca gaaagaagaa tctgattgtt 1980
 ttaaaatgag tcttaaaatt gaatttttag attaaacatg ttaaagagtt ttac

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 639 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..639

(D) OTHER INFORMATION: / Ceres Seq. ID 1450876

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

35 Leu Ser Lys Ser Met Ala Ala Ser Arg Leu Cys Ser Ala Ala Ala Ile
 1 5 10 15
 Ala Ala Ala Phe Thr Ser Met Ser Met Ser Gln Asn Arg Ala Tyr Ala
 20 25 30
 Asp Ser Ser Arg Phe Arg Phe Pro Phe Phe Ser Ser Ser Pro Ser Pro
 35 40 45
 40 Pro Pro Ser Asp Ser Pro Ala Asn Gln Ser Ser Thr Asn Ser Ser Lys
 50 55 60
 Ser Lys Ala Glu Pro Asp Glu Pro Lys Gly Ser Gly Phe Asp Pro Glu
 65 70 75 80
 45 Ala Leu Glu Arg Ala Ala Lys Ala Leu Arg Asp Ile Asn Ser Ser Pro
 85 90 95
 His Ser Lys Gln Val Phe Asp Leu Met Arg Lys Gln Glu Lys Thr Arg
 100 105 110
 Leu Ala Glu Leu Ala Ala Glu Thr Ser His Tyr Glu Ala Ile Gln Ala
 115 120 125
 50 His Asn Asp Ile Gly Arg Gln Gln Lys Leu Ala Glu Asp Gln Arg Asn
 130 135 140
 Leu Leu Gln Thr Gln Ala Gln Thr Lys Ala Gln Asn Leu Arg Tyr Glu
 145 150 155 160
 55 Asp Glu Leu Ala Arg Lys Arg Gln Gln Thr Asp His Glu Ala Gln Arg
 165 170 175
 His His Asn Val Glu Leu Val Lys Met Gln Glu Ala Ser Ser Ile Arg
 180 185 190
 Lys Glu Lys Ala Lys Ile Ala Thr Glu Glu Gln Ile Gln Ala Gln His
 195 200 205
 60 Arg Gln Thr Glu Lys Glu Arg Ala Glu Leu Glu Arg Glu Thr Ile Arg
 210 215 220
 Val Lys Ala Met Ala Glu Ala Glu Gly Arg Ala His Glu Ala Lys Leu

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	225				230					235				240		
	Thr	Glu	Glu	Gln	Asn	Arg	Arg	Leu	Leu	Met	Glu	Arg	Ile	Asn	Gly	Glu
					245					250				255		
5	Arg	Glu	Lys	Trp	Leu	Ala	Ala	Ile	Asn	Thr	Met	Phe	Ser	His	Ile	Glu
				260					265					270		
	Gly	Gly	Phe	Arg	Thr	Leu	Leu	Thr	Asp	Arg	Asn	Lys	Leu	Ile	Met	Thr
				275					280					285		
	Val	Gly	Gly	Ala	Thr	Ala	Leu	Ala	Ala	Gly	Val	Tyr	Thr	Thr	Arg	Glu
		290					295					300				
10	Gly	Ala	Arg	Val	Thr	Trp	Gly	Tyr	Ile	Asn	Arg	Met	Leu	Gly	Gln	Pro
	305					310					315					320
	Ser	Leu	Ile	Arg	Glu	Ser	Ser	Met	Arg	Arg	Phe	Pro	Trp	Thr	Gly	Ser
					325					330					335	
15	Val	Ser	Gln	Phe	Lys	Asn	Arg	Ile	Ser	Gly	Ala	Ala	Ala	Ala	Ser	Ala
				340					345					350		
	Ala	Glu	Gly	Lys	Lys	Pro	Leu	Asp	Asn	Val	Ile	Leu	His	Thr	Ser	Leu
			355					360					365			
	Lys	Lys	Arg	Ile	Glu	Arg	Leu	Ala	Arg	Ala	Thr	Ala	Asn	Thr	Lys	Ser
		370					375					380				
20	His	Gln	Ala	Pro	Phe	Arg	Asn	Met	Met	Phe	Tyr	Gly	Pro	Pro	Gly	Thr
	385					390					395					400
	Gly	Lys	Thr	Met	Val	Ala	Arg	Glu	Ile	Ala	Arg	Lys	Ser	Gly	Leu	Asp
				405						410					415	
25	Tyr	Ala	Met	Met	Thr	Gly	Gly	Asp	Val	Ala	Pro	Leu	Gly	Ser	Gln	Ala
			420					425						430		
	Val	Thr	Lys	Ile	His	Gln	Ile	Phe	Asp	Trp	Ala	Lys	Lys	Ser	Asn	Arg
			435					440					445			
	Gly	Leu	Leu	Leu	Phe	Ile	Asp	Glu	Ala	Asp	Ala	Phe	Leu	Cys	Glu	Arg
		450					455				460					
30	Asn	Ser	Thr	Tyr	Met	Ser	Glu	Ala	Gln	Arg	Ser	Ala	Leu	Asn	Ala	Leu
	465					470					475					480
	Leu	Phe	Arg	Thr	Gly	Asp	Gln	Ser	Arg	Asp	Ile	Val	Leu	Val	Leu	Ala
				485						490					495	
35	Thr	Asn	Arg	Pro	Gly	Asp	Leu	Asp	Ser	Ala	Val	Thr	Asp	Arg	Ile	Asp
			500						505					510		
	Glu	Val	Ile	Glu	Phe	Pro	Leu	Pro	Gly	Glu	Glu	Glu	Arg	Phe	Lys	Leu
			515					520					525			
	Leu	Asn	Leu	Tyr	Leu	Asn	Lys	Tyr	Leu	Lys	Met	Gly	Asp	Asn	Asn	Glu
		530					535					540				
40	Asp	Thr	Lys	Pro	Lys	Trp	Ser	His	Leu	Phe	Lys	Lys	Leu	Ser	Gln	Lys
	545					550					555					560
	Ile	Thr	Val	Glu	Glu	Asp	Leu	Thr	Asp	Lys	Val	Ile	Ser	Glu	Ala	Ala
				565						570					575	
45	Lys	Lys	Thr	Glu	Gly	Phe	Ser	Gly	Arg	Glu	Ile	Ala	Lys	Leu	Val	Ala
			580						585					590		
	Gly	Val	Gln	Ala	Gly	Val	Tyr	Gly	Arg	Ala	Asp	Cys	Val	Leu	Asp	Ser
		595						600				605				
	Gln	Leu	Phe	Lys	Glu	Ile	Val	Glu	Tyr	Lys	Val	Glu	Glu	His	His	Arg
		610					615					620				
50	Arg	His	Met	Leu	Ala	Ser	Glu	Gly	Phe	Gln	Pro	Leu	Leu	Phe	Ser	
	625					630					635					

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..635

(D) OTHER INFORMATION: / Ceres Seq. ID 1450877

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

	Met	Ala	Ala	Ser	Arg	Leu	Cys	Ser	Ala	Ala	Ala	Ile	Ala	Ala	Ala	Phe
	1				5				10						15	
5	Thr	Ser	Met	Ser	Met	Ser	Gln	Asn	Arg	Ala	Tyr	Ala	Asp	Ser	Ser	Arg
				20					25					30		
	Phe	Arg	Phe	Pro	Phe	Phe	Ser	Ser	Ser	Pro	Ser	Pro	Pro	Pro	Ser	Asp
			35					40					45			
	Ser	Pro	Ala	Asn	Gln	Ser	Ser	Thr	Asn	Ser	Ser	Lys	Ser	Lys	Ala	Glu
		50					55					60				
10	Pro	Asp	Glu	Pro	Lys	Gly	Ser	Gly	Phe	Asp	Pro	Glu	Ala	Leu	Glu	Arg
	65					70					75					80
	Ala	Ala	Lys	Ala	Leu	Arg	Asp	Ile	Asn	Ser	Ser	Pro	His	Ser	Lys	Gln
					85					90					95	
15	Val	Phe	Asp	Leu	Met	Arg	Lys	Gln	Glu	Lys	Thr	Arg	Leu	Ala	Glu	Leu
				100					105					110		
	Ala	Ala	Glu	Thr	Ser	His	Tyr	Glu	Ala	Ile	Gln	Ala	His	Asn	Asp	Ile
			115					120					125			
	Gly	Arg	Gln	Gln	Lys	Leu	Ala	Glu	Asp	Gln	Arg	Asn	Leu	Leu	Gln	Thr
			130				135					140				
20	Gln	Ala	Gln	Thr	Lys	Ala	Gln	Asn	Leu	Arg	Tyr	Glu	Asp	Glu	Leu	Ala
	145					150					155					160
	Arg	Lys	Arg	Gln	Gln	Thr	Asp	His	Glu	Ala	Gln	Arg	His	His	Asn	Val
					165					170					175	
25	Glu	Leu	Val	Lys	Met	Gln	Glu	Ala	Ser	Ser	Ile	Arg	Lys	Glu	Lys	Ala
			180						185					190		
	Lys	Ile	Ala	Thr	Glu	Glu	Gln	Ile	Gln	Ala	Gln	His	Arg	Gln	Thr	Glu
			195					200					205			
	Lys	Glu	Arg	Ala	Glu	Leu	Glu	Arg	Glu	Thr	Ile	Arg	Val	Lys	Ala	Met
		210					215					220				
30	Ala	Glu	Ala	Glu	Gly	Arg	Ala	His	Glu	Ala	Lys	Leu	Thr	Glu	Glu	Gln
	225					230					235					240
	Asn	Arg	Arg	Leu	Leu	Met	Glu	Arg	Ile	Asn	Gly	Glu	Arg	Glu	Lys	Trp
					245					250					255	
35	Leu	Ala	Ala	Ile	Asn	Thr	Met	Phe	Ser	His	Ile	Glu	Gly	Gly	Phe	Arg
			260						265					270		
	Thr	Leu	Leu	Thr	Asp	Arg	Asn	Lys	Leu	Ile	Met	Thr	Val	Gly	Gly	Ala
			275					280					285			
	Thr	Ala	Leu	Ala	Ala	Gly	Val	Tyr	Thr	Thr	Arg	Glu	Gly	Ala	Arg	Val
		290					295					300				
40	Thr	Trp	Gly	Tyr	Ile	Asn	Arg	Met	Leu	Gly	Gln	Pro	Ser	Leu	Ile	Arg
	305					310					315					320
	Glu	Ser	Ser	Met	Arg	Arg	Phe	Pro	Trp	Thr	Gly	Ser	Val	Ser	Gln	Phe
				325						330					335	
45	Lys	Asn	Arg	Ile	Ser	Gly	Ala	Ala	Ala	Ala	Ser	Ala	Ala	Glu	Gly	Lys
				340				345						350		
	Lys	Pro	Leu	Asp	Asn	Val	Ile	Leu	His	Thr	Ser	Leu	Lys	Lys	Arg	Ile
			355					360					365			
	Glu	Arg	Leu	Ala	Arg	Ala	Thr	Ala	Asn	Thr	Lys	Ser	His	Gln	Ala	Pro
		370					375					380				
50	Phe	Arg	Asn	Met	Met	Phe	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Met
	385					390					395					400
	Val	Ala	Arg	Glu	Ile	Ala	Arg	Lys	Ser	Gly	Leu	Asp	Tyr	Ala	Met	Met
					405					410					415	
55	Thr	Gly	Gly	Asp	Val	Ala	Pro	Leu	Gly	Ser	Gln	Ala	Val	Thr	Lys	Ile
				420					425					430		
	His	Gln	Ile	Phe	Asp	Trp	Ala	Lys	Lys	Ser	Asn	Arg	Gly	Leu	Leu	Leu
			435					440					445			
	Phe	Ile	Asp	Glu	Ala	Asp	Ala	Phe	Leu	Cys	Glu	Arg	Asn	Ser	Thr	Tyr
		450					455					460				
60	Met	Ser	Glu	Ala	Gln	Arg	Ser	Ala	Leu	Asn	Ala	Leu	Leu	Phe	Arg	Thr
	465					470					475					480
	Gly	Asp	Gln	Ser	Arg	Asp	Ile	Val	Leu	Val	Leu	Ala	Thr	Asn	Arg	Pro

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				485				490					495	
	Gly	Asp	Leu	Asp	Ser	Ala	Val	Thr	Asp	Arg	Ile	Asp	Glu	Val
				500					505				510	
5	Phe	Pro	Leu	Pro	Gly	Glu	Glu	Glu	Arg	Phe	Lys	Leu	Leu	Asn
			515					520					525	
	Leu	Asn	Lys	Tyr	Leu	Lys	Met	Gly	Asp	Asn	Asn	Glu	Asp	Thr
		530					535					540		
	Lys	Trp	Ser	His	Leu	Phe	Lys	Lys	Leu	Ser	Gln	Lys	Ile	Thr
	545					550					555			560
10	Glu	Asp	Leu	Thr	Asp	Lys	Val	Ile	Ser	Glu	Ala	Ala	Lys	Lys
					565					570				575
	Gly	Phe	Ser	Gly	Arg	Glu	Ile	Ala	Lys	Leu	Val	Ala	Gly	Val
				580					585					590
	Gly	Val	Tyr	Gly	Arg	Ala	Asp	Cys	Val	Leu	Asp	Ser	Gln	Leu
15			595				600						605	
	Glu	Ile	Val	Glu	Tyr	Lys	Val	Glu	Glu	His	His	Arg	Arg	His
		610					615					620		
	Ala	Ser	Glu	Gly	Phe	Gln	Pro	Leu	Leu	Phe	Ser			
	625					630				635				
20	(2) INFORMATION FOR SEQ ID NO:257:													
	(i) SEQUENCE CHARACTERISTICS:													
	(A) LENGTH: 617 amino acids													
	(B) TYPE: amino acid													
	(C) STRANDEDNESS:													
25	(D) TOPOLOGY: linear													
	(ii) MOLECULE TYPE: peptide													
	(ix) FEATURE:													
	(A) NAME/KEY: peptide													
	(B) LOCATION: 1..617													
30	(D) OTHER INFORMATION: / Ceres Seq. ID 1450878													
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:													
	Met	Ser	Met	Ser	Gln	Asn	Arg	Ala	Tyr	Ala	Asp	Ser	Ser	Arg
	1				5					10				15
35	Phe	Pro	Phe	Phe	Ser	Ser	Ser	Pro	Ser	Pro	Pro	Pro	Ser	Asp
				20					25					30
	Ala	Asn	Gln	Ser	Ser	Thr	Asn	Ser	Ser	Lys	Ser	Lys	Ala	Glu
			35				40						45	
	Glu	Pro	Lys	Gly	Ser	Gly	Phe	Asp	Pro	Glu	Ala	Leu	Glu	Arg
		50					55					60		
40	Lys	Ala	Leu	Arg	Asp	Ile	Asn	Ser	Ser	Pro	His	Ser	Lys	Gln
	65					70					75			80
	Asp	Leu	Met	Arg	Lys	Gln	Glu	Lys	Thr	Arg	Leu	Ala	Glu	Leu
				85						90				95
45	Glu	Thr	Ser	His	Tyr	Glu	Ala	Ile	Gln	Ala	His	Asn	Asp	Ile
				100					105					110
	Gln	Gln	Lys	Leu	Ala	Glu	Asp	Gln	Arg	Asn	Leu	Leu	Gln	Thr
			115					120					125	
	Gln	Thr	Lys	Ala	Gln	Asn	Leu	Arg	Tyr	Glu	Asp	Glu	Leu	Ala
		130				135					140			
50	Arg	Gln	Gln	Thr	Asp	His	Glu	Ala	Gln	Arg	His	His	Asn	Val
	145					150					155			160
	Val	Lys	Met	Gln	Glu	Ala	Ser	Ser	Ile	Arg	Lys	Glu	Lys	Ala
				165					170					175
55	Ala	Thr	Glu	Glu	Gln	Ile	Gln	Ala	Gln	His	Arg	Gln	Thr	Glu
				180					185				190	
	Arg	Ala	Glu	Leu	Glu	Arg	Glu	Thr	Ile	Arg	Val	Lys	Ala	Met
			195				200					205		
	Ala	Glu	Gly	Arg	Ala	His	Glu	Ala	Lys	Leu	Thr	Glu	Glu	Gln
		210				215						220		
60	Arg	Leu	Leu	Met	Glu	Arg	Ile	Asn	Gly	Glu	Arg	Glu	Lys	Trp
	225					230					235			240
	Ala	Ile	Asn	Thr	Met	Phe	Ser	His	Ile	Glu	Gly	Gly	Phe	Arg

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				245				250					255			
	Leu	Thr	Asp	Arg	Asn	Lys	Leu	Ile	Met	Thr	Val	Gly	Gly	Ala	Thr	Ala
				260					265					270		
5	Leu	Ala	Ala	Gly	Val	Tyr	Thr	Thr	Arg	Glu	Gly	Ala	Arg	Val	Thr	Trp
			275					280					285			
	Gly	Tyr	Ile	Asn	Arg	Met	Leu	Gly	Gln	Pro	Ser	Leu	Ile	Arg	Glu	Ser
		290					295					300				
	Ser	Met	Arg	Arg	Phe	Pro	Trp	Thr	Gly	Ser	Val	Ser	Gln	Phe	Lys	Asn
	305					310					315				320	
10	Arg	Ile	Ser	Gly	Ala	Ala	Ala	Ala	Ser	Ala	Ala	Glu	Gly	Lys	Lys	Pro
				325						330					335	
	Leu	Asp	Asn	Val	Ile	Leu	His	Thr	Ser	Leu	Lys	Lys	Arg	Ile	Glu	Arg
			340						345					350		
15	Leu	Ala	Arg	Ala	Thr	Ala	Asn	Thr	Lys	Ser	His	Gln	Ala	Pro	Phe	Arg
			355					360					365			
	Asn	Met	Met	Phe	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Met	Val	Ala
		370					375					380				
	Arg	Glu	Ile	Ala	Arg	Lys	Ser	Gly	Leu	Asp	Tyr	Ala	Met	Met	Thr	Gly
	385					390					395				400	
20	Gly	Asp	Val	Ala	Pro	Leu	Gly	Ser	Gln	Ala	Val	Thr	Lys	Ile	His	Gln
				405						410					415	
	Ile	Phe	Asp	Trp	Ala	Lys	Lys	Ser	Asn	Arg	Gly	Leu	Leu	Leu	Phe	Ile
			420						425					430		
25	Asp	Glu	Ala	Asp	Ala	Phe	Leu	Cys	Glu	Arg	Asn	Ser	Thr	Tyr	Met	Ser
			435					440					445			
	Glu	Ala	Gln	Arg	Ser	Ala	Leu	Asn	Ala	Leu	Leu	Phe	Arg	Thr	Gly	Asp
		450					455					460				
	Gln	Ser	Arg	Asp	Ile	Val	Leu	Val	Leu	Ala	Thr	Asn	Arg	Pro	Gly	Asp
	465				470						475				480	
30	Leu	Asp	Ser	Ala	Val	Thr	Asp	Arg	Ile	Asp	Glu	Val	Ile	Glu	Phe	Pro
				485						490					495	
	Leu	Pro	Gly	Glu	Glu	Glu	Arg	Phe	Lys	Leu	Leu	Asn	Leu	Tyr	Leu	Asn
			500						505					510		
35	Lys	Tyr	Leu	Lys	Met	Gly	Asp	Asn	Asn	Glu	Asp	Thr	Lys	Pro	Lys	Trp
			515					520					525			
	Ser	His	Leu	Phe	Lys	Lys	Leu	Ser	Gln	Lys	Ile	Thr	Val	Glu	Glu	Asp
		530					535					540				
	Leu	Thr	Asp	Lys	Val	Ile	Ser	Glu	Ala	Ala	Lys	Lys	Thr	Glu	Gly	Phe
	545				550						555				560	
40	Ser	Gly	Arg	Glu	Ile	Ala	Lys	Leu	Val	Ala	Gly	Val	Gln	Ala	Gly	Val
				565						570					575	
	Tyr	Gly	Arg	Ala	Asp	Cys	Val	Leu	Asp	Ser	Gln	Leu	Phe	Lys	Glu	Ile
			580						585					590		
45	Val	Glu	Tyr	Lys	Val	Glu	Glu	His	His	Arg	Arg	His	Met	Leu	Ala	Ser
			595					600					605			
	Glu	Gly	Phe	Gln	Pro	Leu	Leu	Phe	Ser							
		610					615									

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

55 (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1459191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

60	aaccctcttg	gaaagagtct	caacacttgc	agagaaaaag	aacaaggaag	atccccgaaa	60
	atggcaacgg	cgattgtacg	ttcagctctt	tcccagacag	tgactcgcg	agtcggaaga	120
	catccgtcgc	tcctaagcga	aacttttctt	cttcgcgcgg	ccatgacgat	gcttatgaag	180

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ctgcgaagtg ggagaagata acttatctgg gtattgctag ttgcactgct ctagctgtct 240
 atgtttttatc caagggccat catcacggcg aagacaagga gtttccttgg ggtccggatg 300
 gtctgtttga ggtgaagcac aacaaagagc actgagtcct gcgtgggtcat aataacgtct 360
 tctaggttta tttgaaaggc taaaatgttt taccgtatct gttctcaccg tttgtcaacg 420
 atttgctact ccaatctctt ttcttttggg gggaaataaa agttaatact ttgcttgg

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1459192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Asn Pro Leu Gly Lys Ser Leu Asn Thr Cys Arg Glu Lys Glu Gln Gly
 1 5 10 15
 20 Arg Ser Arg Lys Met Ala Thr Ala Ile Val Arg Ser Ala Leu Ser Arg
 20 25 30
 Ala Val Thr Arg Ala Val Arg Arg His Pro Ser Leu Leu Ser Glu Thr
 35 40 45
 25 Phe Pro Leu Pro Pro Ala Met Thr Met Leu Met Lys Leu Arg Ser Gly
 50 55 60
 Arg Arg
 65

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1459193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Pro Ser Trp Lys Glu Ser Gln His Leu Gln Arg Lys Arg Thr Arg Lys
 1 5 10 15
 Ile Pro Glu Asn Gly Asn Gly Asp Cys Thr Phe Ser Ser Phe Pro Ser
 20 25 30
 Ser Asp Ser Arg Ser Pro Lys Thr Ser Val Ala Pro Lys Arg Asn Phe
 35 40 45
 Ser Ser Ser Ala Gly His Asp Asp Ala Tyr Glu Ala Ala Lys Trp Glu
 50 55 60
 Lys Ile Thr Tyr Leu Gly Ile Ala Ser Cys Thr Ala Leu Ala Val Tyr
 65 70 75 80
 50 Val Leu Ser Lys Gly His His His Gly Glu Asp Lys Glu Phe Pro Trp
 85 90 95
 Gly Pro Asp Gly Leu Phe Glu Val Lys His Asn Lys Glu His
 100 105 110

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 741 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

448

(B) LOCATION: 1..741

(D) OTHER INFORMATION: / Ceres Seq. ID 1461848

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

5 atttttagtac attggttgacc atcttttttcg tatagactac tatctctgat ctcttgcgag 60
 ttaagtcagt aactaggaaa attcagaagc gctctcaatc tcaaaaatat ccatggcggc 120
 gattacagaa tttctaccaa aagagtacgg atatgtcggt ctcgtcctcg tcttctactg 180
 tttcctcaac ctctggatgg gtgctcaagt cggcagagct cgcaaaaggt acaacgtccc 240
 gtatccaact ctatatgcaa tagaatcaga aaacaaagat gctaagctct tcaactgtgt 300
 tcagagagga catcaaaact ctttagagat gatgccaatg tatttcatac tgatgatcct 360
 10 cggtgggatg aagcaccctt gtatctgtac tggccttggg ttgctttaca acgttagccg 420
 attcttctac tttaaagggt atgctactgg agatcccatg aagcgtctta cgatcgggaa 480
 atacggtttc ttgggggtgc taggtctgat gatatgtacc atctcgtttg gtgtcactct 540
 gatccttgct taagctactc gtttctgggg ttaatgattc tctggtttgc tcgaagaata 600
 tagaaccaat gcttgtaagc tgtccacaaa acttggtgtaa tacttttagag tttgtcactt 660
 15 ttaaaagttt gtaataaatc atggcttcat agaacagttg aaatttcaca tccgtagacg 720
 ttaataaaga ttgaattat g

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1461849

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

30 Met Ala Ala Ile Thr Glu Phe Leu Pro Lys Glu Tyr Gly Tyr Val Val
 1 5 10 15
 Leu Val Leu Val Phe Tyr Cys Phe Leu Asn Leu Trp Met Gly Ala Gln
 20 25 30
 Val Gly Arg Ala Arg Lys Arg Tyr Asn Val Pro Tyr Pro Thr Leu Tyr
 35 35 40 45
 Ala Ile Glu Ser Glu Asn Lys Asp Ala Lys Leu Phe Asn Cys Val Gln
 50 55 60
 Arg Gly His Gln Asn Ser Leu Glu Met Met Pro Met Tyr Phe Ile Leu
 65 70 75 80
 40 Met Ile Leu Gly Gly Met Lys His Pro Cys Ile Cys Thr Gly Leu Gly
 85 90 95
 Leu Leu Tyr Asn Val Ser Arg Phe Phe Tyr Phe Lys Gly Tyr Ala Thr
 100 105 110
 Gly Asp Pro Met Lys Arg Leu Thr Ile Gly Lys Tyr Gly Phe Leu Gly
 115 120 125
 45 Leu Leu Gly Leu Met Ile Cys Thr Ile Ser Phe Gly Val Thr Leu Ile
 130 135 140
 Leu Ala
 145

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 1461850

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

60 Met Gly Ala Gln Val Gly Arg Ala Arg Lys Arg Tyr Asn Val Pro Tyr
 1 5 10 15

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Pro Thr Leu Tyr Ala Ile Glu Ser Glu Asn Lys Asp Ala Lys Leu Phe
 20 25 30
 Asn Cys Val Gln Arg Gly His Gln Asn Ser Leu Glu Met Met Pro Met
 35 40 45
 5 Tyr Phe Ile Leu Met Ile Leu Gly Gly Met Lys His Pro Cys Ile Cys
 50 55 60
 Thr Gly Leu Gly Leu Leu Tyr Asn Val Ser Arg Phe Phe Tyr Phe Lys
 65 70 75 80
 10 Gly Tyr Ala Thr Gly Asp Pro Met Lys Arg Leu Thr Ile Gly Lys Tyr
 85 90 95
 Gly Phe Leu Gly Leu Leu Gly Leu Met Ile Cys Thr Ile Ser Phe Gly
 100 105 110
 Val Thr Leu Ile Leu Ala
 115

15 (2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

20 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

25 (D) OTHER INFORMATION: / Ceres Seq. ID 1461851

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

Met Met Pro Met Tyr Phe Ile Leu Met Ile Leu Gly Gly Met Lys His
 1 5 10 15
 Pro Cys Ile Cys Thr Gly Leu Gly Leu Leu Tyr Asn Val Ser Arg Phe
 20 25 30
 30 Phe Tyr Phe Lys Gly Tyr Ala Thr Gly Asp Pro Met Lys Arg Leu Thr
 35 40 45
 Ile Gly Lys Tyr Gly Phe Leu Gly Leu Leu Gly Leu Met Ile Cys Thr
 50 55 60
 35 Ile Ser Phe Gly Val Thr Leu Ile Leu Ala
 65 70

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs

40 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

45 (A) NAME/KEY: -

(B) LOCATION: 1..469

(D) OTHER INFORMATION: / Ceres Seq. ID 1472772

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

atatagaata taaccatatt ccggacatga agatcgtgac attggtactc gtcgtcttcg 60
 50 tcatactttc gacatcattc ccggctgcca tcaaagccga agacacggga gatacaggaa 120
 atgtgggagt gacatgtgac gcaaggcagc ttcagccttg ccttgccgag attacgggag 180
 gaggacaacc ctccgggtgca tgttgtgcaa agcttacaga gcaacagtca tgcctatgtg 240
 gtttcgctaa gaacctgagc ttcgcacagt acattagctc tccaaacgct cgcaaagtgc 300
 tccttgcttg caatgttgct tatccactt gttgaaactt atctagattt tataaataaa 360
 55 taaacgaaa gaaataaatt acattatatc aaacgttatg atacaattca accgtttgtg 420
 ttaatgtact ggcttacatg gttaaataaa gtttaatttc ttggttgcc

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

60 (B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

450

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..110

(D) OTHER INFORMATION: / Ceres Seq. ID 1472773

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

```

Ile Glu Tyr Asn His Ile Pro Asp Met Lys Ile Val Thr Leu Val Leu
1      5      10      15
Val Val Phe Val Ile Leu Ser Thr Ser Phe Pro Ala Ala Ile Lys Ala
20     25     30
Glu Asp Thr Gly Asp Thr Gly Asn Val Gly Val Thr Cys Asp Ala Arg
35     40     45
Gln Leu Gln Pro Cys Leu Ala Ala Ile Thr Gly Gly Gly Gln Pro Ser
50     55     60
Gly Ala Cys Cys Ala Lys Leu Thr Glu Gln Gln Ser Cys Leu Cys Gly
65     70     75     80
Phe Ala Lys Asn Pro Ala Phe Ala Gln Tyr Ile Ser Ser Pro Asn Ala
85     90     95
Arg Lys Val Leu Leu Ala Cys Asn Val Ala Tyr Pro Thr Cys
100    105    110

```

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1472774

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

```

Met Lys Ile Val Thr Leu Val Leu Val Val Phe Val Ile Leu Ser Thr
1      5      10      15
Ser Phe Pro Ala Ala Ile Lys Ala Glu Asp Thr Gly Asp Thr Gly Asn
20     25     30
Val Gly Val Thr Cys Asp Ala Arg Gln Leu Gln Pro Cys Leu Ala Ala
35     40     45
Ile Thr Gly Gly Gly Gln Pro Ser Gly Ala Cys Cys Ala Lys Leu Thr
50     55     60
Glu Gln Gln Ser Cys Leu Cys Gly Phe Ala Lys Asn Pro Ala Phe Ala
65     70     75     80
Gln Tyr Ile Ser Ser Pro Asn Ala Arg Lys Val Leu Leu Ala Cys Asn
85     90     95
Val Ala Tyr Pro Thr Cys
100

```

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1056 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1056

(D) OTHER INFORMATION: / Ceres Seq. ID 1533352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

```

aaaaaaaaa accaaagcaa aaaaatggct ttgaaactca cttctccgcc ttcagttttc      60
tcacaatcaa ggagattatc ttcttcttcg ttaattccga taagggtcaaa atccacattc      120
accggatttc gatcgagaac cgggtgtttat ttaagcaaaa cgacggcgct tcagtcgtct      180
acaaaactga gtgtggcggc ggagagtcct gcggcgacaa ttgcgcacgga tgattggggg      240

```

451

aaagtatcgg cggttctgtt tgatatggac ggtgtgcttt gtaacagtga agatctttct 300
 agacgcgccg ccgtggatgt ttttacggag atgggagttg aagtcactgt ggacgatttc 360
 gttcctttta tgggaacagg tgaagccaag tttttaggag gtgttgcttc agtcaaagaa 420
 gttaaaggat ttgatccaga tgcagctaaa aagagattct ttgaaatata tctcgataag 480
 5 tatgcgaagc cagaatctgg gattggattt ccaggagcat tggagcttgt tactgagtgt 540
 aagaacaaag gccttaaagt cgctgttgca tctagtgtct accgtatcaa agttgatgcg 600
 aatctgaaaag ctgctggttt gtctttgacc atgtttgatg ccattgtttc agcagatgcc 660
 tttgagaatt tgaaccagc tccagatatt ttcttggtct ctgcaaagat cttagggtgtg 720
 cctaccagcg agtgtgttgt tattgaagat gcgcttgctg gagtccaagc cgcacaagct 780
 10 gcgaacatga gatgtatagc cgtaaaaact actttatctg aagcaattct taaggatgct 840
 ggtccttcaa tgatacgaga cgatattgga aacatctcaa tcaatgacat tctcactggt 900
 ggctcagatt ctaccagtat gtagtctcaa agaaattcga tggaaaatat cgttcttttc 960
 atgtgtattt tatttcttgt ttactccttt tgaaaacttt tgaataaaagg ggctttcttt 1020
 gtaacgagat tacacattta aaacaatctt ttctgt

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..307

(D) OTHER INFORMATION: / Ceres Seq. ID 1533353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

Lys Lys Lys Asn Gln Ser Lys Lys Met Ala Leu Lys Leu Thr Ser Pro
 1 5 10 15
 Pro Ser Val Phe Ser Gln Ser Arg Arg Leu Ser Ser Ser Ser Leu Ile
 20 25 30
 Pro Ile Arg Ser Lys Ser Thr Phe Thr Gly Phe Arg Ser Arg Thr Gly
 35 40 45
 Val Tyr Leu Ser Lys Thr Thr Ala Leu Gln Ser Ser Thr Lys Leu Ser
 50 55 60
 Val Ala Ala Glu Ser Pro Ala Ala Thr Ile Ala Thr Asp Asp Trp Gly
 65 70 75 80
 Lys Val Ser Ala Val Leu Phe Asp Met Asp Gly Val Leu Cys Asn Ser
 85 90 95
 Glu Asp Leu Ser Arg Arg Ala Ala Val Asp Val Phe Thr Glu Met Gly
 100 105 110
 Val Glu Val Thr Val Asp Asp Phe Val Pro Phe Met Gly Thr Gly Glu
 115 120 125
 Ala Lys Phe Leu Gly Gly Val Ala Ser Val Lys Glu Val Lys Gly Phe
 130 135 140
 Asp Pro Asp Ala Ala Lys Lys Arg Phe Phe Glu Ile Tyr Leu Asp Lys
 145 150 155 160
 Tyr Ala Lys Pro Glu Ser Gly Ile Gly Phe Pro Gly Ala Leu Glu Leu
 165 170 175
 Val Thr Glu Cys Lys Asn Lys Gly Leu Lys Val Ala Val Ala Ser Ser
 180 185 190
 Ala Asp Arg Ile Lys Val Asp Ala Asn Leu Lys Ala Ala Gly Leu Ser
 195 200 205
 Leu Thr Met Phe Asp Ala Ile Val Ser Ala Asp Ala Phe Glu Asn Leu
 210 215 220
 Lys Pro Ala Pro Asp Ile Phe Leu Ala Ala Lys Ile Leu Gly Val
 225 230 235 240
 Pro Thr Ser Glu Cys Val Val Ile Glu Asp Ala Leu Ala Gly Val Gln
 245 250 255
 Ala Ala Gln Ala Ala Asn Met Arg Cys Ile Ala Val Lys Thr Thr Leu
 260 265 270
 60 Ser Glu Ala Ile Leu Lys Asp Ala Gly Pro Ser Met Ile Arg Asp Asp
 275 280 285

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Ile Gly Asn Ile Ser Ile Asn Asp Ile Leu Thr Gly Gly Ser Asp Ser
 290 295 300
 Thr Ser Met
 305

- 5 (2) INFORMATION FOR SEQ ID NO:270:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 299 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 10 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..299
 15 (D) OTHER INFORMATION: / Ceres Seq. ID 1533354
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:
 Met Ala Leu Lys Leu Thr Ser Pro Pro Ser Val Phe Ser Gln Ser Arg
 1 5 10 15
 Arg Leu Ser Ser Ser Ser Leu Ile Pro Ile Arg Ser Lys Ser Thr Phe
 20 20 25 30
 Thr Gly Phe Arg Ser Arg Thr Gly Val Tyr Leu Ser Lys Thr Thr Ala
 35 40 45
 Leu Gln Ser Ser Thr Lys Leu Ser Val Ala Ala Glu Ser Pro Ala Ala
 50 55 60
 25 Thr Ile Ala Thr Asp Asp Trp Gly Lys Val Ser Ala Val Leu Phe Asp
 65 70 75 80
 Met Asp Gly Val Leu Cys Asn Ser Glu Asp Leu Ser Arg Arg Ala Ala
 85 90 95
 Val Asp Val Phe Thr Glu Met Gly Val Glu Val Thr Val Asp Asp Phe
 30 100 105 110
 Val Pro Phe Met Gly Thr Gly Glu Ala Lys Phe Leu Gly Gly Val Ala
 115 120 125
 Ser Val Lys Glu Val Lys Gly Phe Asp Pro Asp Ala Ala Lys Lys Arg
 130 135 140
 35 Phe Phe Glu Ile Tyr Leu Asp Lys Tyr Ala Lys Pro Glu Ser Gly Ile
 145 150 155 160
 Gly Phe Pro Gly Ala Leu Glu Leu Val Thr Glu Cys Lys Asn Lys Gly
 165 170 175
 Leu Lys Val Ala Val Ala Ser Ser Ala Asp Arg Ile Lys Val Asp Ala
 40 180 185 190
 Asn Leu Lys Ala Ala Gly Leu Ser Leu Thr Met Phe Asp Ala Ile Val
 195 200 205
 Ser Ala Asp Ala Phe Glu Asn Leu Lys Pro Ala Pro Asp Ile Phe Leu
 210 215 220
 45 Ala Ala Ala Lys Ile Leu Gly Val Pro Thr Ser Glu Cys Val Val Ile
 225 230 235 240
 Glu Asp Ala Leu Ala Gly Val Gln Ala Ala Gln Ala Ala Asn Met Arg
 245 250 255
 Cys Ile Ala Val Lys Thr Thr Leu Ser Glu Ala Ile Leu Lys Asp Ala
 50 260 265 270
 Gly Pro Ser Met Ile Arg Asp Asp Ile Gly Asn Ile Ser Ile Asn Asp
 275 280 285
 Ile Leu Thr Gly Gly Ser Asp Ser Thr Ser Met
 290 295
- 55 (2) INFORMATION FOR SEQ ID NO:271:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 219 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 60 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

453

(A) NAME/KEY: peptide

(B) LOCATION: 1..219

(D) OTHER INFORMATION: / Ceres Seq. ID 1533355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

5 Met Asp Gly Val Leu Cys Asn Ser Glu Asp Leu Ser Arg Arg Ala Ala
 1 5 10 15
 Val Asp Val Phe Thr Glu Met Gly Val Glu Val Thr Val Asp Asp Phe
 20 25 30
 Val Pro Phe Met Gly Thr Gly Glu Ala Lys Phe Leu Gly Gly Val Ala
 35 40 45
 10 Ser Val Lys Glu Val Lys Gly Phe Asp Pro Asp Ala Ala Lys Lys Arg
 50 55 60
 Phe Phe Glu Ile Tyr Leu Asp Lys Tyr Ala Lys Pro Glu Ser Gly Ile
 65 70 75 80
 15 Gly Phe Pro Gly Ala Leu Glu Leu Val Thr Glu Cys Lys Asn Lys Gly
 85 90 95
 Leu Lys Val Ala Val Ala Ser Ser Ala Asp Arg Ile Lys Val Asp Ala
 100 105 110
 Asn Leu Lys Ala Ala Gly Leu Ser Leu Thr Met Phe Asp Ala Ile Val
 115 120 125
 20 Ser Ala Asp Ala Phe Glu Asn Leu Lys Pro Ala Pro Asp Ile Phe Leu
 130 135 140
 Ala Ala Ala Lys Ile Leu Gly Val Pro Thr Ser Glu Cys Val Val Ile
 145 150 155 160
 25 Glu Asp Ala Leu Ala Gly Val Gln Ala Ala Gln Ala Ala Asn Met Arg
 165 170 175
 Cys Ile Ala Val Lys Thr Thr Leu Ser Glu Ala Ile Leu Lys Asp Ala
 180 185 190
 Gly Pro Ser Met Ile Arg Asp Asp Ile Gly Asn Ile Ser Ile Asn Asp
 195 200 205
 30 Ile Leu Thr Gly Gly Ser Asp Ser Thr Ser Met
 210 215

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1420 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1420

(D) OTHER INFORMATION: / Ceres Seq. ID 1534544

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

45 aaagattctt ggtctccgat ccagtcacct gaagattctc ggagcttctt ttgaccacac 60
 actttcaatg gcggtatgctg tgaacgctca aactccatcg ctctccgagc aatatcattt 120
 ggagaaagaa gtgaagcaag acacaagtgc aaagcctggt gaagtgaag aggtggcacc 180
 agaagttact acacaagctg aagagggttaa gacggagcaa gctaaggaag aatctcctgt 240
 tgaggaagcg gtttctgtag ttgaagagaa gtctgaatct gctcctgaat caacggaagt 300
 50 ggcttctgag gctcctgctg cagcggaaga caatgctgaa gagactcctg ctgctgctga 360
 agaaaataat gacgaaaacg ctagtgaaga agttgctgaa gaaaccctg atgagatcaa 420
 gcttgagaca gctcctgctt gatctcatca ggggtttctt tttttttttt ttttttgaat 480
 tttttcacca agtgttcgtt cacggcattg cttgtcctcc agtatgagta tctccggtgc 540
 tgcagttggt tcaggcagaa atttaagaag agcggtagag tttgggaaaa ctcatgtggt 600
 55 taggcctaaa gggaaacatc aagcaactat tgtctggtta catgggcttg gggacaatgg 660
 ctgagactgg tcccagcttt tggagaccct tccccttcca aatatcaa atggatttgccc 720
 gactgctcct tctcaaccaa taagtttatt tgggtggttt ccctccacag cttggtttga 780
 tgttgtggac atcaatgaag atggacctga tgatatggaa ggattggatg tggctgctgc 840
 acatgttgca aatctgttgt cgaatgagcc tgctgacatt aaattaggtg ttggaggatt 900
 60 cagcatgggt gcggcagcat ctctatatcc tgcaacttgt tttgctctcg gtaaatatgg 960
 aaatggcaat ccaatacccta tcaatttaag cgcaatcata ggcttaagcg gctggcttcc 1020
 ttgtgcaaaag acattggctg gcaaactaga agaggaacag atcaagaacc gagctgcac 1080

454

gttacccatt gttgtctgtc atggaaaagc tgatgatgtg gtaccgttca agtttgggga 1140
 gaaatcttca caggctttgc tttcaaagtg gtttaagaag gtgaccttca aaccttacag 1200
 tgcacttggt caccacacaa tcccacagga gttggatgag ttgtgcgcat ggttgacatc 1260
 cacgctcagc ctogaagggt gatacttcct atgatgtagc tttctgatga aaacccttca 1320
 5 actcttgaga gtttgattga attggatggt tcaggatttc acaatgtttt cattggaata 1380
 tttgtgtaag acacattcgt ctagtagcaa atcttctcct

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 1534545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Lys Ile Leu Gly Leu Arg Ser Ser His Leu Lys Ile Leu Gly Ala Ser
 1 5 10 15
 Phe Asp His Thr Leu Ser Met Ala Asp Ala Val Asn Ala Gln Thr Pro
 20 25 30
 Ser Leu Ser Glu Gln Tyr His Leu Glu Lys Glu Val Lys Gln Asp Thr
 35 40 45
 25 Ser Ala Lys Pro Val Glu Val Lys Glu Val Ala Pro Glu Val Thr Thr
 50 55 60
 Gln Ala Glu Glu Val Lys Thr Glu Gln Ala Lys Glu Glu Ser Pro Val
 65 70 75 80
 Glu Glu Ala Val Ser Val Val Glu Glu Lys Ser Glu Ser Ala Pro Glu
 85 90 95
 30 Ser Thr Glu Val Ala Ser Glu Ala Pro Ala Ala Ala Glu Asp Asn Ala
 100 105 110
 Glu Glu Thr Pro Ala Ala Ala Glu Asn Asn Asp Glu Asn Ala Ser
 115 120 125
 35 Glu Glu Val Ala Glu Glu Thr Pro Asp Glu Ile Lys Leu Glu Thr Ala
 130 135 140
 Pro Ala
 145

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..252

(D) OTHER INFORMATION: / Ceres Seq. ID 1534546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Met Ser Ile Ser Gly Ala Ala Val Gly Ser Gly Arg Asn Leu Arg Arg
 1 5 10 15
 Ala Val Glu Phe Gly Lys Thr His Val Val Arg Pro Lys Gly Lys His
 20 25 30
 55 Gln Ala Thr Ile Val Trp Leu His Gly Leu Gly Asp Asn Gly Ser Ser
 35 40 45
 Trp Ser Gln Leu Leu Glu Thr Leu Pro Leu Pro Asn Ile Lys Trp Ile
 50 55 60
 Cys Pro Thr Ala Pro Ser Gln Pro Ile Ser Leu Phe Gly Gly Phe Pro
 65 70 75 80
 60 Ser Thr Ala Trp Phe Asp Val Val Asp Ile Asn Glu Asp Gly Pro Asp
 85 90 95

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Asp Met Glu Gly Leu Asp Val Ala Ala Ala His Val Ala Asn Leu Leu
 100 105 110
 Ser Asn Glu Pro Ala Asp Ile Lys Leu Gly Val Gly Gly Phe Ser Met
 115 120 125
 5 Gly Ala Ala Thr Ser Leu Tyr Ser Ala Thr Cys Phe Ala Leu Gly Lys
 130 135 140
 Tyr Gly Asn Gly Asn Pro Tyr Pro Ile Asn Leu Ser Ala Ile Ile Gly
 145 150 155 160
 10 Leu Ser Gly Trp Leu Pro Cys Ala Lys Thr Leu Ala Gly Lys Leu Glu
 165 170 175
 Glu Glu Gln Ile Lys Asn Arg Ala Ala Ser Leu Pro Ile Val Val Cys
 180 185 190
 His Gly Lys Ala Asp Asp Val Val Pro Phe Lys Phe Gly Glu Lys Ser
 195 200 205
 15 Ser Gln Ala Leu Leu Ser Asn Gly Phe Lys Lys Val Thr Phe Lys Pro
 210 215 220
 Tyr Ser Ala Leu Gly His His Thr Ile Pro Gln Glu Leu Asp Glu Leu
 225 230 235 240
 20 Cys Ala Trp Leu Thr Ser Thr Leu Ser Leu Glu Gly
 245 250

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1534547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

Met Glu Gly Leu Asp Val Ala Ala Ala His Val Ala Asn Leu Leu Ser
 1 5 10 15
 35 Asn Glu Pro Ala Asp Ile Lys Leu Gly Val Gly Gly Phe Ser Met Gly
 20 25 30
 Ala Ala Thr Ser Leu Tyr Ser Ala Thr Cys Phe Ala Leu Gly Lys Tyr
 35 40 45
 40 Gly Asn Gly Asn Pro Tyr Pro Ile Asn Leu Ser Ala Ile Ile Gly Leu
 50 55 60
 Ser Gly Trp Leu Pro Cys Ala Lys Thr Leu Ala Gly Lys Leu Glu Glu
 65 70 75 80
 Glu Gln Ile Lys Asn Arg Ala Ala Ser Leu Pro Ile Val Val Cys His
 85 90 95
 45 Gly Lys Ala Asp Asp Val Val Pro Phe Lys Phe Gly Glu Lys Ser Ser
 100 105 110
 Gln Ala Leu Leu Ser Asn Gly Phe Lys Lys Val Thr Phe Lys Pro Tyr
 115 120 125
 50 Ser Ala Leu Gly His His Thr Ile Pro Gln Glu Leu Asp Glu Leu Cys
 130 135 140
 Ala Trp Leu Thr Ser Thr Leu Ser Leu Glu Gly
 145 150 155

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1592 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1592

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(D) OTHER INFORMATION: / Ceres Seq. ID 1567172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

5 gtagtctctc tttttataac cacttctcga aaactgaaac ctttgtagag agaaccata 60
 gttcgataaa acattctttt tgcaactgag acttggcaac ttggttttac tcaaagtaag 120
 atttcttctt gttgatggtg ataagttcaa tatgatgaaa agtttggcta gtgcggttg 180
 agggaagacg gcgagggcat gtgatagctg cgtgaagagg cgggcacgtt ggtattgcgc 240
 aGctgatgat gccttttctt gccatgcttg tgacggttcg gtccactcgg caaacctct 300
 tgctcgtaga cagcagagag ttcgcttgaa atcggttagc gccggaaaat atcgccatgc 360
 ctgcgccctt caccaagcca cgtggcatca gggatttaca cgtaaagctc ggacccacg 420
 10 tggaggcaag aagagccaca cgatggtttt tcatgatctt gtgccggaga tgagcacgga 480
 ggatcaagcg gagagttacg aggtggaaga gcagctcata tttgaggtgc cggatgatgaa 540
 ctcgatggtt gaggagcaat gctttaacca atccctggag aaacagaatg agtttccaat 600
 gatgccctta agtttcaaga gtagtgacga agaagatgac gacaacgctg agagttgtct 660
 gaatggtttg ttcccaaccg acatggaact agctcagttc acagctgacg tggagactct 720
 15 actcgggtga ggggatcgag agtttcattc catagaagaa ctagggttag gtgagatggt 780
 aaagatcgaa aaagaggagg tggagggaaga ggaaggagtt gtgacaagag aagtgcata 840
 tcaagatgaa ggtgatgaga catccccatt tgaaataagc tttgactacg agtacacaca 900
 caagaccaca ttcgatgaag gagaagaaga tgagaaagaa gacgtgatga agaattgtat 960
 ggagatggga gtgaatgaga tgagtgggtg gattaaagaa gagaagaagg agaaggctct 1020
 20 tatgcttaga ttggactatg aatcagtcac ttccacttgg ggaggccaag ggatcccatg 1080
 gaccgcccg gtgccatctg aaatagacct cgacatggtt tgtttcccaa cccataccat 1140
 gggtgaaagt ggagcagagg ctcatcatca caaccacttc cgcggcctaG ggttacacct 1200
 aggagatgct ggggatggag gaagagaggc tagggtttca agataccgag agaaaaggag 1260
 gacaaggttg ttctccaaga agataaggta cgaggtagct aaattgaatg cagataaaag 1320
 25 gcttcgcatg aaaggaaggt tcgtcaagag atcttcaatt ggtgttgctc actaaagaac 1380
 ttaattaatt atggatatta aattactttg ctctcatctt gcttttttgt tgctatagtt 1440
 ttggtgattg ttagctttct ttttctgcat tcatagagaa ttttgacgt ttttgtgagc 1500
 tacgtatgta cataaatata tcaccaaaaa atgtgactat cttgtaagca ctgatttata 1560
 tagtcgatat aacgtgaatt ttgattgctg gt

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..407

(D) OTHER INFORMATION: / Ceres Seq. ID 1567173

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Met Met Lys Ser Leu Ala Ser Ala Val Gly Lys Thr Ala Arg Ala
 1 5 10 15
 Cys Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr Cys Ala Ala Asp
 20 25 30
 Asp Ala Phe Leu Cys His Ala Cys Asp Gly Ser Val His Ser Ala Asn
 35 40 45
 Pro Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys Ser Ala Ser Ala
 50 55 60
 Gly Lys Tyr Arg His Ala Ser Pro Pro His Gln Ala Thr Trp His Gln
 65 70 75 80
 Gly Phe Thr Arg Lys Ala Arg Thr Pro Arg Gly Gly Lys Lys Ser His
 85 90 95
 Thr Met Val Phe His Asp Leu Val Pro Glu Met Ser Thr Glu Asp Gln
 100 105 110
 Ala Glu Ser Tyr Glu Val Glu Glu Gln Leu Ile Phe Glu Val Pro Val
 115 120 125
 Met Asn Ser Met Val Glu Glu Gln Cys Phe Asn Gln Ser Leu Glu Lys
 130 135 140
 60 Gln Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu
 145 150 155 160
 Glu Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr

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				165					170					175			
	Asp	Met	Glu	Leu	Ala	Gln	Phe	Thr	Ala	Asp	Val	Glu	Thr	Leu	Leu	Gly	
				180					185					190			
5	Gly	Gly	Asp	Arg	Glu	Phe	His	Ser	Ile	Glu	Glu	Leu	Gly	Leu	Gly	Glu	
			195					200					205				
	Met	Leu	Lys	Ile	Glu	Lys	Glu	Val	Glu	Glu	Glu	Glu	Gly	Val	Val		
		210					215					220					
	Thr	Arg	Glu	Val	His	Asp	Gln	Asp	Glu	Gly	Asp	Glu	Thr	Ser	Pro	Phe	
	225				230						235					240	
10	Glu	Ile	Ser	Phe	Asp	Tyr	Glu	Tyr	Thr	His	Lys	Thr	Thr	Phe	Asp	Glu	
				245						250					255		
	Gly	Glu	Glu	Asp	Glu	Lys	Glu	Asp	Val	Met	Lys	Asn	Val	Met	Glu	Met	
				260					265					270			
15	Gly	Val	Asn	Glu	Met	Ser	Gly	Gly	Ile	Lys	Glu	Glu	Lys	Lys	Glu	Lys	
			275					280					285				
	Ala	Leu	Met	Leu	Arg	Leu	Asp	Tyr	Glu	Ser	Val	Ile	Ser	Thr	Trp	Gly	
		290					295					300					
	Gly	Gln	Gly	Ile	Pro	Trp	Thr	Ala	Arg	Val	Pro	Ser	Glu	Ile	Asp	Leu	
	305					310					315				320		
20	Asp	Met	Val	Cys	Phe	Pro	Thr	His	Thr	Met	Gly	Glu	Ser	Gly	Ala	Glu	
				325						330					335		
	Ala	His	His	His	Asn	His	Phe	Arg	Gly	Leu	Gly	Leu	His	Leu	Gly	Asp	
				340					345					350			
25	Ala	Gly	Asp	Gly	Gly	Arg	Glu	Ala	Arg	Val	Ser	Arg	Tyr	Arg	Glu	Lys	
			355					360					365				
	Arg	Arg	Thr	Arg	Leu	Phe	Ser	Lys	Lys	Ile	Arg	Tyr	Glu	Val	Arg	Lys	
		370					375					380					
	Leu	Asn	Ala	Asp	Lys	Arg	Pro	Arg	Met	Lys	Gly	Arg	Phe	Val	Lys	Arg	
	385					390					395					400	
30	Ser	Ser	Ile	Gly	Val	Ala	His										
					405												

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 1567174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

45	Met	Lys	Ser	Leu	Ala	Ser	Ala	Val	Gly	Gly	Lys	Thr	Ala	Arg	Ala	Cys
	1			5					10						15	
	Asp	Ser	Cys	Val	Lys	Arg	Arg	Ala	Arg	Trp	Tyr	Cys	Ala	Ala	Asp	Asp
			20						25					30		
	Ala	Phe	Leu	Cys	His	Ala	Cys	Asp	Gly	Ser	Val	His	Ser	Ala	Asn	Pro
			35					40					45			
50	Leu	Ala	Arg	Arg	His	Glu	Arg	Val	Arg	Leu	Lys	Ser	Ala	Ser	Ala	Gly
		50					55					60				
	Lys	Tyr	Arg	His	Ala	Ser	Pro	Pro	His	Gln	Ala	Thr	Trp	His	Gln	Gly
	65				70					75					80	
	Phe	Thr	Arg	Lys	Ala	Arg	Thr	Pro	Arg	Gly	Gly	Lys	Lys	Ser	His	Thr
55				85						90					95	
	Met	Val	Phe	His	Asp	Leu	Val	Pro	Glu	Met	Ser	Thr	Glu	Asp	Gln	Ala
				100					105					110		
	Glu	Ser	Tyr	Glu	Val	Glu	Glu	Gln	Leu	Ile	Phe	Glu	Val	Pro	Val	Met
			115					120					125			
60	Asn	Ser	Met	Val	Glu	Glu	Gln	Cys	Phe	Asn	Gln	Ser	Leu	Glu	Lys	Gln
		130					135					140				
	Asn	Glu	Phe	Pro	Met	Met	Pro	Leu	Ser	Phe	Lys	Ser	Ser	Asp	Glu	Glu

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145 150 155 160
 Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr Asp
 165 170 175
 5 Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly Gly
 180 185 190
 Gly Asp Arg Glu Phe His Ser Ile Glu Glu Leu Gly Leu Gly Glu Met
 195 200 205
 Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Glu Gly Val Val Thr
 210 215 220
 10 Arg Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe Glu
 225 230 235 240
 Ile Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu Gly
 245 250 255
 15 Glu Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met Gly
 260 265 270
 Val Asn Glu Met Ser Gly Gly Ile Lys Glu Glu Lys Lys Glu Lys Ala
 275 280 285
 Leu Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly Gly
 290 295 300
 20 Gln Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu Asp
 305 310 315 320
 Met Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu Ala
 325 330 335
 25 His His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp Ala
 340 345 350
 Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys Arg
 355 360 365
 Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys Leu
 370 375 380
 30 Asn Ala Asp Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg Ser
 385 390 395 400
 Ser Ile Gly Val Ala His
 405
 (2) INFORMATION FOR SEQ ID NO:279:
 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..310
 (D) OTHER INFORMATION: / Ceres Seq. ID 1567175
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:
 Met Val Phe His Asp Leu Val Pro Glu Met Ser Thr Glu Asp Gln Ala
 1 5 10 15
 Glu Ser Tyr Glu Val Glu Glu Gln Leu Ile Phe Glu Val Pro Val Met
 20 25 30
 50 Asn Ser Met Val Glu Glu Gln Cys Phe Asn Gln Ser Leu Glu Lys Gln
 35 40 45
 Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu Glu
 50 55 60
 55 Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr Asp
 65 70 75 80
 Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly Gly
 85 90 95
 Gly Asp Arg Glu Phe His Ser Ile Glu Glu Leu Gly Leu Gly Glu Met
 100 105 110
 60 Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Glu Gly Val Val Thr
 115 120 125
 Arg Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe Glu

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130 135 140
 Ile Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu Gly
 145 150 155 160
 Glu Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met Gly
 5 165 170 175
 Val Asn Glu Met Ser Gly Gly Ile Lys Glu Glu Lys Lys Glu Lys Ala
 180 185 190
 Leu Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly Gly
 195 200 205
 10 Gln Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu Asp
 210 215 220
 Met Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu Ala
 225 230 235 240
 15 His His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp Ala
 245 250 255
 Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys Arg
 260 265 270
 Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys Leu
 275 280 285
 20 Asn Ala Asp Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg Ser
 290 295 300
 Ser Ile Gly Val Ala His
 305 310

(2) INFORMATION FOR SEQ ID NO:280:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 520 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..520

(D) OTHER INFORMATION: / Ceres Seq. ID 1567555

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

aaaaattccg cagaattgat tatcgctcatt tcgttaagga tctctgtggg gtttgatcga 60
 atttcatagc gaaggagaga gtgagagaga gattgaagca gtaatggcag gaacatctgg 120
 attgctcaac gcagtgaagc caaagatcca aacgattgat attcaggccg ccgctggatg 180
 gggaatcgcc gccgcagccg gtgccatctg ggtcgctcaa ccatttggtt ggataaagaa 240
 40 gacattcatt gaccaccccc caactgaaga gaagtgaat atcaccaaga ttcaagacta 300
 agtgaagagt tttccagttt ctaagtttgt taccgcctct ttggcgtgga gctgaataaa 360
 ttttggttct tttctggggc tttctggttt catttcttca atgtttgact gatttgctct 420
 ctcaaatgtt ataacaacaa agaaaagcac ttactccaag ttacttgaaa agagaaccca 480
 ttttgcatct atcatgagtt attatttTcc atgtcaaagt

45 (2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1567536

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Met Ala Gly Thr Ser Gly Leu Leu Asn Ala Val Lys Pro Lys Ile Gln
 1 5 10 15
 Thr Ile Asp Ile Gln Ala Ala Ala Gly Trp Gly Ile Ala Ala Ala
 20 25 30
 60 Gly Ala Ile Trp Val Val Gln Pro Phe Gly Trp Ile Lys Lys Thr Phe
 35 40 45

460

Ile Asp Pro Pro Pro Thr Glu Glu Lys
50 55

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 765 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..765
(D) OTHER INFORMATION: / Ceres Seq. ID 1569689

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

15 aacccaaaat ttcttcgtct ctgtctccaa aatcgaatca aaatctctaa agtttcaatt      60
   tttttgttct gttctttttt ttttttaaag aatggcttca atttctgcaa ctttgccttc      120
   gccattgtta ctcacacaga gaaaatccaa tctcacatcg attcaaaaac tcccattttc      180
   tctaactcga ggtacgaatg atctttctcc attatctctt actcgaaacc ctagcagcat      240
   cagtctgatg gtgaaagcta gtggagaaag ctcagattca tcgactgatc tcgacgttgt      300
20 tagtacgatt cagaatgttt gggataagtc tgaagatagg ttaggtctta ttgggtttggg      360
   ttttRgctgg tattgtagct ctttgggcat cattgaatct catcacggca attgacaaat      420
   tgsccgttat ctcgagcgga ttcgaaactag ttggtatctt gttctccacg tggttcacat      480
   atcgatatct cttgttcaaa ccggacagac aggagctttc gaaaattgtc aagaaatcag      540
   tagcggatat acttggccag tgaaccttgt gtgtgtgata atacTttcat ctttgaaga      600
25 tgatttgttt gcaagtttgt aaaattacat gacagggtgg ttggtgtttc tagtccaata      660
   atgtcatgca tttgaaacct gtaaatactt tattgttggt ttttggttgt gagcaaaaatc      720
   aatcttttct aatttcaaag attctctttt atgattatac gtttt

```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..66
(D) OTHER INFORMATION: / Ceres Seq. ID 1569690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

40 Asn Gln Lys Phe Leu Arg Leu Cys Leu Gln Asn Arg Ile Lys Ile Ser
   1      5      10      15
   Lys Val Ser Ile Phe Leu Phe Cys Ser Phe Phe Phe Leu Lys Asn Gly
   20      25      30
   Phe Asn Phe Cys Asn Phe Ala Phe Ala Ile Val Thr His Thr Glu Lys
45 35      40      45
   Ile Gln Ser His Ile Asp Ser Lys Thr Pro Ile Phe Ser Asn Ser Arg
   50      55      60
   Tyr Glu
65

```

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..107
(D) OTHER INFORMATION: / Ceres Seq. ID 1569691

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Met Ala Ser Ile Ser Ala Thr Leu Pro Ser Pro Leu Leu Leu Thr Gln

1					5					10					15				
Arg	Lys	Ser	Asn	Leu	Thr	Ser	Ile	Gln	Lys	Leu	Pro	Phe	Ser	Leu	Thr				
				20					25					30					
Arg	Gly	Thr	Asn	Asp	Leu	Ser	Pro	Leu	Ser	Leu	Thr	Arg	Asn	Pro	Ser				
				35					40					45					
Ser	Ile	Ser	Leu	Met	Val	Lys	Ala	Ser	Gly	Glu	Ser	Ser	Asp	Ser	Ser				
				50					55					60					
Thr	Asp	Leu	Asp	Val	Val	Ser	Thr	Ile	Gln	Asn	Val	Trp	Asp	Lys	Ser				
65					70					75					80				
Glu	Asp	Arg	Leu	Gly	Leu	Ile	Gly	Leu	Gly	Phe	Xaa	Trp	Tyr	Cys	Ser				
				85					90					95					
Ser	Leu	Gly	Ile	Glu	Ser	His	His	Gly	Asn										
				100					105										

(i) SEQUENCE CHARACTERISTICS:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1569692

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Met	Val	Lys	Ala	Ser	Gly	Glu	Ser	Ser	Asp	Ser	Ser	Thr	Asp	Leu	Asp
1				5					10					15	
Val	Val	Ser	Thr	Ile	Gln	Asn	Val	Trp	Asp	Lys	Ser	Glu	Asp	Arg	Leu
			20					25					30		
Gly	Leu	Ile	Gly	Leu	Gly	Phe	Xaa	Trp	Tyr	Cys	Ser	Ser	Leu	Gly	Ile
		35					40					45			
Ile	Glu	Ser	His	His	Gly	Asn									
	50					55									

(2) INFORMATION FOR SEO ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 782 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..782

(D) OTHER INFORMATION: / Ceres Seq. ID 1571042

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

atcaacaaaa	acaaaacata	aaaaacaagt	ggaagcttta	aaacgagagg	gagagagcaa	60
aaatggcgac	gtcgggaacg	tacgtgacgg	aagttcgcgt	aaaaggatcg	gccgagaaat	120
actacaagag	gtggaagaac	gagaaccatg	tcttccttga	tgtatctcgg	caccacatcc	180
aaaatgtttac	cgttcacgaa	ggcgaacatg	actctcacgg	Gtctatcagg	agttggaact	240
acacatggga	tggaaaggag	gaggtgttca	aggagagaag	agagatagac	gatgagacca	300
aaacgttgac	gttaagagga	cttgagggtc	acgtgatgga	gcagctcaaa	gtgtacgacg	360
tcgtctacca	attcatctcc	aaatctgagg	atacctgcgt	cgccaaaatc	actttaatat	420
gggagaagcg	caacgatgat	tccccagaac	caagcggcta	catgaaattc	gtcaagagct	480
tggttgctga	catgggaaac	cacgttagca	aaacttaatc	atcattccca	cagtcgtcgt	540
catcatcatc	atcatcatca	tcatcatcat	catcatcatc	atcatcatca	tcatcatcat	600
catcatcatc	atcatcata	tctcgattta	taagtttaaga	tgttttcagt	ataataaatg	660
gggtcttgtg	gatcgttcat	ttctatgtgt	aaaccgtttg	gtttctgtatg	atgcttcgat	720
atattgttat	gttcatgatc	atatgtcggg	ttcgatataa	tgattcttaa	gattaattta	780

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..151
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571043
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

10	Met	Ala	Thr	Ser	Gly	Thr	Tyr	Val	Thr	Glu	Val	Pro	Leu	Lys	Gly	Ser
	1				5					10					15	
	Ala	Glu	Lys	Tyr	Tyr	Lys	Arg	Trp	Lys	Asn	Glu	Asn	His	Val	Phe	Pro
				20					25					30		
15	Asp	Ala	Ile	Gly	His	His	Ile	Gln	Asn	Val	Thr	Val	His	Glu	Gly	Glu
			35					40					45			
	His	Asp	Ser	His	Gly	Ser	Ile	Arg	Ser	Trp	Asn	Tyr	Thr	Trp	Asp	Gly
		50					55				60					
	Lys	Glu	Glu	Val	Phe	Lys	Glu	Arg	Arg	Glu	Ile	Asp	Asp	Glu	Thr	Lys
		65				70				75					80	
20	Thr	Leu	Thr	Leu	Arg	Gly	Leu	Glu	Gly	His	Val	Met	Glu	Gln	Leu	Lys
					85					90					95	
	Val	Tyr	Asp	Val	Val	Tyr	Gln	Phe	Ile	Pro	Lys	Ser	Glu	Asp	Thr	Cys
				100				105						110		
	Ile	Gly	Lys	Ile	Thr	Leu	Ile	Trp	Glu	Lys	Arg	Asn	Asp	Asp	Ser	Pro
25			115					120					125			
	Glu	Pro	Ser	Gly	Tyr	Met	Lys	Phe	Val	Lys	Ser	Leu	Val	Ala	Asp	Met
		130					135					140				
	Gly	Asn	His	Val	Ser	Lys	Thr									
	145					150										

(2) INFORMATION FOR SEQ ID NO:288:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 718 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 35 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..718
 40 (D) OTHER INFORMATION: / Ceres Seq. ID 1571079
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

	attcaaagac	atacaaaata	attgagtttt	tttttttttaa	ttagaaacaa	atgggggttga	60
	gtggtggttct	tcattgtggag	gttgaggtta	agtctccggc	tgaaaagtgc	tgggtagccc	120
	tcggcgacgg	catcaatctc	ttcccaataag	ctttccctaa	cgactacaaa	accatccaag	180
45	ttctagccgg	cgacggcaac	gctcctggct	ccattcgcct	cattacttat	ggagaaggat	240
	ctccactggt	gaagatatcg	gcggagagga	tcgaagcagt	ggatttggag	aacaaaagca	300
	tgtcatacag	catcattggc	ggcgaaatgt	tggagtacta	caaacggtc	aaaggaacca	360
	tcaccgttat	tcctaagaac	ggtggcagcc	ttctgaaatg	gtctggtgag	tttgagaaga	420
	ccgccccatga	gattgatgac	ccacacgtca	tcaaggactt	tgctgtcaag	aacttcaaag	480
50	agatagatga	gtatctcctt	aagcaaacta	gtgcctaaca	ctagaacctt	taaattatat	540
	Maagagggtt	cgatcgtctc	tataagattt	ttctaattaa	gaagtgaat	aaagtgaac	600
	ctctttatga	atatccaagt	ttgtgatttc	ggagtttatg	cagcctagta	ggccataagc	660
	tttttacaaa	agccaattta	gtcgaacatt	ttgaaaaaat	cgaacctttt	ggtaaagc	

(2) INFORMATION FOR SEQ ID NO:289:
 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 60 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide

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(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 1571080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

5 Met Gly Leu Ser Gly Val Leu His Val Glu Val Glu Val Lys Ser Pro
 1 5 10 15
 Ala Glu Lys Phe Trp Val Ala Leu Gly Asp Gly Ile Asn Leu Phe Pro
 20 25 30
 Lys Ala Phe Pro Asn Asp Tyr Lys Thr Ile Gln Val Leu Ala Gly Asp
 35 40 45
 10 Gly Asn Ala Pro Gly Ser Ile Arg Leu Ile Thr Tyr Gly Glu Gly Ser
 50 55 60
 Pro Leu Val Lys Ile Ser Ala Glu Arg Ile Glu Ala Val Asp Leu Glu
 65 70 75 80
 Asn Lys Ser Met Ser Tyr Ser Ile Ile Gly Glu Met Leu Glu Tyr
 85 90 95
 15 Tyr Lys Thr Phe Lys Gly Thr Ile Thr Val Ile Pro Lys Asn Gly Gly
 100 105 110
 Ser Leu Leu Lys Trp Ser Gly Glu Phe Glu Lys Thr Ala His Glu Ile
 115 120 125
 20 Asp Asp Pro His Val Ile Lys Asp Phe Ala Val Lys Asn Phe Lys Glu
 130 135 140
 Ile Asp Glu Tyr Leu Leu Lys Gln Thr Ser Ala
 145 150 155

(2) INFORMATION FOR SEQ ID NO:290:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 808 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..808

(D) OTHER INFORMATION: / Ceres Seq. ID 1572097

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

atcaacaaaa acaaaacata aaaaacaagt ggaagcttta aaacgagagg gatagagcaa 60
 aaatggcgac gtcgggaacg tacgtgacgg aagttccgct aaaaggatcg gccgagaaat 120
 actacaagag gtggaagaac gagaaccatg tcttccctga tgctatcggc caccacatcc 180
 40 aaaatgttac cgttcacgaa ggcgaacatg actctcacgg gtctatcagg agttggaact 240
 acacatggga tggaaaggag gaggtgttca aggagagaag agagatagac gatgagacca 300
 aaacgttgac gttaagagga cttgagggtc acgtgatgga gcagctcaaa gtgtacgacg 360
 tcgtctacca attcattccc aaatctgagg atacctgcac cggcaaaatc actttaatat 420
 gggagaagcg caacgatgat tccccagaac caagcggcta catgaaattc gtcaagagct 480
 45 tgggttgctga catgggaaac cacgttagCC CcAAAAAAAA AAAAAAAAAa cttaatcatc 540
 attcccacag tcgtcgtcat catcatcatc atcatcatca tcatcatcat catcatcatc 600
 atcatcatca tcatcatcat catcatcatc atcactatct cgatttataa gttaagatgt 660
 tttcagtata ataaatgggg tcttggtgat cgttcatttc tatgtgtaaa ccgtttggtt 720
 ctgtatgatg cttcgatata ttgttatgtt catgatcata tgtcgggttc gatataatga 780
 ttcttaagat taatttacta cacatttc

50 (2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1572098

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser

1				5				10				15			
Ala	Glu	Lys	Tyr	Tyr	Lys	Arg	Trp	Lys	Asn	Glu	Asn	His	Val	Phe	Pro
			20				25				30				
Asp	Ala	Ile	Gly	His	His	Ile	Gln	Asn	Val	Thr	Val	His	Glu	Gly	Glu
			35				40				45				
His	Asp	Ser	His	Gly	Ser	Ile	Arg	Ser	Trp	Asn	Tyr	Thr	Trp	Asp	Gly
			50				55				60				
Lys	Glu	Glu	Val	Phe	Lys	Glu	Arg	Arg	Glu	Ile	Asp	Asp	Glu	Thr	Lys
65				70				75				80			
Thr	Leu	Thr	Leu	Arg	Gly	Leu	Glu	Gly	His	Val	Met	Glu	Gln	Leu	Lys
			85				90				95				
Val	Tyr	Asp	Val	Val	Tyr	Gln	Phe	Ile	Pro	Lys	Ser	Glu	Asp	Thr	Cys
			100				105				110				
Ile	Gly	Lys	Ile	Thr	Leu	Ile	Trp	Glu	Lys	Arg	Asn	Asp	Asp	Ser	Pro
			115				120				125				
Glu	Pro	Ser	Gly	Tyr	Met	Lys	Phe	Val	Lys	Ser	Leu	Val	Ala	Asp	Met
			130				135				140				
Gly	Asn	His	Val	Ser	Pro	Lys	Lys	Lys	Lys	Lys	Lys	Leu	Asn	His	His
145				150				155				160			
Ser	His	Ser	Arg	Arg	His	His	His	His	His	His	His	His	His	His	His
			165				170				175				
His	His	His	His	His	His	His	His	His	His	His	His	His	His	His	Tyr
			180				185				190				
Leu	Asp	Leu													
			195												

(i) SEQUENCE CHARACTERISTICS:

- ```

 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..104
 (D) OTHER INFORMATION: / Ceres Seq. ID 1572099
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

```

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- ```
(A) LENGTH: 583 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:
      (A) NAME/KEY: -
      (B) LOCATION: 1..583
      (D) OTHER INFORMATION: / Ceres Seq. ID 1572890
```


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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

```

aaaaacaaaa ataaaaaaaa catcgacaaa gaaaataaaa gatttgtaga atcaactaag      60
aaaatggcta gcactatgat gactacattg cctcagttca atgggtcttcg agccaccaaaa    120
atctctgcag ctctgtgata aggccctggca agtggttcagc ccatgagacg caagggaaat    180
5  ggagctttgg gtgcaaagtg tgacttcatac ggttcacaa caaatctgat aatggtaacg    240
tcgacgaccc tgattttggt cgcggggaga ttcggacttg cgccatcagc caataggaag    300
gcgacagctg gacttaggtt ggaggcacgt gactcaggtc tacaaacggg tgaccgggcc    360
gggttcacgc ttgcggacac tttggcttgt ggcaccgttg gtcatatcat cgggtgtagga    420
gttgctcttg gccttaaaaa cattggtgct atttgaagtt cctaaagctc ttttatttgt    480
10 atttgtaaaa Atttgtagat tttataaaca atattctcat gcacctgaac gagatctaata 540
ggattttaca agtctttatg tttatcttat aatgttgat  cgc

```

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 151 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```

20 (A) NAME/KEY: peptide
    (B) LOCATION: 1..151
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572891

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

```

25 Lys Asn Lys Asn Lys Lys Asn Ile Ala Gln Glu Asn Lys Arg Phe Val
    1           5           10           15
    Glu Ser Thr Lys Lys Met Ala Ser Thr Met Met Thr Thr Leu Pro Gln
        20           25           30
    Phe Asn Gly Leu Arg Ala Thr Lys Ile Ser Ala Ala Pro Val Gln Gly
        35           40           45
30  Leu Ala Ser Val Gln Pro Met Arg Arg Lys Gly Asn Gly Ala Leu Gly
    50           55           60
    Ala Lys Cys Asp Phe Ile Gly Ser Ser Thr Asn Leu Ile Met Val Thr
    65           70           75           80
    Ser Thr Thr Leu Ile Leu Phe Ala Gly Arg Phe Gly Leu Ala Pro Ser
35  85           90           95
    Ala Asn Arg Lys Ala Thr Ala Gly Leu Arg Leu Glu Ala Arg Asp Ser
        100          105          110
    Gly Leu Gln Thr Gly Asp Pro Ala Gly Phe Thr Leu Ala Asp Thr Leu
        115          120          125
40  Ala Cys Gly Thr Val Gly His Ile Ile Gly Val Gly Val Val Leu Gly
    130          135          140
    Leu Lys Asn Ile Gly Ala Ile
    145          150

```

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

```

45 (A) LENGTH: 130 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```

50 (A) NAME/KEY: peptide
    (B) LOCATION: 1..130
    (D) OTHER INFORMATION: / Ceres Seq. ID 1572892

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

```

55 Met Ala Ser Thr Met Met Thr Thr Leu Pro Gln Phe Asn Gly Leu Arg
    1           5           10           15
    Ala Thr Lys Ile Ser Ala Ala Pro Val Gln Gly Leu Ala Ser Val Gln
        20           25           30
60  Pro Met Arg Arg Lys Gly Asn Gly Ala Leu Gly Ala Lys Cys Asp Phe
    35           40           45
    Ile Gly Ser Ser Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Ile

```

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50 55 60
 Leu Phe Ala Gly Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala
 65 70 75 80
 Thr Ala Gly Leu Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly
 85 90 95
 Asp Pro Ala Gly Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val
 100 105 110
 Gly His Ile Ile Gly Val Gly Val Val Leu Gly Leu Lys Asn Ile Gly
 115 120 125

Ala Ile
 130

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..126

(D) OTHER INFORMATION: / Ceres Seq. ID 1572893

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Met Thr Thr Leu Pro Gln Phe Asn Gly Leu Arg Ala Thr Lys Ile
 1 5 10 15
 Ser Ala Ala Pro Val Gln Gly Leu Ala Ser Val Gln Pro Met Arg Arg
 20 25 30
 Lys Gly Asn Gly Ala Leu Gly Ala Lys Cys Asp Phe Ile Gly Ser Ser
 35 40 45
 Thr Asn Leu Ile Met Val Thr Ser Thr Thr Leu Ile Leu Phe Ala Gly
 50 55 60
 Arg Phe Gly Leu Ala Pro Ser Ala Asn Arg Lys Ala Thr Ala Gly Leu
 65 70 75 80
 Arg Leu Glu Ala Arg Asp Ser Gly Leu Gln Thr Gly Asp Pro Ala Gly
 85 90 95
 Phe Thr Leu Ala Asp Thr Leu Ala Cys Gly Thr Val Gly His Ile Ile
 100 105 110
 Gly Val Gly Val Val Leu Gly Leu Lys Asn Ile Gly Ala Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 748 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..748

(D) OTHER INFORMATION: / Ceres Seq. ID 1573606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ccttctcact tcaaattcat aatctctcta cttctctctc tctctaaatt caaaaatggc 60
 gaaactggtg atgttggttg ttctttgtat cttaccggcg ataGccatgg cggcaaggag 120
 gagtaatatt ggaaagaata caatggtggt tcaaggtagc acttactgtg acatttgcaa 180
 attcggtctc gagactcctg aatcctccta cttcatcccc ggtgcaacgg tgaagctatc 240
 atgcaaagac aggaagacaa tggaagaggt ttacacagac aaagctgtat cggacaaaga 300
 aggaaagtat aagttcattg tccacgacga tcacagagac cagatgtgcg atgttttgct 360
 tgtgaaaagc tcggataaaa cctgctctaa aatctccgtt ggacgtgaga agtctcgtgt 420
 gatcttgaac cattacagtg gcattgcctc gcagatcaga catgctaaca acatgggatt 480
 cgagaaagaa gtgagtgtat tgttctgtct tgctttgttt cagaagtata tggttgatga 540
 agatgaggat gatattaaaa accatctcta atctctctgt ttaatcttat gatctgctgt 600
 tttcttcatt aatgagtttc gagttatgga agagatatat ttgtatttgt ttgattactt 660

467

atttggttgtc tttagagatg ttgactctgg tgatcggata actatctggt tgtgtaagct 720
 tcttatatat tgatgtgtca tttccttg

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..171

(D) OTHER INFORMATION: / Ceres Seq. ID 1573607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

15 Met Ala Lys Leu Val Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile
 1 5 10 15
 Ala Met Ala Ala Arg Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val
 20 25 30
 Gln Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro
 20 35 40 45
 Glu Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys
 50 55 60
 Asp Arg Lys Thr Met Glu Val Tyr Thr Asp Lys Ala Val Ser Asp
 65 70 75 80
 25 Lys Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln
 85 90 95
 Met Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys
 100 105 110
 Ile Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser
 30 115 120 125
 Gly Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys
 130 135 140
 Glu Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val
 145 150 155 160
 35 Asp Glu Asp Glu Asp Asp Ile Lys Asn His Leu
 165 170

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 1573608

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

50 Met Leu Leu Val Leu Cys Ile Leu Pro Ala Ile Ala Met Ala Arg
 1 5 10 15
 Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val Gln Gly Ser Thr Tyr
 20 25 30
 Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu Ser Ser Tyr Phe
 35 40 45
 55 Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp Arg Lys Thr Met
 50 55 60
 Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys Glu Gly Lys Tyr
 65 70 75 80
 Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met Cys Asp Val Leu
 85 90 95
 60 Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile Ser Val Gly Arg
 100 105 110

468

Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly Ile Ala Ser Gln
 115 120 125
 Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu Val Ser Asp Val
 130 135 140
 5 Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp Glu Asp Glu Asp
 145 150 155 160
 Asp Ile Lys Asn His Leu
 165

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 1573609

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

Met Ala Ala Arg Arg Ser Asn Ile Gly Lys Asn Thr Met Val Val Gln
 1 5 10 15
 Gly Ser Thr Tyr Cys Asp Ile Cys Lys Phe Gly Phe Glu Thr Pro Glu
 20 25 30
 25 Ser Ser Tyr Phe Ile Pro Gly Ala Thr Val Lys Leu Ser Cys Lys Asp
 35 40 45
 Arg Lys Thr Met Glu Glu Val Tyr Thr Asp Lys Ala Val Ser Asp Lys
 50 55 60
 Glu Gly Lys Tyr Lys Phe Ile Val His Asp Asp His Arg Asp Gln Met
 65 70 75 80
 30 Cys Asp Val Leu Leu Val Lys Ser Ser Asp Lys Thr Cys Ser Lys Ile
 85 90 95
 Ser Val Gly Arg Glu Lys Ser Arg Val Ile Leu Asn His Tyr Ser Gly
 100 105 110
 35 Ile Ala Ser Gln Ile Arg His Ala Asn Asn Met Gly Phe Glu Lys Glu
 115 120 125
 Val Ser Asp Val Phe Cys Ser Ala Leu Phe Gln Lys Tyr Met Val Asp
 130 135 140
 Glu Asp Glu Asp Asp Ile Lys Asn His Leu
 145 150

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 704 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..704

(D) OTHER INFORMATION: / Ceres Seq. ID 1573861

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

aaaaaatcga atcaaaatct cttaaagtttc aattttttttg ttctgttctt tttttttttt 60
 taaagaatgg cttcaatttc tgcaactttg ccttcgccat tgttactcac acagagaaaa 120
 55 tccaatctca catcgattca aaaactccca ttttctctaa ctcgaggtac gaatgatott 180
 tctccattat ctcttactcg aaacctagc agcatcagtc tgatgggtgaa agctagtggg 240
 gaaagctcag attcatcgac tgatctcgac gttgttagta cgattcagaa tgtttgggat 300
 aagtctgaaa ataggttagg tcttattggt ttgggttttg ctggtattgt agctctttgg 360
 gcatcattga atctcatcac ggcaattgac aaattgcccg ttatctcgag cggattcgaa 420
 60 ctagtttgta tcttgttctc cacgtgggtc acatatcgat atctcttggt caaacgggac 480
 agacaggagc tttcgaaaat tgtcaagaaa tcagtagcgg atatacttgg cAcagtgaac 540
 cttgtgtgtg tgataatact tcatcttttg aagatgattt gtttgcaagt ttgtaaaatt 600

469

acatgacagg gtggttggttg tttctagtcc aataatgtca tgcatttgaa acctgtaaat 660
 actttattgt tgggttttgg ttgtgagcaa aatcaatcct ttct

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 1573862

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

15 Met Ala Ser Ile Ser Ala Thr Leu Pro Ser Pro Leu Leu Thr Gln
 1 5 10 15
 Arg Lys Ser Asn Leu Thr Ser Ile Gln Lys Leu Pro Phe Ser Leu Thr
 20 20 25 30
 Arg Gly Thr Asn Asp Leu Ser Pro Leu Ser Leu Thr Arg Asn Pro Ser
 20 35 40 45
 Ser Ile Ser Leu Met Val Lys Ala Ser Gly Glu Ser Ser Asp Ser Ser
 50 55 60
 Thr Asp Leu Asp Val Val Ser Thr Ile Gln Asn Val Trp Asp Lys Ser
 65 70 75 80
 25 Glu Asn Arg Leu Gly Leu Ile Gly Leu Gly Phe Ala Gly Ile Val Ala
 85 90 95
 Leu Trp Ala Ser Leu Asn Leu Ile Thr Ala Ile Asp Lys Leu Pro Val
 100 105 110
 Ile Ser Ser Gly Phe Glu Leu Val Gly Ile Leu Phe Ser Thr Trp Phe
 30 115 120 125
 Thr Tyr Arg Tyr Leu Leu Phe Lys Pro Asp Arg Gln Glu Leu Ser Lys
 130 135 140
 Ile Val Lys Lys Ser Val Ala Asp Ile Leu Gly Thr Val Asn Leu Val
 145 150 155 160
 35 Cys Val Ile Ile Leu His Leu Trp Lys Met Ile Cys Leu Gln Val Cys
 165 170 175
 Lys Ile Thr

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 1573863

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

50 Met Val Lys Ala Ser Gly Glu Ser Ser Ser Ser Thr Asp Leu Asp
 1 5 10 15
 Val Val Ser Thr Ile Gln Asn Val Trp Asp Lys Ser Glu Asn Arg Leu
 20 25 30
 55 Gly Leu Ile Gly Leu Gly Phe Ala Gly Ile Val Ala Leu Trp Ala Ser
 35 40 45
 Leu Asn Leu Ile Thr Ala Ile Asp Lys Leu Pro Val Ile Ser Ser Gly
 50 55 60
 Phe Glu Leu Val Gly Ile Leu Phe Ser Thr Trp Phe Thr Tyr Arg Tyr
 60 65 70 75 80
 Leu Leu Phe Lys Pro Asp Arg Gln Glu Leu Ser Lys Ile Val Lys Lys
 85 90 95

470

Ser Val Ala Asp Ile Leu Gly Thr Val Asn Leu Val Cys Val Ile Ile
 100 105 110
 Leu His Leu Trp Lys Met Ile Cys Leu Gln Val Cys Lys Ile Thr
 115 120 125

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 662 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..662

(D) OTHER INFORMATION: / Ceres Seq. ID 1574093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

attttttctt tctctctctc ctrcctaagc aaaactaaaa caagctatgg ctggtatgct 60
 tcccggagtt gagtgtgcaa ggaggcggcg cttccacggt ggtgctcctc cgattgaatc 120
 ctccaacaca gtttctgtgg cggctgcggc gggacacgctc tggacacggc gaccatcggt 180
 ctctcttttac actaccaatc atgagagcca ccaggcccat gtctccttct cggagagaag 240
 tgtttaggaat aaatcttatg gagaagacaa cgatgagaaa cttgacggag cagccaaaga 300
 ggcaaagcag aggcctaaca agcggctgag aatcccacca cgtacaagtt caggcaaat 360
 ggtaaagaca aagggaataa attggagcaa ggaaagggta aacctctcgg ggacttaccg 420
 accgaggtgg Gtcgggttaa agaagagccg aggaaggttg atggaatggt tcaagcggcg 480
 agttaggga caacaagatt gtgctatatg tctagaccgg ttcaagaagg gtgagacctt 540
 ggtacaccta ccattgtgcc ataagtttca ctccatatgc ttattgcctt ggctagacac 600
 taatgtttat tgcccatatt gtagaactga tatttggaat taaatgttat atttttgatg 660
 tc

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 1574094

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

Met Ala Gly Met Leu Pro Gly Val Glu Cys Ala Arg Arg Arg Arg Phe
 1 5 10 15
 His Gly Gly Ala Pro Pro Ile Glu Ser Ser Asn Thr Ala Ser Val Ala
 20 25 30
 Ala Ala Ala Gly His Val Trp Thr Arg Arg Pro Ser Phe Ser Leu Tyr
 35 40 45
 Thr Thr Asn His Glu Ser His Gln Ala His Val Ser Phe Ser Glu Arg
 50 55 60
 Ser Val Arg Asn Lys Ser Tyr Gly Glu Asp Asn Asp Glu Lys Leu Asp
 65 70 75 80
 Gly Ala Ala Lys Glu Ala Lys Gln Arg Leu Asn Lys Arg Leu Arg Ile
 85 90 95
 Pro Pro Arg Thr Ser Ser Gly Lys Met Val Lys Thr Lys Gly Ile Asn
 100 105 110
 Trp Ser Lys Glu Arg Val Asn Leu Ser Gly Thr Tyr Arg Pro Arg Trp
 115 120 125
 Val Gly Leu Lys Lys Ser Arg Gly Arg Leu Met Glu Trp Phe Lys Arg
 130 135 140
 Arg Val Arg Glu Gln Gln Asp Cys Ala Ile Cys Leu Asp Arg Phe Lys
 145 150 155 160
 Lys Gly Glu Thr Leu Val His Leu Pro Cys Ala His Lys Phe His Ser
 165 170 175

471

Ile Cys Leu Leu Pro Trp Leu Asp Thr Asn Val Tyr Cys Pro Tyr Cys
 180 185 190
 Arg Thr Asp Ile Trp Asn
 195

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 195 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..195

(D) OTHER INFORMATION: / Ceres Seq. ID 1574095

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

Met Leu Pro Gly Val Glu Cys Ala Arg Arg Arg Phe His Gly Gly
 1 5 10 15
 Ala Pro Pro Ile Glu Ser Ser Asn Thr Ala Ser Val Ala Ala Ala Ala
 20 20 25 30
 Gly His Val Trp Thr Arg Arg Pro Ser Phe Ser Leu Tyr Thr Thr Asn
 35 40 45
 His Glu Ser His Gln Ala His Val Ser Phe Ser Glu Arg Ser Val Arg
 50 55 60
 Asn Lys Ser Tyr Gly Glu Asp Asn Asp Glu Lys Leu Asp Gly Ala Ala
 65 70 75 80
 Lys Glu Ala Lys Gln Arg Leu Asn Lys Arg Leu Arg Ile Pro Pro Arg
 85 90 95
 Thr Ser Ser Gly Lys Met Val Lys Thr Lys Gly Ile Asn Trp Ser Lys
 100 105 110
 Glu Arg Val Asn Leu Ser Gly Thr Tyr Arg Pro Arg Trp Val Gly Leu
 115 120 125
 Lys Lys Ser Arg Gly Arg Leu Met Glu Trp Phe Lys Arg Arg Val Arg
 130 135 140
 Glu Gln Gln Asp Cys Ala Ile Cys Leu Asp Arg Phe Lys Lys Gly Glu
 145 150 155 160
 Thr Leu Val His Leu Pro Cys Ala His Lys Phe His Ser Ile Cys Leu
 165 170 175
 Leu Pro Trp Leu Asp Thr Asn Val Tyr Cys Pro Tyr Cys Arg Thr Asp
 180 185 190
 Ile Trp Asn
 195

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 725 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..725

(D) OTHER INFORMATION: / Ceres Seq. ID 1580388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

ctcacacaaa aatacaacaa cttagatcag tctcaaaggg ggaaaaaaaaa cttaaaagaa 60
 acattaagag gcaacacaaa tcacacaaaa gatcaaattg aagcctaaga agaaggcaaa 120
 aagtgagaag caatggctac catgttgaag gtctctcttg tattgtcatt gttaggtttt 180
 ctggtgatcg ctgtcgtgac tccatcggcg gcgaacccat tcaggaagag cgtagttctc 240
 ggagggaagt caggcgttcc aaacattcgg accaacaggg aaattcaaca acttggaagg 300
 tactgcgtgg agcaattcaa tcaacaagca cagaacgagc aaggaaacat aggatccatt 360
 gcgaaaacag acacggcaat ttcgaatcca ttgcaattta gccgagtagt gtctgctcag 420
 aaacaggtcg tcgctggact caaatactat ctaaggattg aagtcactca acccaatggc 480

472

tctaccagga tgtttgactc tgttgtggtt attcaaccat ggctccattc taagcagttg 540
 ctcggtttca ctccctgttg cagtcctgtc tactaacttt atttcttctt attcgactta 600
 aatttccata atatgatcaa gaaaagacta aaaggtgtat gatacaaagc tattaagaat 660
 ggggtaatag ttgggtttca tgatatgttt acgttggttca taaataaaaa caagttgtta 720
 ttagg

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 1580389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Met Ala Thr Met Leu Lys Val Ser Leu Val Leu Ser Leu Leu Gly Phe
 1 5 10 15
 Leu Val Ile Ala Val Val Thr Pro Ser Ala Ala Asn Pro Phe Arg Lys
 20 25 30
 Ser Val Val Leu Gly Gly Lys Ser Gly Val Pro Asn Ile Arg Thr Asn
 35 40 45
 Arg Glu Ile Gln Gln Leu Gly Arg Tyr Cys Val Glu Gln Phe Asn Gln
 50 55 60
 Gln Ala Gln Asn Glu Gln Gly Asn Ile Gly Ser Ile Ala Lys Thr Asp
 65 70 75 80
 Thr Ala Ile Ser Asn Pro Leu Gln Phe Ser Arg Val Val Ser Ala Gln
 85 90 95
 Lys Gln Val Val Ala Gly Leu Lys Tyr Tyr Leu Arg Ile Glu Val Thr
 100 105 110
 Gln Pro Asn Gly Ser Thr Arg Met Phe Asp Ser Val Val Val Ile Gln
 115 120 125
 Pro Trp Leu His Ser Lys Gln Leu Leu Gly Phe Thr Pro Val Val Ser
 130 135 140
 Pro Val Tyr
 145

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..144

(D) OTHER INFORMATION: / Ceres Seq. ID 1580390

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Met Leu Lys Val Ser Leu Val Leu Ser Leu Leu Gly Phe Leu Val Ile
 1 5 10 15
 Ala Val Val Thr Pro Ser Ala Ala Asn Pro Phe Arg Lys Ser Val Val
 20 25 30
 Leu Gly Gly Lys Ser Gly Val Pro Asn Ile Arg Thr Asn Arg Glu Ile
 35 40 45
 Gln Gln Leu Gly Arg Tyr Cys Val Glu Gln Phe Asn Gln Gln Ala Gln
 50 55 60
 Asn Glu Gln Gly Asn Ile Gly Ser Ile Ala Lys Thr Asp Thr Ala Ile
 65 70 75 80
 Ser Asn Pro Leu Gln Phe Ser Arg Val Val Ser Ala Gln Lys Gln Val
 85 90 95
 Val Ala Gly Leu Lys Tyr Tyr Leu Arg Ile Glu Val Thr Gln Pro Asn

473

100 105 110
 Gly Ser Thr Arg Met Phe Asp Ser Val Val Val Ile Gln Pro Trp Leu
 115 120 125
 His Ser Lys Gln Leu Leu Gly Phe Thr Pro Val Val Ser Pro Val Tyr
 130 135 140

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..675

(D) OTHER INFORMATION: / Ceres Seq. ID 1582959

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

tgggcaaggc aacaaacata atcaacttaa atcttatcta ctttctatatt ctttttaaatc 60
 aaaattaccg ttcttaacta tggcgaagtg gtttttcact atcttcttgg tttttgccct 120
 agcctcagct ttagcttggtg gcgcaagaaa cgtcccagta ggcctctctg accaaaagaa 180
 ctacctcgga tatggtggcg gatattccgg cgttggagac aatgggtttac cctttggtgg 240
 cgtcgggtgga ggtgtgtctg gtcccggagg taatcttggg tatgggggat ttggtggtgc 300
 tgggtggcggc ttaggcgggtg gtttggggcg tggagcaggc agtggattag gcggtggcct 360
 aggtggtgga agtgggaattg gtgccggaac cagtggagga agtaccggag gagttcattt 420
 cccttgagtt gttacttttg tttttaaggc gtcatacggg ccttattaag ctagggtctag 480
 cttaagatga tgtcataata ataatttatc atatctcttt aggggtttta actttggtat 540
 tatgaattat cattagctgt ttaacgtgcg tcttaagtta ctattttaac gtatgtttga 600
 atcagtctag tggcttgtcg tgtcatggct tgggtccattt tcaaattcta ctttgacott 660
 ttcgagtgtt tcacc

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 1582960

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

Met Ala Lys Trp Phe Phe Thr Ile Phe Leu Val Phe Ala Leu Ala Ser
 1 5 10 15
 Ala Leu Ala Cys Gly Ala Arg Asn Val Pro Val Gly Leu Ser Asp Gln
 20 25 30
 Lys Asn Tyr Leu Gly Tyr Gly Gly Tyr Ser Gly Val Gly Asp Asn
 35 40 45
 Gly Leu Pro Phe Gly Gly Val Gly Gly Gly Val Ser Gly Pro Gly Gly
 50 55 60
 Asn Leu Gly Tyr Gly Gly Phe Gly Gly Ala Gly Gly Gly Leu Gly Gly
 65 70 75 80
 Gly Leu Gly Gly Gly Ala Gly Ser Gly Leu Gly Gly Gly Leu Gly Gly
 85 90 95
 Gly Ser Gly Ile Gly Ala Gly Thr Ser Gly Gly Ser Thr Gly Gly Val
 100 105 110
 His Phe Pro
 115

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1076 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

474

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(ix) FEATURE:

(A) NAME/KEY: -
(B) LOCATION: 1..1076
(D) OTHER INFORMATION: / Ceres Seq. ID 1663221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

```

5  aacacgagct taccgattct cttcgctctca acatttaggg tttcagagat cggctgattt      60
   tcacatccac aagtatggcg actcaaatca gcaagaagag aaagtttgta gcgcatggtg      120
10  tattctacgc tgaattgaat gaggttctca caagagagct agcagaggat ggttactctg      180
   gtgttgaggt tagggttact ccaatgagga ctgagattat catcagagct actcgtactc      240
   agaatgttct tgggtgagaag gggaggagaa ttaggggaatt gacatctctt gtccagaaga      300
   gattcaagtt tccagttgac agtggtgagc tctatgctga gaagggttaac aacagaggtc      360
   tctgtgccat tgctcaggct gagtctctac gttacaagct tctcgggtgtt cttgctgttc      420
15  gcagggcctg ttatggtggt ttgagatttg ttatggagag tggagctaag ggatgtgagg      480
   tcatcgtgag tggaaagctc cgtgctgcac gtgctaagtc catgaagttc aaggatggtt      540
   acatggtttc atctgggtcaa ccaactaagg aatacatcga tgctgcagtg agacatgttt      600
   tgctcagaca ggggggtgtt ggaatcaagg tgaagatcat gcttgactgg gaccctacgg      660
   gcaaatcagg accaaagaca ccattgcctg atgttgatgat cattcatgct cctaaagatg      720
20  atgttgatcta ctctgcacct gctcaggctg ctgctccagt tactcttggt caagaagctc      780
   cactcacaac cgtagattac cctgagatga ttctctccagt ggcttagaga agaccttttt      840
   tactattact ccattgggatt ttgttctttt tggtataact tttctacttt tgacactctc      900
   tagtcgtatc tcttatatcc tccaagcaga caagtttttt ctcattgttg ttcttaacct      960
25  atgtcaagtt ttctggaggt tgaatgcttt tagttccatg atttttttgt tcttaagact     1020
   cgtaataaga aaaagaatga cgacaacaat gcctgggtatt tgatgttggt actttg

```

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..250

(D) OTHER INFORMATION: / Ceres Seq. ID 1663222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

```

Met Ala Thr Gln Ile Ser Lys Lys Arg Lys Phe Val Ala Asp Gly Val
1      5      10      15
40  Phe Tyr Ala Glu Leu Asn Glu Val Leu Thr Arg Glu Leu Ala Glu Asp
      20      25      30
   Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Met Arg Thr Glu Ile
      35      40      45
45  Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu Gly Glu Lys Gly Arg
      50      55      60
   Arg Ile Arg Glu Leu Thr Ser Leu Val Gln Lys Arg Phe Lys Phe Pro
      65      70      75      80
   Val Asp Ser Val Glu Leu Tyr Ala Glu Lys Val Asn Asn Arg Gly Leu
      85      90      95
50  Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly
      100     105     110
   Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu Arg Phe Val Met Glu
      115     120     125
   Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser Gly Lys Leu Arg Ala
55  130     135     140
   Ala Arg Ala Lys Ser Met Lys Phe Lys Asp Gly Tyr Met Val Ser Ser
      145     150     155     160
   Gly Gln Pro Thr Lys Glu Tyr Ile Asp Ala Ala Val Arg His Val Leu
      165     170     175
60  Leu Arg Gln Gly Val Leu Gly Ile Lys Val Lys Ile Met Leu Asp Trp
      180     185     190
   Asp Pro Thr Gly Lys Ser Gly Pro Lys Thr Pro Leu Pro Asp Val Val

```

475

195 200 205
 Ile Ile His Ala Pro Lys Asp Asp Val Val Tyr Ser Ala Pro Ala Gln
 210 215 220
 Ala Ala Ala Pro Val Thr Leu Val Gln Glu Ala Pro Leu Thr Thr Val
 225 230 235 240
 Asp Tyr Pro Glu Met Ile Pro Pro Val Ala
 245 250

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..207
 (D) OTHER INFORMATION: / Ceres Seq. ID 1663223

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu
 1 5 10 15
 Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser Leu Val Gln Lys
 20 25 30
 Arg Phe Lys Phe Pro Val Asp Ser Val Glu Leu Tyr Ala Glu Lys Val
 35 40 45
 Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr
 50 55 60
 Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu
 65 70 75 80
 Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser
 85 90 95
 Gly Lys Leu Arg Ala Ala Arg Ala Lys Ser Met Lys Phe Lys Asp Gly
 100 105 110
 Tyr Met Val Ser Ser Gly Gln Pro Thr Lys Glu Tyr Ile Asp Ala Ala
 115 120 125
 Val Arg His Val Leu Leu Arg Gln Gly Val Leu Gly Ile Lys Val Lys
 130 135 140
 Ile Met Leu Asp Trp Asp Pro Thr Gly Lys Ser Gly Pro Lys Thr Pro
 145 150 155 160
 Leu Pro Asp Val Val Ile Ile His Ala Pro Lys Asp Asp Val Val Tyr
 165 170 175
 Ser Ala Pro Ala Gln Ala Ala Ala Pro Val Thr Leu Val Gln Glu Ala
 180 185 190
 Pro Leu Thr Thr Val Asp Tyr Pro Glu Met Ile Pro Pro Val Ala
 195 200 205

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 488 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..488
 (D) OTHER INFORMATION: / Ceres Seq. ID 1663275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

gtgactaaat ttctagggtt ttgaagagtc tctctcgtcg ccgtttgtta ttcctctgtg 60
 agcaaatacga cgaaatgggt cactctaatag tatggaactc tcatccgaag aagtacggtc 120
 ctggatctcg tttatgccgt gtgtgcggga actcgacagg tctgatccgg aagtatggtt 180
 tgaactgctg cagacagtgt ttccgtagca acgctaagga gattggattc attaatgacc 240
 gttaatcaag caccaacttc atgattgatg cttaatgata taaacatgaa ggcgtcgatg 300

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ggtatggcctt ttaagctttt gtagtttttg aaatttttac ttttgagaac cattgttatt 360
 ttgggagtta attaagttgt tgaacctcat taagcatgtc ttattttgga ttaatgatgt 420
 tttggctatt ctcgtatttt tgttttatca gtcaaatttg actaagaaga atttgcttgt 480
 tattagcc

5 (2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..56

15 (D) OTHER INFORMATION: / Ceres Seq. ID 1663276

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

Met Gly His Ser Asn Val Trp Asn Ser His Pro Lys Lys Tyr Gly Pro
 1 5 10 15
 Gly Ser Arg Leu Cys Arg Val Cys Gly Asn Ser His Gly Leu Ile Arg
 20 20 25 30
 Lys Tyr Gly Leu Asn Cys Cys Arg Gln Cys Phe Arg Ser Asn Ala Lys
 35 40 45
 Glu Ile Gly Phe Ile Lys Tyr Arg
 50 55

25 (2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

35 (D) OTHER INFORMATION: / Ceres Seq. ID 1663277

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

Met Glu Leu Ser Ser Glu Glu Val Arg Ser Trp Ile Ser Phe Met Pro
 1 5 10 15
 Cys Val Arg Glu Leu Ala Arg Ser Asp Pro Glu Val Trp Phe Glu Leu
 40 20 25 30
 Leu Gln Thr Val Phe Pro
 35

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 759 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..759

(D) OTHER INFORMATION: / Ceres Seq. ID 1665304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

55 atcaacaaaa aaaaaacata aaaaacaagt ggaagcttta aaacgagagg gagagagcaa 60
 aaatggcgac gtcgggaacg tacgtgacgg aagttccgct aaaaggatcg gccgagaaat 120
 actacaagag gtggaagaac gagaaccatg tcttcctga tgctatcggc caccacatcc 180
 aaaatgttac cgttcacgaa ggcgaacatg actctcacgg gtctatcagg agttggaact 240
 acacatggga tggaaaggag gaggtgttca aggagagaag agagatagac gatgagacca 300
 60 aaacgttgac gttaagagga cttgagggtc acgtgatgga gcagctcaaa gtgtacgacg 360
 tcgtctacca attcattccc aaatctgagg atacctgcat cggcaaaatc actttaatat 420
 gggagaagcg caacgatgat tccccagaac caagcggcta catgaaattc gtcaagagct 480

477

tggttgctga catgggaaac cacgtagca aaacttaatc atcattccca cagtcgtcgt 540
 cgctgcgcac atcatcatca tcatcatcat catcatcatc atcatcatca tcatcatcat 600
 catcactatc tcgatttata agttaagatg ttttcagtat aataaatggg gtcttggtga 660
 tcgttcattt ctatgtgtaa accgtttggg tctgtatgat gcttcgatat attggttatgt 720
 tcatgatcat atgtcgggtt cgatataatg attcttaag

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..151

(D) OTHER INFORMATION: / Ceres Seq. ID 1665305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser
 1 5 10 15
 20 Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro
 20 25 30
 Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu
 35 40 45
 25 His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly
 50 55 60
 Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys
 65 70 75 80
 Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys
 85 90 95
 30 Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys
 100 105 110
 Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg Asn Asp Asp Ser Pro
 115 120 125
 35 Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Ser Leu Val Ala Asp Met
 130 135 140
 Gly Asn His Val Ser Lys Thr
 145 150

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 602 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..602

(D) OTHER INFORMATION: / Ceres Seq. ID 1709970

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

gaagtctctt atatataagt atcgagagaa ttagggtttt ctagtctagt gtttccggga 60
 gcagcctgag caggaggaag aagacgaaga agaagaggag cagctactac catggttctg 120
 ggacggagct ttgtcgtttc agtggacaga agatttaccc aggaagagga attaggttta 180
 tccgatctga ttctcaggtt ttcttgtttc ttaactcaaa atgtaagagg tacttcata 240
 acaagttgaa gccatccaag cttgcatgga ctgccatgta cagaaagcaa cncaagaagg 300
 55 atgcagcaca agaggctgtg aagagaagga gacgtgccac caagaagcca tactcaaggt 360
 ccattgttgg tgctaccttg gaagtaattc agaagaagag agctgagaag cctgaagttc 420
 gtgatgcagc cagggaagct gctctgcgtg agatcaagga aagaatcaaa aagaccaaag 480
 atgaaaagaa ggctaagaag gtggaatttg cttctaagca acagaagggtc aaggctaatt 540
 tccccaaagc tgctgctgca tccaagggtc ctaagggtggg aggtggtggt ggcaaagcgt 600
 ga

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

478

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1709971

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

```

Met Tyr Arg Lys Gln Xaa Lys Lys Asp Ala Ala Gln Glu Ala Val Lys
1      5      10      15
Arg Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
      20      25      30
Ala Thr Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
      35      40      45
Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
      50      55      60
Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Val Glu Phe Ala Ser
20 65      70      75      80
Lys Gln Gln Lys Val Lys Ala Asn Phe Pro Lys Ala Ala Ala Ala Ser
      85      90      95
Lys Gly Pro Lys Val Gly Gly Gly Gly Gly Lys Arg
      100     105

```

25 (2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1709972

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

```

Met Gln Pro Gly Lys Leu Leu Cys Val Arg Ser Arg Lys Glu Ser Lys
1      5      10      15
Arg Pro Lys Met Lys Arg Arg Leu Arg Arg Trp Asn Leu Leu Leu Ser
40 20      25      30
Asn Arg Arg Ser Arg Leu Ile Ser Pro Lys Leu Leu Leu His Pro Arg
      35      40      45
Val Leu Arg Trp Glu Val Val Val Ala Asn Ala
      50      55

```

45 (2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..726

(D) OTHER INFORMATION: / Ceres Seq. ID 1711273

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

```

atcttcttgt ctctctctca tttcttggtta ttatccacga acgaagaaaa acctagaaaa      60
cagttgaaga aagaaaatca caagagaagc catggccgga attggaccga ttactcagga      120
ttgggaacca gttgtgatcc gcaagagagc tcctaacgct gcagctaagc gcgacgagaa      180
gactgtcaac gccgctcgtc gaagcggcgc cgatattgag accgttcgaa aattcaatgc      240
tggatcgaac aaggctgcat caagcggcac ctccctgaac acaaagaagc tagatgatga      300
tactgagaac ttatctcatg atcgtgtgcc cactgaattg aagaaagcca tcatgcaagc      360

```

479

tagaggggag aasaagctga ctcagtccca acttgcccat ctgatcaatg agaagccaca 420
 agtgatccaa gaatacagat cggggaaagc aattccgaat caacagatcc tttcaaagct 480
 ggagagggca cttgggtgcta aactccgtgg aaagaagtag aagtttagaa caaagctctt 540
 aaaggtaaca aaaagctgat cgcagtttct ctccagtcca catgctttac catatcctaa 600
 5 aaactatatac tatgtatggt ttggtttaat ggcgtagtag tttgttgcca ggaatctttc 660
 atgatgtaag aaaaacaaag ctgtttggaa ccttttgtca ttataaataa tctcttctct 720
 ttcttt

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1711274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

20 Met Ala Gly Ile Gly Pro Ile Thr Gln Asp Trp Glu Pro Val Val Ile
 1 5 10 15
 Arg Lys Arg Ala Pro Asn Ala Ala Ala Lys Arg Asp Glu Lys Thr Val
 20 25 30
 25 Asn Ala Ala Arg Arg Ser Gly Ala Asp Ile Glu Thr Val Arg Lys Phe
 35 40 45
 Asn Ala Gly Ser Asn Lys Ala Ala Ser Ser Gly Thr Ser Leu Asn Thr
 50 55 60
 Lys Lys Leu Asp Asp Asp Thr Glu Asn Leu Ser His Asp Arg Val Pro
 65 70 75 80
 30 Thr Glu Leu Lys Lys Ala Ile Met Gln Ala Arg Gly Glu Xaa Lys Leu
 85 90 95
 Thr Gln Ser Gln Leu Ala His Leu Ile Asn Glu Lys Pro Gln Val Ile
 100 105 110
 Gln Glu Tyr Glu Ser Gly Lys Ala Ile Pro Asn Gln Gln Ile Leu Ser
 115 120 125
 35 Lys Leu Glu Arg Ala Leu Gly Ala Lys Leu Arg Gly Lys Lys
 130 135 140

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 686 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..686

(D) OTHER INFORMATION: / Ceres Seq. ID 1715423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

50 aacaataaaa caaagtgatt tattatggcg ttaagagaga tgataataga tgagagtgat 60
 gacatagaga gctacagtga tcaatctctt tgtcttgata aagccaagga gcttcttgct 120
 ctcacaaac tacccacggg attgttgcca ttgaaggata tgacggaagt tgggtacaac 180
 aaaacaaaag gggttggtg gatgaggctg agaagcaaga ttgagcatatc attccgtgag 240
 ataggtcgca aggttttata tgacacggYa gataactgcg tttgttgagg accgccgtat 300
 55 gaggagactt accggagtca aaagcaaaaga gctcatgatc tgggttcctg tgaatgatat 360
 cttcatcaaa gagaaagatc ctgagaagat cacctttgct aataccaccg gcctgtcacg 420
 aacatttaaa gtttcagcat ttcaatgtga aggttgataa ataaaaagaa aagaggagta 480
 accagacttc cttgatgaaa gcaaccaata aagaacagaa gttgttccat actcaataag 540
 agatagttta attaaatatc aaggacacgc ctttcttaca atgaattgct tatggatcat 600
 60 cacagtaaat aaacaggttc tgcaattgat gccttgatgt ataacagtga gtttccaatc 660
 aacatattag aatcgattca ttggtt

(2) INFORMATION FOR SEQ ID NO:326:

480

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 1715424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

```

Met Ala Leu Arg Glu Met Ile Ile Asp Glu Ser Asp Asp Ile Glu Ser
1      5      10      15
Tyr Ser Asp Gln Ser Leu Cys Leu Asp Lys Ala Lys Glu Leu Leu Ala
15     20     25     30
Leu Ile Lys Leu Pro Thr Gly Leu Leu Pro Leu Lys Asp Met Thr Glu
35     40     45
Val Gly Tyr Asn Lys Thr Lys Gly Phe Val Trp Met Arg Leu Arg Ser
50     55     60
Lys Ile Glu His Thr Phe Arg Glu Ile Gly Arg Arg Val Leu Tyr Asp
65     70     75     80
Thr Xaa Asp Asn Cys Val Cys
85

```

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..82

(D) OTHER INFORMATION: / Ceres Seq. ID 1715425

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

```

Met Ile Ile Asp Glu Ser Asp Asp Ile Glu Ser Tyr Ser Asp Gln Ser
1      5      10      15
Leu Cys Leu Asp Lys Ala Lys Glu Leu Leu Ala Leu Ile Lys Leu Pro
20     25     30
Thr Gly Leu Leu Pro Leu Lys Asp Met Thr Glu Val Gly Tyr Asn Lys
35     40     45
Thr Lys Gly Phe Val Trp Met Arg Leu Arg Ser Lys Ile Glu His Thr
50     55     60
Phe Arg Glu Ile Gly Arg Arg Val Leu Tyr Asp Thr Xaa Asp Asn Cys
65     70     75     80
Val Cys

```

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1715426

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

```

Met Thr Arg Xaa Ile Thr Ala Phe Val Glu Asp Arg Arg Met Arg Arg
1      5      10      15
Leu Thr Gly Val Lys Ser Lys Glu Leu Met Ile Trp Val Pro Val Asn

```


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20 25 30
 Asp Ile Phe Ile Lys Glu Lys Asp Pro Glu Lys Ile Thr Phe Ala Asn
 35 40 45
 Thr Thr Gly Leu Ser Arg Thr Phe Lys Val Ser Ala Phe Gln Cys Glu
 5 50 55 60

Gly
 65

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 829 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..829

(D) OTHER INFORMATION: / Ceres Seq. ID 1715962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

20 aaaaacgccg tcgagaaatc tccctctagg gtttctttga tcaaaccaga gagccgtcag 60
 ggagagcaaaa acaaagatcg gagaagatga agacgattct ttcttccgaa acgatggaca 120
 tccccgacag tggtaccatc aaggttcacg ctaaagtgat cgaagtcgaa ggacctcgcg 180
 ggaagcttgt tcgcgatttc aagcatctca acctcgattt ccagctgacg aaggatccag 240
 agactggaaa gaagaagctt aagatcgatt cgtgggtttgg aacacgcaaa accagcgcct 300
 25 ccatacagaac cgctcttagc cacgtcgata acttgatctc cgggtgttacc agaggtttcc 360
 gttacaagat gaggttcgtg tacgcccatt ttcccatcaa cgccctccatc ggcggtgacg 420
 gaaagtctat cgagatccgt aacttccttg gcgagaagaa ggtgaggaag gtagagatgt 480
 tggatggtgt aacCattggt cgaYctgaga aggtgaagga tgagattggt cttgacggta 540
 acgacatcga gcttgtttca aggtcatgcg ctttgatcaa ccagaaatgt cacgtgaaga 600
 30 agaaggatat caggaagttt cttgatggta tctatggttag cgagaaaagc aagatcgtag 660
 aggaagaatg aatgcccata tcatcgctctt agctcctatt tcttgctctt tgaatgtag 720
 tttcgtttta tggaccaaatt ccaccggtgt tgcaaaactc tggtatccc ttgttcctt 780
 tttgtgttcg agattttatt tacttatgca caagtttttg agacgagct

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..194

(D) OTHER INFORMATION: / Ceres Seq. ID 1715963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Met Lys Thr Ile Leu Ser Ser Glu Thr Met Asp Ile Pro Asp Ser Val
 1 5 10 15
 Thr Ile Lys Val His Ala Lys Val Ile Glu Val Glu Gly Pro Arg Gly
 20 25 30
 50 Lys Leu Val Arg Asp Phe Lys His Leu Asn Leu Asp Phe Gln Leu Ile
 35 40 45
 Lys Asp Pro Glu Thr Gly Lys Lys Lys Leu Lys Ile Asp Ser Trp Phe
 50 55 60
 Gly Thr Arg Lys Thr Ser Ala Ser Ile Arg Thr Ala Leu Ser His Val
 65 70 75 80
 55 Asp Asn Leu Ile Ser Gly Val Thr Arg Gly Phe Arg Tyr Lys Met Arg
 85 90 95
 Phe Val Tyr Ala His Phe Pro Ile Asn Ala Ser Ile Gly Gly Asp Gly
 100 105 110
 60 Lys Ser Ile Glu Ile Arg Asn Phe Leu Gly Glu Lys Lys Val Arg Lys
 115 120 125
 Val Glu Met Leu Asp Gly Val Thr Ile Val Arg Xaa Glu Lys Val Lys

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130 135 140
 Asp Glu Ile Val Leu Asp Gly Asn Asp Ile Glu Leu Val Ser Arg Ser
 145 150 155 160
 Cys Ala Leu Ile Asn Gln Lys Cys His Val Lys Lys Lys Asp Ile Arg
 5 165 170 175
 Lys Phe Leu Asp Gly Ile Tyr Val Ser Glu Lys Ser Lys Ile Val Glu
 180 185 190
 Glu Glu

10 (2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..185

20 (D) OTHER INFORMATION: / Ceres Seq. ID 1715964

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Met Asp Ile Pro Asp Ser Val Thr Ile Lys Val His Ala Lys Val Ile
 1 5 10 15
 Glu Val Glu Gly Pro Arg Gly Lys Leu Val Arg Asp Phe Lys His Leu
 25 20 25 30
 Asn Leu Asp Phe Gln Leu Ile Lys Asp Pro Glu Thr Gly Lys Lys Lys
 35 40 45
 Leu Lys Ile Asp Ser Trp Phe Gly Thr Arg Lys Thr Ser Ala Ser Ile
 50 55 60
 Arg Thr Ala Leu Ser His Val Asp Asn Leu Ile Ser Gly Val Thr Arg
 30 65 70 75 80
 Gly Phe Arg Tyr Lys Met Arg Phe Val Tyr Ala His Phe Pro Ile Asn
 85 90 95
 Ala Ser Ile Gly Asp Gly Lys Ser Ile Glu Ile Arg Asn Phe Leu
 35 100 105 110
 Gly Glu Lys Lys Val Arg Lys Val Glu Met Leu Asp Gly Val Thr Ile
 115 120 125
 Val Arg Xaa Glu Lys Val Lys Asp Glu Ile Val Leu Asp Gly Asn Asp
 130 135 140
 Ile Glu Leu Val Ser Arg Ser Cys Ala Leu Ile Asn Gln Lys Cys His
 40 145 150 155 160
 Val Lys Lys Lys Asp Ile Arg Lys Phe Leu Asp Gly Ile Tyr Val Ser
 165 170 175
 Glu Lys Ser Lys Ile Val Glu Glu Glu
 45 180 185

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

50 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

55 (B) LOCATION: 1..100

(D) OTHER INFORMATION: / Ceres Seq. ID 1715965

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

Met Arg Phe Val Tyr Ala His Phe Pro Ile Asn Ala Ser Ile Gly Gly
 1 5 10 15
 Asp Gly Lys Ser Ile Glu Ile Arg Asn Phe Leu Gly Glu Lys Lys Val
 60 20 25 30
 Arg Lys Val Glu Met Leu Asp Gly Val Thr Ile Val Arg Xaa Glu Lys

483

35 40 45
 Val Lys Asp Glu Ile Val Leu Asp Gly Asn Asp Ile Glu Leu Val Ser
 50 55 60
 Arg Ser Cys Ala Leu Ile Asn Gln Lys Cys His Val Lys Lys Lys Asp
 5 65 70 75 80
 Ile Arg Lys Phe Leu Asp Gly Ile Tyr Val Ser Glu Lys Ser Lys Ile
 85 90 95
 Val Glu Glu Glu
 100
 (2) INFORMATION FOR SEQ ID NO:333:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 675 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..675
 20 (D) OTHER INFORMATION: / Ceres Seq. ID 1808584
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:
 aacttgctcac ctgcagagaa agaaagaagc cctagatttt gtcaaaaggc ggttgccagaa 60
 caaaaaacca tggccggaat tggaccgata actcaggatt gggagccggt ggtgatccgt 120
 aagaaacccg ctaacgcccgc tgccaagcgc gacgagaaaa ctgtcaacgc cgctcgtcga 180
 25 tccggcgccg atatcgagac cgtcagaaaa ttcaatgctg gaaccaacaa ggcggcatca 240
 agcggcacat ctctgaacac aaaaatgctt gatgatgaca ctgagaacct tactcatgaa 300
 cgtgtgccta ctgagctaaa gaaagccatt atgcaagcca ggacagacaa gaagctaacc 360
 cagtcccaac ttgtctcaat catcaatgag aagccacaag tgattcaaga gtatgagtct 420
 ggcaaagcta taccacaacca gcaaatcctt tctaagctgg agagagcgct tggagctaag 480
 30 cttcgtggaa agaagtgagc caagttctac tgatgtagca agtaacaaga atcaatgctt 540
 tcgtctaatt ccgtaacttt gccagaaga atatcttctg attgtaagaa agcaaaaccg 600
 tttgaatggt tgtttcgttg atggaatctc tatctcataa actcatatca atataataac 660
 ttgggtcttt tcattc
 (2) INFORMATION FOR SEQ ID NO:334:
 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..165
 (D) OTHER INFORMATION: / Ceres Seq. ID 1808585
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:
 Asn Leu Ser Pro Ala Glu Lys Glu Arg Ser Pro Arg Phe Cys Gln Lys
 1 5 10 15
 Ala Val Ala Glu Gln Lys Thr Met Ala Gly Ile Gly Pro Ile Thr Gln
 20 25 30
 50 Asp Trp Glu Pro Val Val Ile Arg Lys Lys Pro Ala Asn Ala Ala Ala
 35 40 45
 Lys Arg Asp Glu Lys Thr Val Asn Ala Ala Arg Arg Ser Gly Ala Asp
 50 55 60
 Ile Glu Thr Val Arg Lys Phe Asn Ala Gly Thr Asn Lys Ala Ala Ser
 55 65 70 75 80
 Ser Gly Thr Ser Leu Asn Thr Lys Met Leu Asp Asp Asp Thr Glu Asn
 85 90 95
 Leu Thr His Glu Arg Val Pro Thr Glu Leu Lys Lys Ala Ile Met Gln
 100 105 110
 60 Ala Arg Thr Asp Lys Lys Leu Thr Gln Ser Gln Leu Ala Gln Ile Ile
 115 120 125
 Asn Glu Lys Pro Gln Val Ile Gln Glu Tyr Glu Ser Gly Lys Ala Ile

484

130 135 140
 Pro Asn Gln Gln Ile Leu Ser Lys Leu Glu Arg Ala Leu Gly Ala Lys
 145 150 155 160
 Leu Arg Gly Lys Lys

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..142

(D) OTHER INFORMATION: / Ceres Seq. ID 1808586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

Met Ala Gly Ile Gly Pro Ile Thr Gln Asp Trp Glu Pro Val Val Ile
 1 5 10 15
 Arg Lys Lys Pro Ala Asn Ala Ala Lys Arg Asp Glu Lys Thr Val
 20 25 30
 Asn Ala Ala Arg Arg Ser Gly Ala Asp Ile Glu Thr Val Arg Lys Phe
 35 40 45
 Asn Ala Gly Thr Asn Lys Ala Ala Ser Ser Gly Thr Ser Leu Asn Thr
 50 55 60
 Lys Met Leu Asp Asp Asp Thr Glu Asn Leu Thr His Glu Arg Val Pro
 65 70 75 80
 Thr Glu Leu Lys Lys Ala Ile Met Gln Ala Arg Thr Asp Lys Lys Leu
 85 90 95
 Thr Gln Ser Gln Leu Ala Gln Ile Ile Asn Glu Lys Pro Gln Val Ile
 100 105 110
 Gln Glu Tyr Glu Ser Gly Lys Ala Ile Pro Asn Gln Gln Ile Leu Ser
 115 120 125
 Lys Leu Glu Arg Ala Leu Gly Ala Lys Leu Arg Gly Lys Lys
 130 135 140

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 630 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..630

(D) OTHER INFORMATION: / Ceres Seq. ID 1808591

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

aacactacaa caattttcat acctcatatt ctcttccatg gcaaccacca agcacctcct 60
 cctcttctct ctcacatcatg ctatcatcac cattacatct tccacttcac ttccatttct 120
 cacgacggag caaaacacaa tcgcaaccaa aatcatagac gcaatggtct caagtggctc 180
 tttcgaagat tggagcggag cgcttcctcaa caacaacgac gaattaaacg gtccagtcct 240
 aacttcaact ctcttcctcc ccaaaacatc cgtggaagga atcaacgcca cgtcaccact 300
 agttgcttct taccatattg ttccacaatg gcttgacttc tccgtcataa gtctcatgat 360
 gcctttctct cgcaccccta cactcctctc tggacactct atagtcgtta ccaacaattc 420
 agcttctggt tttactcttg atggtgttct catctctgag ccagatttat tctgtctctcc 480
 tactatagtt atccatcgaa tggcttttcc atttaacttc tctcgttacg gtggtggcga 540
 tatatagtta tttacttttg attcgcttct ccactttggt tctttctact tttactaata 600
 cactttcaaa taattaacaa cgaacttgac

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: amino acid

485

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

5 (A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 1808592

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

10 Thr Leu Gln Gln Phe Ser Tyr Leu Ile Phe Ser Ser Met Ala Thr Thr
 1 5 10 15
 Lys His Leu Leu Leu Phe Leu Leu Ile Ile Ala Ile Ile Thr Ile Thr
 20 25 30
 Ser Ser Thr Ser Leu Pro Phe Leu Thr Thr Glu Gln Asn Gln Ile Ala
 35 40 45
 15 Thr Lys Ile Ile Asp Ala Met Val Ser Ser Gly Ser Phe Glu Asp Trp
 50 55 60
 Ser Gly Ala Phe Leu Asn Asn Asn Asp Glu Leu Asn Gly Pro Val Leu
 65 70 75 80
 20 Thr Ser Thr Leu Phe Leu Pro Lys Thr Ser Val Glu Gly Ile Asn Ala
 85 90 95
 Thr Ser Pro Leu Val Ala Ser Tyr His Ile Val Pro Gln Trp Leu Asp
 100 105 110
 Phe Ser Val Ile Ser Leu Met Met Pro Phe Ser Arg Ile Pro Thr Leu
 115 120 125
 25 Leu Ser Gly His Ser Ile Val Val Thr Asn Asn Ser Ala Ser Gly Phe
 130 135 140
 Thr Leu Asp Gly Val Leu Ile Ser Glu Pro Asp Leu Phe Val Ser Pro
 145 150 155 160
 30 Thr Ile Val Ile His Arg Met Ala Phe Pro Phe Asn Phe Ser Arg Tyr
 165 170 175
 Gly Gly Gly Asp Ile
 180

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 1808593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

45 Met Ala Thr Thr Lys His Leu Leu Leu Phe Leu Leu Ile Ile Ala Ile
 1 5 10 15
 Ile Thr Ile Thr Ser Ser Thr Ser Leu Pro Phe Leu Thr Thr Glu Gln
 20 25 30
 Asn Gln Ile Ala Thr Lys Ile Ile Asp Ala Met Val Ser Ser Gly Ser
 35 40 45
 50 Phe Glu Asp Trp Ser Gly Ala Phe Leu Asn Asn Asn Asp Glu Leu Asn
 50 55 60
 Gly Pro Val Leu Thr Ser Thr Leu Phe Leu Pro Lys Thr Ser Val Glu
 65 70 75 80
 55 Gly Ile Asn Ala Thr Ser Pro Leu Val Ala Ser Tyr His Ile Val Pro
 85 90 95
 Gln Trp Leu Asp Phe Ser Val Ile Ser Leu Met Met Pro Phe Ser Arg
 100 105 110
 Ile Pro Thr Leu Leu Ser Gly His Ser Ile Val Val Thr Asn Asn Ser
 115 120 125
 60 Ala Ser Gly Phe Thr Leu Asp Gly Val Leu Ile Ser Glu Pro Asp Leu
 130 135 140

486

Phe Val Ser Pro Thr Ile Val Ile His Arg Met Ala Phe Pro Phe Asn
 145 150 155 160
 Phe Ser Arg Tyr Gly Gly Asp Ile
 165

5 (2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

15 (D) OTHER INFORMATION: / Ceres Seq. ID 1808594

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

Met Val Ser Ser Gly Ser Phe Glu Asp Trp Ser Gly Ala Phe Leu Asn
 1 5 10 15
 Asn Asn Asp Glu Leu Asn Gly Pro Val Leu Thr Ser Thr Leu Phe Leu
 20 20 25 30
 Pro Lys Thr Ser Val Glu Gly Ile Asn Ala Thr Ser Pro Leu Val Ala
 35 40 45
 Ser Tyr His Ile Val Pro Gln Trp Leu Asp Phe Ser Val Ile Ser Leu
 50 55 60
 25 Met Met Pro Phe Ser Arg Ile Pro Thr Leu Leu Ser Gly His Ser Ile
 65 70 75 80
 Val Val Thr Asn Asn Ser Ala Ser Gly Phe Thr Leu Asp Gly Val Leu
 85 90 95
 Ile Ser Glu Pro Asp Leu Phe Val Ser Pro Thr Ile Val Ile His Arg
 30 100 105 110
 Met Ala Phe Pro Phe Asn Phe Ser Arg Tyr Gly Gly Gly Asp Ile
 115 120 125

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..717

(D) OTHER INFORMATION: / Ceres Seq. ID 1920563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

45 cttgtttata ctaatgacca aggagagact gttaaaggag tttgctcaaa tttcttgtgt 60
 gatttggcac ccggaagtga tgtaagctg actggctcctg taggcaaaga aatgcttatg 120
 cctaaggatc caaacgccac cgtaattatg cttgccacag ggacaggaat tgctcctttc 180
 aggtctttct tatggaagat gttctttgag aaacatgatg actacaagtt caatggctta 240
 gcttggttgt tcttgggtgt accaaccact agctcattgc tctaccaaga ggagtttgat 300
 50 aagatgaaag caaaggcccc cgagaacttc aggggtggatt acgcgataag cagagaacaa 360
 gcgaacgata aaggagagaaa aatgtatatc cagactcgga tggcacagta cgcagctgaa 420
 ttatgggagt tgttgaagaa agacaacatc tttgtttaca tgtgtggact caagggaatg 480
 gagaaaggaa ttgatgacat tatggtctca ttggctgcaa atgacggtat tgactggttt 540
 gattacaaga agcagttgaa gaaggcagag caatggaacg ttgaagtcta ctgatcaaaa 600
 55 agcctttgac atttctgtag caaagtatag ctgaacaaaa ctgtaatttt cgcttccgaa 660
 tttctgtatt ttgaagataa gttttttaga tatgtttatac taaaaaaaga gttcttt

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

60 (D) TOPOLOGY: linear

487

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..197

5 (D) OTHER INFORMATION: / Ceres Seq. ID 1920564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

Leu Val Tyr Thr Asn Asp Gln Gly Glu Thr Val Lys Gly Val Cys Ser
 1 5 10 15
 Asn Phe Leu Cys Asp Leu Ala Pro Gly Ser Asp Val Lys Leu Thr Gly
 10 20 25 30
 Pro Val Gly Lys Glu Met Leu Met Pro Lys Asp Pro Asn Ala Thr Val
 35 40 45
 Ile Met Leu Ala Thr Gly Thr Gly Ile Ala Pro Phe Arg Ser Phe Leu
 50 55 60
 15 Trp Lys Met Phe Phe Glu Lys His Asp Asp Tyr Lys Phe Asn Gly Leu
 65 70 75 80
 Ala Trp Leu Phe Leu Gly Val Pro Thr Thr Ser Ser Leu Leu Tyr Gln
 85 90 95
 Glu Glu Phe Asp Lys Met Lys Ala Lys Ala Pro Glu Asn Phe Arg Val
 100 105 110
 20 Asp Tyr Ala Ile Ser Arg Glu Gln Ala Asn Asp Lys Gly Glu Lys Met
 115 120 125
 Tyr Ile Gln Thr Arg Met Ala Gln Tyr Ala Ala Glu Leu Trp Glu Leu
 130 135 140
 25 Leu Lys Lys Asp Asn Thr Phe Val Tyr Met Cys Gly Leu Lys Gly Met
 145 150 155 160
 Glu Lys Gly Ile Asp Asp Ile Met Val Ser Leu Ala Ala Asn Asp Gly
 165 170 175
 30 Ile Asp Trp Phe Asp Tyr Lys Lys Gln Leu Lys Lys Ala Glu Gln Trp
 180 185 190
 Asn Val Glu Val Tyr
 195

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 160 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..160

(D) OTHER INFORMATION: / Ceres Seq. ID 1920565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

45 Met Leu Met Pro Lys Asp Pro Asn Ala Thr Val Ile Met Leu Ala Thr
 1 5 10 15
 Gly Thr Gly Ile Ala Pro Phe Arg Ser Phe Leu Trp Lys Met Phe Phe
 20 25 30
 50 Glu Lys His Asp Asp Tyr Lys Phe Asn Gly Leu Ala Trp Leu Phe Leu
 35 40 45
 Gly Val Pro Thr Thr Ser Ser Leu Leu Tyr Gln Glu Glu Phe Asp Lys
 50 55 60
 Met Lys Ala Lys Ala Pro Glu Asn Phe Arg Val Asp Tyr Ala Ile Ser
 65 70 75 80
 55 Arg Glu Gln Ala Asn Asp Lys Gly Glu Lys Met Tyr Ile Gln Thr Arg
 85 90 95
 Met Ala Gln Tyr Ala Ala Glu Leu Trp Glu Leu Leu Lys Lys Asp Asn
 100 105 110
 60 Thr Phe Val Tyr Met Cys Gly Leu Lys Gly Met Glu Lys Gly Ile Asp
 115 120 125
 Asp Ile Met Val Ser Leu Ala Ala Asn Asp Gly Ile Asp Trp Phe Asp
 130 135 140

488

Tyr Lys Lys Gln Leu Lys Lys Ala Glu Gln Trp Asn Val Glu Val Tyr
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1920566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

Met Pro Lys Asp Pro Asn Ala Thr Val Ile Met Leu Ala Thr Gly Thr
 1 5 10 15
 Gly Ile Ala Pro Phe Arg Ser Phe Leu Trp Lys Met Phe Phe Glu Lys
 20 25 30
 His Asp Asp Tyr Lys Phe Asn Gly Leu Ala Trp Leu Phe Leu Gly Val
 35 40 45
 Pro Thr Thr Ser Ser Leu Leu Tyr Gln Glu Glu Phe Asp Lys Met Lys
 50 55 60
 Ala Lys Ala Pro Glu Asn Phe Arg Val Asp Tyr Ala Ile Ser Arg Glu
 65 70 75 80
 Gln Ala Asn Asp Lys Gly Glu Lys Met Tyr Ile Gln Thr Arg Met Ala
 85 90 95
 Gln Tyr Ala Ala Glu Leu Trp Glu Leu Leu Lys Lys Asp Asn Thr Phe
 100 105 110
 Val Tyr Met Cys Gly Leu Lys Gly Met Glu Lys Gly Ile Asp Asp Ile
 115 120 125
 Met Val Ser Leu Ala Ala Asn Asp Gly Ile Asp Trp Phe Asp Tyr Lys
 130 135 140
 Lys Gln Leu Lys Lys Ala Glu Gln Trp Asn Val Glu Val Tyr
 145 150 155

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2192

(D) OTHER INFORMATION: / Ceres Seq. ID 1974419

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

aattcaagtc atctctatcc gtcaacaata caaaccaacc ttctcaattc ctctcttttc 60
 atccacattt tcactagcta atggcttcta gttcaatgag cacctcatca tggacagcta 120
 gagaggacaa gcaattcgaa atggcggttg cgaaattcga caaggacact cctgaccggt 180
 50 ggcaaaaaat tgcaagggca gttggtggga aatcaactga agaagtaaag cgacactatg 240
 aattgctcct tagggatgtg aatgacattg agtcaggacg ctatccacaa cctagattat 300
 gttccgcggc ggcgatagct gctgcgttca cttcaatgtc gatgtcacag aaccgcgctt 360
 acgctgactc gcgatttcgc tttcctttct tctcttcttc acctccggca gaagaatctc 420
 caaccgatca taagtcttct tcgaattcta aatcggagac taaacctgac tccgatgagc 480
 55 cttaaaggatc tggtttcgat cctgagtcac tggaaagagg tgctaaagct cttcgtgaaa 540
 tcaatagctc tcctcattcc aaacagggtg ttgatcta at gcgaaagcag gagaagactc 600
 gattagctga attagcggct gagaaagaac ataatgaagc tattcaagct agcaaggaca 660
 ttgaaagaca gcggaattg gcagaggatc agagaaattt agtgacgcaa caggcccaag 720
 cgaaagcgca aaatcttaga tatgaggatg agttggccag gaagagaatg cagacagata 780
 60 atgaagctca gagacggcat aatgctgaat tggtttcgat gcaagaagca tcttctatac 840
 ggaaagagaa agcaagaatt gccacggaag aacagattca agcacagcag cgcgagactg 900
 agaaagagag agcggaaact gagcgagaaa caattcgcgt gaaagctatg gctgaggctg 960

489

aaggccgagc tcatgaagct aaactcactg aggagcagaa tagaagaatg cttctagata 1020
 agataaatgg tgaaagggag aaatggcttg cagcaatcaa cagcactttc agtcacattg 1080
 aaggaggagt aaggacctta ttaactgatc gaagtaaatt gattatgact gttggaggag 1140
 5 ttacggcatt agccgctggg gtttacacaa ctcgagaagg tgctagggtt acctgggggtt 1200
 atatcaatag aattcttggg cagccatcac tgatcagaga atcttccatg ggccgattcc 1260
 catgggcagg ctgagtgtct cagtttaaga acaaacttag cacagctgca ggggcagcag 1320
 catctgcaga aggagaaaag cctcttgaaa atgtaattct ccacgttct ttgaagacga 1380
 gaattgagcg tcttgcaaga gccacagcaa ataccaagtc acataaagca ccattccgaa 1440
 acatgatgtt ttatgggcct ccagggtaccg gaaaaactat ggtggcgagg gagattgctc 1500
 10 ggaagtcggg tcttgattat gctatgatga caggaggaga tgttgctcct cttggtgcac 1560
 aggctgttac aaagatccat gaaatatttg attgggctaa gaaatcaaac aaagggttac 1620
 tgcttttcat cgatgaagct gatgctttcc tatgcgaacg taacagcact tacatgagtg 1680
 aggctcagcg cagcgctctg aacgcgttgc tctttcgaac cgggtgatcaa tcgcgggaca 1740
 tagtccttgt cctggctaca aacagacctg gagatctcga cagtgcagtc actgacagga 1800
 15 tcgacgaagt tatcgagttt cctctccctg gtgaagaaga acgcttcaag ctcctcaagc 1860
 tctatctcaa caagtaccta atgggtgacg acaagaaagg tgagaaagac tcaaacctta 1920
 aatggagcaa cttgttcaag aagaagaagt cacagaagat aaccattgaa ggagacctaa 1980
 ccgaccaagt gattaaagaa gctgcaaaaa agacagaagg cttttctggt cgtgaaatcg 2040
 ctaagcttgt cgccggtgtt caagctgcgg tatatggacg acaggattgt gtcttggatt 2100
 20 cccaactttt tgaagaaatt gtggattata agatcgaaga acatcaccag agaatcagac 2160
 ttgcgactga aggtggccaa tcgtttccgt ag

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 703 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..703

(D) OTHER INFORMATION: / Ceres Seq. ID 1974420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

35 Met Ala Ser Ser Ser Met Ser Thr Ser Ser Trp Thr Ala Arg Glu Asp
 1 5 10 15
 Lys Gln Phe Glu Met Ala Leu Ala Lys Phe Asp Lys Asp Thr Pro Asp
 20 25 30
 Arg Trp Gln Lys Ile Ala Arg Ala Val Gly Gly Lys Ser Thr Glu Glu
 35 40 45
 40 Val Lys Arg His Tyr Glu Leu Leu Arg Asp Val Asn Asp Ile Glu
 50 55 60
 Ser Gly Arg Tyr Pro Gln Pro Arg Leu Cys Ser Ala Ala Ala Ile Ala
 65 70 75 80
 45 Ala Ala Phe Thr Ser Met Ser Met Ser Gln Asn Arg Ala Tyr Ala Asp
 85 90 95
 Ser Arg Phe Arg Phe Pro Phe Phe Ser Ser Ser Pro Pro Ala Glu Glu
 100 105 110
 Ser Pro Thr Asp His Lys Ser Ser Ser Asn Ser Lys Ser Glu Thr Lys
 115 120 125
 50 Pro Asp Ser Asp Glu Pro Lys Gly Ser Gly Phe Asp Pro Glu Ser Leu
 130 135 140
 Glu Arg Gly Ala Lys Ala Leu Arg Glu Ile Asn Ser Ser Pro His Ser
 145 150 155 160
 55 Lys Gln Val Phe Asp Leu Met Arg Lys Gln Glu Lys Thr Arg Leu Ala
 165 170 175
 Glu Leu Ala Ala Glu Lys Glu His Asn Glu Ala Ile Gln Ala Ser Lys
 180 185 190
 Asp Ile Glu Arg Gln Arg Lys Leu Ala Glu Asp Gln Arg Asn Leu Val
 195 200 205
 60 Gln Gln Gln Ala Gln Ala Lys Ala Gln Asn Leu Arg Tyr Glu Asp Glu
 210 215 220
 Leu Ala Arg Lys Arg Met Gln Thr Asp Asn Glu Ala Gln Arg Arg His

490

	225				230					235				240
	Asn	Ala	Glu	Leu	Val	Ser	Met	Gln	Glu	Ala	Ser	Ser	Ile	Arg
					245					250				Lys
5	Lys	Ala	Arg	Ile	Ala	Thr	Glu	Glu	Gln	Ile	Gln	Ala	Gln	Gln
				260					265				270	Arg
	Thr	Glu	Lys	Glu	Arg	Ala	Glu	Leu	Glu	Arg	Glu	Thr	Ile	Arg
			275				280					285	Val	Lys
	Ala	Met	Ala	Glu	Ala	Glu	Gly	Arg	Ala	His	Glu	Ala	Lys	Leu
		290					295				300		Thr	Glu
10	Glu	Gln	Asn	Arg	Arg	Met	Leu	Leu	Asp	Lys	Ile	Asn	Gly	Glu
	305					310					315			Arg
	Lys	Trp	Leu	Ala	Ala	Ile	Asn	Thr	Thr	Phe	Ser	His	Ile	Glu
				325						330				Gly
	Val	Arg	Thr	Leu	Leu	Thr	Asp	Arg	Ser	Lys	Leu	Ile	Met	Thr
15				340						345			350	Val
	Gly	Val	Thr	Ala	Leu	Ala	Ala	Gly	Val	Tyr	Thr	Thr	Arg	Glu
		355					360					365	Gly	Ala
	Arg	Val	Thr	Trp	Gly	Tyr	Ile	Asn	Arg	Ile	Leu	Gly	Gln	Pro
		370					375					380	Ser	Leu
20	Ile	Arg	Glu	Ser	Ser	Met	Gly	Arg	Phe	Pro	Trp	Ala	Gly	Ser
	385					390					395			Val
	Gln	Phe	Lys	Asn	Lys	Leu	Ser	Thr	Ala	Ala	Gly	Ala	Ala	Ser
				405						410				Ala
	Glu	Gly	Glu	Lys	Pro	Leu	Glu	Asn	Val	Ile	Leu	His	Arg	Ser
25				420					425				430	Leu
	Thr	Arg	Ile	Glu	Arg	Leu	Ala	Arg	Ala	Thr	Ala	Asn	Thr	Lys
		435					440					445	Ser	His
	Lys	Ala	Pro	Phe	Arg	Asn	Met	Met	Phe	Tyr	Gly	Pro	Pro	Gly
		450				455					460			Thr
30	Lys	Thr	Met	Val	Ala	Arg	Glu	Ile	Ala	Arg	Lys	Ser	Gly	Leu
	465					470					475			Asp
	Ala	Met	Met	Thr	Gly	Gly	Asp	Val	Ala	Pro	Leu	Gly	Ala	Gln
				485						490				Ala
	Thr	Lys	Ile	His	Glu	Ile	Phe	Asp	Trp	Ala	Lys	Lys	Ser	Asn
35				500					505					Lys
	Leu	Leu	Leu	Phe	Ile	Asp	Glu	Ala	Asp	Ala	Phe	Leu	Cys	Glu
		515					520					525	Arg	Asn
	Ser	Thr	Tyr	Met	Ser	Glu	Ala	Gln	Arg	Ser	Ala	Leu	Asn	Ala
		530					535					540	Leu	Leu
40	Phe	Arg	Thr	Gly	Asp	Gln	Ser	Arg	Asp	Ile	Val	Leu	Val	Leu
	545					550					555			Ala
	Asn	Arg	Pro	Gly	Asp	Leu	Asp	Ser	Ala	Val	Thr	Asp	Arg	Ile
				565						570				Asp
	Val	Ile	Glu	Phe	Pro	Leu	Pro	Gly	Glu	Glu	Glu	Arg	Phe	Lys
45				580					585				590	Leu
	Lys	Leu	Tyr	Leu	Asn	Lys	Tyr	Leu	Met	Gly	Asp	Asp	Lys	Lys
		595						600				605	Gly	Glu
	Lys	Asp	Ser	Asn	Leu	Lys	Trp	Ser	Asn	Leu	Phe	Lys	Lys	Lys
		610					615					620	Lys	Ser
50	Gln	Lys	Ile	Thr	Ile	Glu	Gly	Asp	Leu	Thr	Asp	Gln	Val	Ile
	625					630					635			Glu
	Ala	Ala	Lys	Lys	Thr	Glu	Gly	Phe	Ser	Gly	Arg	Glu	Ile	Ala
				645						650				Lys
	Val	Ala	Gly	Val	Gln	Ala	Ala	Val	Tyr	Gly	Arg	Gln	Asp	Cys
55				660					665				670	Val
	Asp	Ser	Gln	Leu	Phe	Glu	Glu	Ile	Val	Asp	Tyr	Lys	Ile	Glu
		675					680					685	Glu	His
	His	Gln	Arg	Ile	Arg	Leu	Ala	Thr	Glu	Gly	Gly	Gln	Ser	Phe
		690					695					700	Pro	
60	(2)	INFORMATION FOR SEQ ID NO:346:												
		(i) SEQUENCE CHARACTERISTICS:												
		(A) LENGTH: 698 amino acids												

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(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..698
 (D) OTHER INFORMATION: / Ceres Seq. ID 1974421
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

10	Met	Ser	Thr	Ser	Ser	Trp	Thr	Ala	Arg	Glu	Asp	Lys	Gln	Phe	Glu	Met
	1			5						10					15	
	Ala	Leu	Ala	Lys	Phe	Asp	Lys	Asp	Thr	Pro	Asp	Arg	Trp	Gln	Lys	Ile
				20					25					30		
	Ala	Arg	Ala	Val	Gly	Gly	Lys	Ser	Thr	Glu	Glu	Val	Lys	Arg	His	Tyr
15			35				40						45			
	Glu	Leu	Leu	Leu	Arg	Asp	Val	Asn	Asp	Ile	Glu	Ser	Gly	Arg	Tyr	Pro
		50					55					60				
	Gln	Pro	Arg	Leu	Cys	Ser	Ala	Ala	Ala	Ile	Ala	Ala	Ala	Phe	Thr	Ser
	65					70					75					80
20	Met	Ser	Met	Ser	Gln	Asn	Arg	Ala	Tyr	Ala	Asp	Ser	Arg	Phe	Arg	Phe
					85					90					95	
	Pro	Phe	Phe	Ser	Ser	Ser	Pro	Pro	Ala	Glu	Glu	Ser	Pro	Thr	Asp	His
				100					105					110		
	Lys	Ser	Ser	Ser	Asn	Ser	Lys	Ser	Glu	Thr	Lys	Pro	Asp	Ser	Asp	Glu
25			115						120					125		
	Pro	Lys	Gly	Ser	Gly	Phe	Asp	Pro	Glu	Ser	Leu	Glu	Arg	Gly	Ala	Lys
		130					135					140				
	Ala	Leu	Arg	Glu	Ile	Asn	Ser	Ser	Pro	His	Ser	Lys	Gln	Val	Phe	Asp
	145					150					155					160
30	Leu	Met	Arg	Lys	Gln	Glu	Lys	Thr	Arg	Leu	Ala	Glu	Leu	Ala	Ala	Glu
					165					170					175	
	Lys	Glu	His	Asn	Glu	Ala	Ile	Gln	Ala	Ser	Lys	Asp	Ile	Glu	Arg	Gln
				180					185					190		
	Arg	Lys	Leu	Ala	Glu	Asp	Gln	Arg	Asn	Leu	Val	Gln	Gln	Gln	Ala	Gln
35			195					200					205			
	Ala	Lys	Ala	Gln	Asn	Leu	Arg	Tyr	Glu	Asp	Glu	Leu	Ala	Arg	Lys	Arg
		210					215					220				
	Met	Gln	Thr	Asp	Asn	Glu	Ala	Gln	Arg	Arg	His	Asn	Ala	Glu	Leu	Val
	225					230					235					240
40	Ser	Met	Gln	Glu	Ala	Ser	Ser	Ile	Arg	Lys	Glu	Lys	Ala	Arg	Ile	Ala
					245					250					255	
	Thr	Glu	Glu	Gln	Ile	Gln	Ala	Gln	Gln	Arg	Glu	Thr	Glu	Lys	Glu	Arg
				260						265					270	
	Ala	Glu	Leu	Glu	Arg	Glu	Thr	Ile	Arg	Val	Lys	Ala	Met	Ala	Glu	Ala
45			275					280					285			
	Glu	Gly	Arg	Ala	His	Glu	Ala	Lys	Leu	Thr	Glu	Glu	Gln	Asn	Arg	Arg
		290					295					300				
	Met	Leu	Leu	Asp	Lys	Ile	Asn	Gly	Glu	Arg	Glu	Lys	Trp	Leu	Ala	Ala
	305					310					315					320
50	Ile	Asn	Thr	Thr	Phe	Ser	His	Ile	Glu	Gly	Gly	Val	Arg	Thr	Leu	Leu
					325					330					335	
	Thr	Asp	Arg	Ser	Lys	Leu	Ile	Met	Thr	Val	Gly	Gly	Val	Thr	Ala	Leu
				340					345					350		
	Ala	Ala	Gly	Val	Tyr	Thr	Thr	Arg	Glu	Gly	Ala	Arg	Val	Thr	Trp	Gly
55			355					360					365			
	Tyr	Ile	Asn	Arg	Ile	Leu	Gly	Gln	Pro	Ser	Leu	Ile	Arg	Glu	Ser	Ser
		370					375					380				
	Met	Gly	Arg	Phe	Pro	Trp	Ala	Gly	Ser	Val	Ser	Gln	Phe	Lys	Asn	Lys
	385					390					395					400
60	Leu	Ser	Thr	Ala	Ala	Gly	Ala	Ala	Ala	Ser	Ala	Glu	Gly	Glu	Lys	Pro
					405						410				415	
	Leu	Glu	Asn	Val	Ile	Leu	His	Arg	Ser	Leu	Lys	Thr	Arg	Ile	Glu	Arg

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420 425 430
 Leu Ala Arg Ala Thr Ala Asn Thr Lys Ser His Lys Ala Pro Phe Arg
 435 440 445
 5 Asn Met Met Phe Tyr Gly Pro Pro Gly Thr Gly Lys Thr Met Val Ala
 450 455 460
 Arg Glu Ile Ala Arg Lys Ser Gly Leu Asp Tyr Ala Met Met Thr Gly
 465 470 475 480
 Gly Asp Val Ala Pro Leu Gly Ala Gln Ala Val Thr Lys Ile His Glu
 485 490 495
 10 Ile Phe Asp Trp Ala Lys Lys Ser Asn Lys Gly Leu Leu Leu Phe Ile
 500 505 510
 Asp Glu Ala Asp Ala Phe Leu Cys Glu Arg Asn Ser Thr Tyr Met Ser
 515 520 525
 15 Glu Ala Gln Arg Ser Ala Leu Asn Ala Leu Leu Phe Arg Thr Gly Asp
 530 535 540
 Gln Ser Arg Asp Ile Val Leu Val Leu Ala Thr Asn Arg Pro Gly Asp
 545 550 555 560
 Leu Asp Ser Ala Val Thr Asp Arg Ile Asp Glu Val Ile Glu Phe Pro
 565 570 575
 20 Leu Pro Gly Glu Glu Glu Arg Phe Lys Leu Leu Lys Leu Tyr Leu Asn
 580 585 590
 Lys Tyr Leu Met Gly Asp Asp Lys Lys Gly Glu Lys Asp Ser Asn Leu
 595 600 605
 25 Lys Trp Ser Asn Leu Phe Lys Lys Lys Ser Gln Lys Ile Thr Ile
 610 615 620
 Glu Gly Asp Leu Thr Asp Gln Val Ile Lys Glu Ala Ala Lys Lys Thr
 625 630 635 640
 Glu Gly Phe Ser Gly Arg Glu Ile Ala Lys Leu Val Ala Gly Val Gln
 645 650 655
 30 Ala Ala Val Tyr Gly Arg Gln Asp Cys Val Leu Asp Ser Gln Leu Phe
 660 665 670
 Glu Glu Ile Val Asp Tyr Lys Ile Glu Glu His His Gln Arg Ile Arg
 675 680 685
 35 Leu Ala Thr Glu Gly Gly Gln Ser Phe Pro
 690 695
 (2) INFORMATION FOR SEQ ID NO:347:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 683 amino acids
 (B) TYPE: amino acid
 40 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 45 (B) LOCATION: 1..683
 (D) OTHER INFORMATION: / Ceres Seq. ID 1974422
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:
 Met Ala Leu Ala Lys Phe Asp Lys Asp Thr Pro Asp Arg Trp Gln Lys
 1 5 10 15
 50 Ile Ala Arg Ala Val Gly Gly Lys Ser Thr Glu Glu Val Lys Arg His
 20 25 30
 Tyr Glu Leu Leu Arg Asp Val Asn Asp Ile Glu Ser Gly Arg Tyr
 35 40 45
 55 Pro Gln Pro Arg Leu Cys Ser Ala Ala Ala Ile Ala Ala Ala Phe Thr
 50 55 60
 Ser Met Ser Met Ser Gln Asn Arg Ala Tyr Ala Asp Ser Arg Phe Arg
 65 70 75 80
 Phe Pro Phe Phe Ser Ser Ser Pro Pro Ala Glu Glu Ser Pro Thr Asp
 85 90 95
 60 His Lys Ser Ser Asn Ser Lys Ser Glu Thr Lys Pro Asp Ser Asp
 100 105 110
 Glu Pro Lys Gly Ser Gly Phe Asp Pro Glu Ser Leu Glu Arg Gly Ala

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		115				120					125					
	Lys	Ala	Leu	Arg	Glu	Ile	Asn	Ser	Ser	Pro	His	Ser	Lys	Gln	Val	Phe
		130					135					140				
5	Asp	Leu	Met	Arg	Lys	Gln	Glu	Lys	Thr	Arg	Leu	Ala	Glu	Leu	Ala	Ala
	145					150					155					160
	Glu	Lys	Glu	His	Asn	Glu	Ala	Ile	Gln	Ala	Ser	Lys	Asp	Ile	Glu	Arg
					165					170						175
	Gln	Arg	Lys	Leu	Ala	Glu	Asp	Gln	Arg	Asn	Leu	Val	Gln	Gln	Gln	Ala
					180					185					190	
10	Gln	Ala	Lys	Ala	Gln	Asn	Leu	Arg	Tyr	Glu	Asp	Glu	Leu	Ala	Arg	Lys
					195					200					205	
	Arg	Met	Gln	Thr	Asp	Asn	Glu	Ala	Gln	Arg	Arg	His	Asn	Ala	Glu	Leu
	210						215					220				
15	Val	Ser	Met	Gln	Glu	Ala	Ser	Ser	Ile	Arg	Lys	Glu	Lys	Ala	Arg	Ile
	225					230					235					240
	Ala	Thr	Glu	Glu	Gln	Ile	Gln	Ala	Gln	Gln	Arg	Glu	Thr	Glu	Lys	Glu
					245					250						255
	Arg	Ala	Glu	Leu	Glu	Arg	Glu	Thr	Ile	Arg	Val	Lys	Ala	Met	Ala	Glu
					260					265					270	
20	Ala	Glu	Gly	Arg	Ala	His	Glu	Ala	Lys	Leu	Thr	Glu	Glu	Gln	Asn	Arg
					275				280						285	
	Arg	Met	Leu	Leu	Asp	Lys	Ile	Asn	Gly	Glu	Arg	Glu	Lys	Trp	Leu	Ala
	290						295					300				
25	Ala	Ile	Asn	Thr	Thr	Phe	Ser	His	Ile	Glu	Gly	Gly	Val	Arg	Thr	Leu
	305					310					315					320
	Leu	Thr	Asp	Arg	Ser	Lys	Leu	Ile	Met	Thr	Val	Gly	Gly	Val	Thr	Ala
					325					330						335
	Leu	Ala	Ala	Gly	Val	Tyr	Thr	Thr	Arg	Glu	Gly	Ala	Arg	Val	Thr	Trp
					340				345					350		
30	Gly	Tyr	Ile	Asn	Arg	Ile	Leu	Gly	Gln	Pro	Ser	Leu	Ile	Arg	Glu	Ser
					355				360					365		
	Ser	Met	Gly	Arg	Phe	Pro	Trp	Ala	Gly	Ser	Val	Ser	Gln	Phe	Lys	Asn
	370						375					380				
35	Lys	Leu	Ser	Thr	Ala	Ala	Gly	Ala	Ala	Ala	Ser	Ala	Glu	Gly	Glu	Lys
	385					390					395					400
	Pro	Leu	Glu	Asn	Val	Ile	Leu	His	Arg	Ser	Leu	Lys	Thr	Arg	Ile	Glu
					405					410						415
	Arg	Leu	Ala	Arg	Ala	Thr	Ala	Asn	Thr	Lys	Ser	His	Lys	Ala	Pro	Phe
					420				425					430		
40	Arg	Asn	Met	Met	Phe	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Met	Val
					435				440					445		
	Ala	Arg	Glu	Ile	Ala	Arg	Lys	Ser	Gly	Leu	Asp	Tyr	Ala	Met	Met	Thr
	450						455					460				
45	Gly	Gly	Asp	Val	Ala	Pro	Leu	Gly	Ala	Gln	Ala	Val	Thr	Lys	Ile	His
	465					470				475						480
	Glu	Ile	Phe	Asp	Trp	Ala	Lys	Lys	Ser	Asn	Lys	Gly	Leu	Leu	Leu	Phe
					485					490						495
	Ile	Asp	Glu	Ala	Asp	Ala	Phe	Leu	Cys	Glu	Arg	Asn	Ser	Thr	Tyr	Met
					500				505					510		
50	Ser	Glu	Ala	Gln	Arg	Ser	Ala	Leu	Asn	Ala	Leu	Leu	Phe	Arg	Thr	Gly
					515				520					525		
	Asp	Gln	Ser	Arg	Asp	Ile	Val	Leu	Val	Leu	Ala	Thr	Asn	Arg	Pro	Gly
					530				535			540				
55	Asp	Leu	Asp	Ser	Ala	Val	Thr	Asp	Arg	Ile	Asp	Glu	Val	Ile	Glu	Phe
	545					550					555					560
	Pro	Leu	Pro	Gly	Glu	Glu	Glu	Arg	Phe	Lys	Leu	Leu	Lys	Leu	Tyr	Leu
					565					570						575
	Asn	Lys	Tyr	Leu	Met	Gly	Asp	Asp	Lys	Lys	Gly	Glu	Lys	Asp	Ser	Asn
					580				585					590		
60	Leu	Lys	Trp	Ser	Asn	Leu	Phe	Lys	Lys	Lys	Ser	Gln	Lys	Ile	Thr	
					595				600			605				
	Ile	Glu	Gly	Asp	Leu	Thr	Asp	Gln	Val	Ile	Lys	Glu	Ala	Ala	Lys	Lys

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610 615 620
 Thr Glu Gly Phe Ser Gly Arg Glu Ile Ala Lys Leu Val Ala Gly Val
 625 630 635 640
 Gln Ala Ala Val Tyr Gly Arg Gln Asp Cys Val Leu Asp Ser Gln Leu
 5 645 650 655
 Phe Glu Glu Ile Val Asp Tyr Lys Ile Glu Glu His His Gln Arg Ile
 660 665 670
 Arg Leu Ala Thr Glu Gly Gly Gln Ser Phe Pro
 675 680
 10 (2) INFORMATION FOR SEQ ID NO:348:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 953 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..953
 20 (D) OTHER INFORMATION: / Ceres Seq. ID 1975983
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:
 aaaaaagata aaacaaaagc tgaaaggagg aaaccagagg aaggagacga cgaccaccac 60
 cacaacgcat ctacagctctt ccttaatcca tggcagacaa gggccgcccg ttgccgaagt 120
 ttggaagagc tgagatgcgt tgtggtggtg gcgtcgctc cttcttcaat ctcatcgcaa 180
 25 tcatgatcat atccgagact aatcgccgtg agatctccaa gtacctcttc aaagagggtg 240
 tttgttttgc caaaaaggat ttcaatttac cacaacatcc tttgattgag agtgttccaa 300
 atctgcaagt tatcaagttg atgcagagtt tcaaactctaa ggaatatgtg agagagacct 360
 ttgcttggat gcattactac tggttcctca caaatgaagg tattgacttt cttaggactt 420
 accttaatat cccatctgag attgttcttg ctactctgaa gaagcaacag aagcctcttg 480
 30 gtcgaccttt tggaggtggt ggtgaccgtc cccgtggccc tcctcggtgt gatggagaga 540
 ggaggttttg tgacagagat ggataccgtg gaggtcctaa atcaggtgga gagtatggtg 600
 acaaggctgg agcacctgct gattaccagc ctggcttcag ggggtggagct agtggagcaa 660
 ggcaagggtt tggctgtgga gctggtggtt ttggtggtgg tgctggtcca gctgctggat 720
 ctgatctacc ttgaaaagga ctttcttgtt tctttttggt cttatttaag gttacatagc 780
 35 accttattga gaacgaatgt gtcttttggg actttgtttc tttctcttaa accatttcac 840
 aatatgattg tttttttacg ttagaatttt atgaagaaat gttggatcgt tacatgaatc 900
 tttttacact gtctctcttt ttaaattctc ctatttagtt tttttcgaag ctt
 (2) INFORMATION FOR SEQ ID NO:349:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 214 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 45 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..214
 (D) OTHER INFORMATION: / Ceres Seq. ID 1975984
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:
 50 Met Ala Asp Lys Gly Arg Pro Leu Pro Lys Phe Gly Arg Ala Glu Met
 1 5 10 15
 Arg Cys Gly Gly Gly Val Ala Ser Phe Asn Leu Ile Ala Ile Met
 20 25 30
 Ile Ile Ser Glu Thr Asn Arg Arg Glu Ile Ser Lys Tyr Leu Phe Lys
 55 35 40 45
 Glu Gly Val Leu Phe Ala Lys Lys Asp Phe Asn Leu Pro Gln His Pro
 50 55 60
 Leu Ile Glu Ser Val Pro Asn Leu Gln Val Ile Lys Leu Met Gln Ser
 65 70 75 80
 60 Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Phe Ala Trp Met His Tyr
 85 90 95
 Tyr Trp Phe Leu Thr Asn Glu Gly Ile Asp Phe Leu Arg Thr Tyr Leu

495

100 105 110
 Asn Leu Pro Ser Glu Ile Val Pro Ala Thr Leu Lys Lys Gln Gln Lys
 115 120 125
 5 Pro Leu Gly Arg Pro Phe Gly Gly Gly Asp Arg Pro Arg Gly Pro
 130 135 140
 Pro Arg Gly Asp Gly Glu Arg Arg Phe Gly Asp Arg Asp Gly Tyr Arg
 145 150 155 160
 Gly Gly Pro Lys Ser Gly Gly Glu Tyr Gly Asp Lys Ala Gly Ala Pro
 165 170 175
 10 Ala Asp Tyr Gln Pro Gly Phe Arg Gly Gly Ala Ser Gly Ala Arg Gln
 180 185 190
 Gly Phe Gly Arg Gly Ala Gly Gly Phe Gly Gly Gly Ala Gly Pro Ala
 195 200 205
 Ala Gly Ser Asp Leu Pro
 210
 (2) INFORMATION FOR SEQ ID NO:350:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 199 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 25 (B) LOCATION: 1..199
 (D) OTHER INFORMATION: / Ceres Seq. ID 1975985
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:
 Met Arg Cys Gly Gly Gly Val Ala Ser Phe Phe Asn Leu Ile Ala Ile
 1 5 10 15
 30 Met Ile Ile Ser Glu Thr Asn Arg Arg Glu Ile Ser Lys Tyr Leu Phe
 20 25 30
 Lys Glu Gly Val Leu Phe Ala Lys Lys Asp Phe Asn Leu Pro Gln His
 35 35 40 45
 Pro Leu Ile Glu Ser Val Pro Asn Leu Gln Val Ile Lys Leu Met Gln
 50 55 60
 Ser Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Phe Ala Trp Met His
 65 70 75 80
 Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Asp Phe Leu Arg Thr Tyr
 85 90 95
 40 Leu Asn Leu Pro Ser Glu Ile Val Pro Ala Thr Leu Lys Lys Gln Gln
 100 105 110
 Lys Pro Leu Gly Arg Pro Phe Gly Gly Gly Asp Arg Pro Arg Gly
 115 120 125
 45 Pro Pro Arg Gly Asp Gly Glu Arg Arg Phe Gly Asp Arg Asp Gly Tyr
 130 135 140
 Arg Gly Gly Pro Lys Ser Gly Gly Glu Tyr Gly Asp Lys Ala Gly Ala
 145 150 155 160
 Pro Ala Asp Tyr Gln Pro Gly Phe Arg Gly Gly Ala Ser Gly Ala Arg
 165 170 175
 50 Gln Gly Phe Gly Arg Gly Ala Gly Gly Phe Gly Gly Gly Ala Gly Pro
 180 185 190
 Ala Ala Gly Ser Asp Leu Pro
 195
 (2) INFORMATION FOR SEQ ID NO:351:
 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 60 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide

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(B) LOCATION: 1..183

(D) OTHER INFORMATION: / Ceres Seq. ID 1975986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

5 Met Ile Ile Ser Glu Thr Asn Arg Arg Glu Ile Ser Lys Tyr Leu Phe
 1 5 10 15
 Lys Glu Gly Val Leu Phe Ala Lys Lys Asp Phe Asn Leu Pro Gln His
 20 25 30
 Pro Leu Ile Glu Ser Val Pro Asn Leu Gln Val Ile Lys Leu Met Gln
 35 40 45
 10 Ser Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Phe Ala Trp Met His
 50 55 60
 Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Asp Phe Leu Arg Thr Tyr
 65 70 75 80
 Leu Asn Leu Pro Ser Glu Ile Val Pro Ala Thr Leu Lys Lys Gln Gln
 85 90 95
 15 Lys Pro Leu Gly Arg Pro Phe Gly Gly Gly Asp Arg Pro Arg Gly
 100 105 110
 Pro Pro Arg Gly Asp Gly Glu Arg Arg Phe Gly Asp Arg Asp Gly Tyr
 115 120 125
 20 Arg Gly Gly Pro Lys Ser Gly Gly Glu Tyr Gly Asp Lys Ala Gly Ala
 130 135 140
 Pro Ala Asp Tyr Gln Pro Gly Phe Arg Gly Gly Ala Ser Gly Ala Arg
 145 150 155 160
 Gln Gly Phe Gly Arg Gly Ala Gly Gly Phe Gly Gly Gly Ala Gly Pro
 165 170 175
 25 Ala Ala Gly Ser Asp Leu Pro
 180

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1027 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1027

(D) OTHER INFORMATION: / Ceres Seq. ID 1976019

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

40 atcgaaatta gggtttcgcg ttaggagaag aagttaaagc aaaacacata caaacgcagt 60
 caccttctct gtcgcctcct tcttcaatct catcgcaatc atgatcatat ccgagactaa 120
 tcgccgtgag atctccaagt acctcttcaa agagggtgtt ttgtttgccaa aaaaggattt 180
 caatttaccac caacatcctt tgattgagag tgttccaaat ctgcaagtta tcaagttgat 240
 gcagagtttc aatatctaagg aatatgtgag agagaccttt gcttgatgc attactactg 300
 45 gttcctcaca aatgaaggta ttgactttct taggacttac cttaatctcc catctgagat 360
 tgttcctgct actctgaaga agcaacagaa gcctcttggt cgaccttttg gaggtggtgg 420
 tgaccgtccc cgtggccctc ctcgtggtga tggagagagg aggtttggtg acagagatgg 480
 ataccgtgga ggtcctaaat caggtggaga gtatggtgac aaggctggag cacctgctga 540
 ttaccagcct ggcttcaggg gtggagctag tggagcaagg caagggtttg gtcgtggagc 600
 50 tgggtggtttt ggtggtggtg ctggtccagc tgctggatct gatctacctt gaaaaggaga 660
 caatacagct cagccaaaagc caaggccttt atcaccttac acaatgtacg cggacatgaa 720
 gcctccaaca tcaccacttc catctccagt caccaatcat tagctatgtg agacgagaat 780
 tggcctccta aaccctggag cttcttctta attgcaggtt gtaaacaatg agtaagagag 840
 tgatggggca attcagtttt gcaggtatga atcagtgagc ttatttgtac aataatacaa 900
 55 tattcatcaa catgccttat atatgagttc tacttttttt ctctgttca acgatcaatg 960
 cagtaaccat attgttacc cttctcatac atatatgatg acccaaatta attatcatta 1020
 ggctttc

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:

60

497

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

5 (A) NAME/KEY: peptide
(B) LOCATION: 1..183
(D) OTHER INFORMATION: / Ceres Seq. ID 1976020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

Met Ile Ile Ser Glu Thr Asn Arg Arg Glu Ile Ser Lys Tyr Leu Phe
1 5 10 15
10 Lys Glu Gly Val Leu Phe Ala Lys Lys Asp Phe Asn Leu Pro Gln His
20 25 30
Pro Leu Ile Glu Ser Val Pro Asn Leu Gln Val Ile Lys Leu Met Gln
35 40 45
15 Ser Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Phe Ala Trp Met His
50 55 60
Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Asp Phe Leu Arg Thr Tyr
65 70 75 80
Leu Asn Leu Pro Ser Glu Ile Val Pro Ala Thr Leu Lys Lys Gln Gln
85 90 95
20 Lys Pro Leu Gly Arg Pro Phe Gly Gly Gly Gly Asp Arg Pro Arg Gly
100 105 110
Pro Pro Arg Gly Asp Gly Glu Arg Arg Phe Gly Asp Arg Asp Gly Tyr
115 120 125
25 Arg Gly Gly Pro Lys Ser Gly Gly Glu Tyr Gly Asp Lys Ala Gly Ala
130 135 140
Pro Ala Asp Tyr Gln Pro Gly Phe Arg Gly Gly Ala Ser Gly Ala Arg
145 150 155 160
Gln Gly Phe Gly Arg Gly Ala Gly Gly Phe Gly Gly Gly Ala Gly Pro
165 170 175
30 Ala Ala Gly Ser Asp Leu Pro
180

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 137 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

40 (A) NAME/KEY: peptide
(B) LOCATION: 1..137
(D) OTHER INFORMATION: / Ceres Seq. ID 1976021

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

Met Gln Ser Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Phe Ala Trp
45 1 5 10 15
Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Asp Phe Leu Arg
20 25 30
Thr Tyr Leu Asn Leu Pro Ser Glu Ile Val Pro Ala Thr Leu Lys Lys
35 40 45
50 Gln Gln Lys Pro Leu Gly Arg Pro Phe Gly Gly Gly Gly Asp Arg Pro
50 55 60
Arg Gly Pro Pro Arg Gly Asp Gly Glu Arg Arg Phe Gly Asp Arg Asp
65 70 75 80
Gly Tyr Arg Gly Gly Pro Lys Ser Gly Gly Glu Tyr Gly Asp Lys Ala
55 85 90 95
Gly Ala Pro Ala Asp Tyr Gln Pro Gly Phe Arg Gly Gly Ala Ser Gly
100 105 110
Ala Arg Gln Gly Phe Gly Arg Gly Ala Gly Gly Phe Gly Gly Gly Ala
115 120 125
60 Gly Pro Ala Ala Gly Ser Asp Leu Pro
130 135

(2) INFORMATION FOR SEQ ID NO:355:

498

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..121

(D) OTHER INFORMATION: / Ceres Seq. ID 1976022

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met His Tyr Tyr Trp Phe Leu Thr Asn Glu Gly Ile Asp Phe Leu Arg
 1 5 10 15
 Thr Tyr Leu Asn Leu Pro Ser Glu Ile Val Pro Ala Thr Leu Lys Lys
 20 25 30
 Gln Gln Lys Pro Leu Gly Arg Pro Phe Gly Gly Gly Gly Asp Arg Pro
 35 40 45
 Arg Gly Pro Pro Arg Gly Asp Gly Glu Arg Arg Phe Gly Asp Arg Asp
 50 55 60
 Gly Tyr Arg Gly Gly Pro Lys Ser Gly Gly Glu Tyr Gly Asp Lys Ala
 65 70 75 80
 Gly Ala Pro Ala Asp Tyr Gln Pro Gly Phe Arg Gly Gly Ala Ser Gly
 85 90 95
 Ala Arg Gln Gly Phe Gly Arg Gly Ala Gly Gly Phe Gly Gly Gly Ala
 100 105 110
 Gly Pro Ala Ala Gly Ser Asp Leu Pro
 115 120

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..478

(D) OTHER INFORMATION: / Ceres Seq. ID 1976673

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

aaattcaatc tcttccaatt tctcttcttc ttctctcgca cgcgttaatg gcggcttcgt 60
 tctcactcac gagcttcac tcttcatct caccattcaa atctcaaacc aaacctacac 120
 caccacaaa tctcactctt ccttctccaa ctatctccca aaggcgaaga aatgatctcg 180
 ctatcgaatc aatggcggtc gaagaatctt cttcaaccgc ttcttcactt tcctctgagc 240
 ttgcttctgt gatatgcccc tcgcttgctt actccaacac gctcttcttc agttctggat 300
 acaatgtgca agtggttgggt gaagataacg agtcagagga gaggcttggtg aatcgattta 360
 ggagagaagt gatgagaact ggtgttatac aggaatgtaa gaggagaaga tactttgaga 420
 ataaacaaga tgagaagaaa cgtaggactc gtgatgctgc taagcgtaat aagaaaag

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..158

(D) OTHER INFORMATION: / Ceres Seq. ID 1976674

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

Ile Gln Ser Leu Pro Ile Ser Leu Leu Leu Pro Arg Asp Ala Leu Met
 1 5 10 15
 Ala Ala Ser Phe Ser Leu Thr Ser Phe Ile Ser Phe Ile Ser Pro Phe

499

20 25 30
 Lys Ser Gln Thr Lys Pro Thr Pro Pro Pro Asn Leu Thr Leu Pro Ser
 35 40 45
 5 Pro Thr Ile Ser Gln Arg Arg Arg Asn Asp Leu Ala Ile Glu Ser Met
 50 55 60
 Ala Val Glu Glu Ser Ser Thr Ala Ser Ser Leu Ser Ser Glu Leu
 65 70 75 80
 Ala Ser Val Ile Cys Pro Ser Leu Ala Tyr Ser Asn Thr Leu Phe Phe
 85 90 95
 10 Ser Ser Gly Tyr Asn Val Gln Val Phe Val Glu Asp Asn Glu Ser Glu
 100 105 110
 Glu Arg Leu Val Asn Arg Phe Arg Arg Glu Val Met Arg Thr Gly Val
 115 120 125
 15 Ile Gln Glu Cys Lys Arg Arg Arg Tyr Phe Glu Asn Lys Gln Asp Glu
 130 135 140
 Lys Lys Arg Arg Thr Arg Asp Ala Ala Lys Arg Asn Lys Lys
 145 150 155

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 143 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..143

(D) OTHER INFORMATION: / Ceres Seq. ID 1976675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

30 Met Ala Ala Ser Phe Ser Leu Thr Ser Phe Ile Ser Phe Ile Ser Pro
 1 5 10 15
 Phe Lys Ser Gln Thr Lys Pro Thr Pro Pro Pro Asn Leu Thr Leu Pro
 20 25 30
 35 Ser Pro Thr Ile Ser Gln Arg Arg Arg Asn Asp Leu Ala Ile Glu Ser
 35 40 45
 Met Ala Val Glu Glu Ser Ser Thr Ala Ser Ser Leu Ser Ser Glu
 50 55 60
 Leu Ala Ser Val Ile Cys Pro Ser Leu Ala Tyr Ser Asn Thr Leu Phe
 65 70 75 80
 40 Phe Ser Ser Gly Tyr Asn Val Gln Val Phe Val Glu Asp Asn Glu Ser
 85 90 95
 Glu Glu Arg Leu Val Asn Arg Phe Arg Arg Glu Val Met Arg Thr Gly
 100 105 110
 Val Ile Gln Glu Cys Lys Arg Arg Tyr Phe Glu Asn Lys Gln Asp
 115 120 125
 45 Glu Lys Lys Arg Arg Thr Arg Asp Ala Ala Lys Arg Asn Lys Lys
 130 135 140

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..95

(D) OTHER INFORMATION: / Ceres Seq. ID 1976676

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

60 Met Ala Val Glu Glu Ser Ser Ser Thr Ala Ser Ser Leu Ser Ser Glu
 1 5 10 15
 Leu Ala Ser Val Ile Cys Pro Ser Leu Ala Tyr Ser Asn Thr Leu Phe

500

20 25 30
 Phe Ser Ser Gly Tyr Asn Val Gln Val Phe Val Glu Asp Asn Glu Ser
 35 40 45
 5 Glu Glu Arg Leu Val Asn Arg Phe Arg Arg Glu Val Met Arg Thr Gly
 50 55 60
 Val Ile Gln Glu Cys Lys Arg Arg Arg Tyr Phe Glu Asn Lys Gln Asp
 65 70 75 80
 Glu Lys Lys Arg Arg Thr Arg Asp Ala Ala Lys Arg Asn Lys Lys
 85 90 95
 10 (2) INFORMATION FOR SEQ ID NO:360:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1076 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 15 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1076
 20 (D) OTHER INFORMATION: / Ceres Seq. ID 2025186
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:
 aatcatttgc agaagaaaaa taaaaaaaaa aaacagagaa aaggagatat ggaatcaatc 60
 ggagtcctta tgatgtgccc catgtcctcc tacctcgaga acgagcttga gaagcgcttc 120
 aaccttcttc gcttctggac ttctccggag aaatccgtcc tcctagaaac tcatcggaac 180
 25 tccatccgcg ccgtcgttgg gaatgcttct gccggcgccg atgctcagct catcagcgat 240
 ctgccc aacc ttgagattgt atccagcttc agcgctcgggc tcgacaagat cgatttgagg 300
 aaatgcaaag aaaaagggat ccgcgtcacc aacacccccg acgttctcac cgaagacgtc 360
 gcagatctcg ccacgaggct tatcctggct ctccctcgac ggctgtgtga gtgcgatcgc 420
 tatgtaagga gcggaataat gaagcaagggt gaattccaac tctactacaa gtttagtgga 480
 30 aaatccgtgg ggatcattgg tctaggtaga attgggactg ccacgcgcaa gagggctgaa 540
 gccttttagct gcccaatcaa ttactactca agaaccatta agcctgatgt cgcctacaag 600
 tattatccga cgggtggttga ccttgctcaa aactcagaca tcctcgctcg cgcgatgccg 660
 ttgaccgagc agaccagaca cattgtggac cggcagggtca tggatgcatt aggagctaag 720
 35 ggcgtcctca taaacattgg ccgtggacca catgttgatg agcaagagct tattaaagct 780
 ctaacagaag gccgcctagg tggggctgcc cttgatgtgt ttgagcagga gcctcacgtg 840
 cccgaggagc tctttggcct tgagaatgta gttctcctcc ctacgcttgg gaggggcact 900
 gtggaaacac ggaatgccat ggccgatctt gtcgtgggta acttgggaag gcacttttct 960
 gggaaatcac ttctgactcc ggctgcttga gtcattgtgac acatttggga tttgggttca 1020
 cttcatttga aagggttttta tggttaacgaa ctcatgaaaa gggttaatttc tcttcc
 40 (2) INFORMATION FOR SEQ ID NO:361:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 45 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..329
 50 (D) OTHER INFORMATION: / Ceres Seq. ID 2025187
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:
 Asn His Leu Gln Lys Lys Asn Lys Lys Lys Lys Gln Arg Lys Gly Asp
 1 5 10 15
 55 Met Glu Ser Ile Gly Val Leu Met Met Cys Pro Met Ser Ser Tyr Leu
 20 25 30
 Glu Asn Glu Leu Glu Lys Arg Phe Asn Leu Leu Arg Phe Trp Thr Ser
 35 40 45
 Pro Glu Lys Ser Val Leu Leu Glu Thr His Arg Asn Ser Ile Arg Ala
 50 55 60
 60 Val Val Gly Asn Ala Ser Ala Gly Ala Asp Ala Gln Leu Ile Ser Asp
 65 70 75 80
 Leu Pro Asn Leu Glu Ile Val Ser Ser Phe Ser Val Gly Leu Asp Lys

501

				85					90					95		
	Ile	Asp	Leu	Gly	Lys	Cys	Lys	Glu	Lys	Gly	Ile	Arg	Val	Thr	Asn	Thr
				100					105					110		
5	Pro	Asp	Val	Leu	Thr	Glu	Asp	Val	Ala	Asp	Leu	Ala	Ile	Gly	Leu	Ile
			115					120					125			
	Leu	Ala	Leu	Leu	Arg	Arg	Leu	Cys	Glu	Cys	Asp	Arg	Tyr	Val	Arg	Ser
			130				135				140					
	Gly	Lys	Trp	Lys	Gln	Gly	Glu	Phe	Gln	Leu	Thr	Thr	Lys	Phe	Ser	Gly
	145				150					155					160	
10	Lys	Ser	Val	Gly	Ile	Ile	Gly	Leu	Gly	Arg	Ile	Gly	Thr	Ala	Ile	Ala
				165					170						175	
	Lys	Arg	Ala	Glu	Ala	Phe	Ser	Cys	Pro	Ile	Asn	Tyr	Tyr	Ser	Arg	Thr
			180						185					190		
15	Ile	Lys	Pro	Asp	Val	Ala	Tyr	Lys	Tyr	Tyr	Pro	Thr	Val	Val	Asp	Leu
			195					200					205			
	Ala	Gln	Asn	Ser	Asp	Ile	Leu	Val	Val	Ala	Cys	Pro	Leu	Thr	Glu	Gln
			210				215					220				
	Thr	Arg	His	Ile	Val	Asp	Arg	Gln	Val	Met	Asp	Ala	Leu	Gly	Ala	Lys
	225				230					235					240	
20	Gly	Val	Leu	Ile	Asn	Ile	Gly	Arg	Gly	Pro	His	Val	Asp	Glu	Gln	Glu
				245					250						255	
	Leu	Ile	Lys	Ala	Leu	Thr	Glu	Gly	Arg	Leu	Gly	Gly	Ala	Ala	Leu	Asp
			260						265					270		
25	Val	Phe	Glu	Gln	Glu	Pro	His	Val	Pro	Glu	Glu	Leu	Phe	Gly	Leu	Glu
			275				280						285			
	Asn	Val	Val	Leu	Leu	Pro	His	Val	Gly	Ser	Gly	Thr	Val	Glu	Thr	Arg
			290				295					300				
	Asn	Ala	Met	Ala	Asp	Leu	Val	Val	Gly	Asn	Leu	Glu	Ala	His	Phe	Ser
	305				310					315					320	
30	Gly	Lys	Ser	Leu	Leu	Thr	Pro	Val	Val							
				325												

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..313

(D) OTHER INFORMATION: / Ceres Seq. ID 2025188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

45	Met	Glu	Ser	Ile	Gly	Val	Leu	Met	Met	Cys	Pro	Met	Ser	Ser	Tyr	Leu
	1			5						10					15	
	Glu	Asn	Glu	Leu	Glu	Lys	Arg	Phe	Asn	Leu	Leu	Arg	Phe	Trp	Thr	Ser
			20					25					30			
	Pro	Glu	Lys	Ser	Val	Leu	Leu	Glu	Thr	His	Arg	Asn	Ser	Ile	Arg	Ala
			35				40					45				
50	Val	Val	Gly	Asn	Ala	Ser	Ala	Gly	Ala	Asp	Ala	Gln	Leu	Ile	Ser	Asp
			50			55					60					
	Leu	Pro	Asn	Leu	Glu	Ile	Val	Ser	Ser	Phe	Ser	Val	Gly	Leu	Asp	Lys
	65				70					75					80	
55	Ile	Asp	Leu	Gly	Lys	Cys	Lys	Glu	Lys	Gly	Ile	Arg	Val	Thr	Asn	Thr
			85						90					95		
	Pro	Asp	Val	Leu	Thr	Glu	Asp	Val	Ala	Asp	Leu	Ala	Ile	Gly	Leu	Ile
			100					105					110			
	Leu	Ala	Leu	Leu	Arg	Arg	Leu	Cys	Glu	Cys	Asp	Arg	Tyr	Val	Arg	Ser
			115				120					125				
60	Gly	Lys	Trp	Lys	Gln	Gly	Glu	Phe	Gln	Leu	Thr	Thr	Lys	Phe	Ser	Gly
			130			135					140					
	Lys	Ser	Val	Gly	Ile	Ile	Gly	Leu	Gly	Arg	Ile	Gly	Thr	Ala	Ile	Ala

502

145 150 155 160
 Lys Arg Ala Glu Ala Phe Ser Cys Pro Ile Asn Tyr Tyr Ser Arg Thr
 165 170 175
 5 Ile Lys Pro Asp Val Ala Tyr Lys Tyr Tyr Pro Thr Val Val Asp Leu
 180 185 190
 Ala Gln Asn Ser Asp Ile Leu Val Ala Cys Pro Leu Thr Glu Gln
 195 200 205
 Thr Arg His Ile Val Asp Arg Gln Val Met Asp Ala Leu Gly Ala Lys
 210 215 220
 10 Gly Val Leu Ile Asn Ile Gly Arg Gly Pro His Val Asp Glu Gln Glu
 225 230 235 240
 Leu Ile Lys Ala Leu Thr Glu Gly Arg Leu Gly Gly Ala Ala Leu Asp
 245 250 255
 15 Val Phe Glu Gln Glu Pro His Val Pro Glu Glu Leu Phe Gly Leu Glu
 260 265 270
 Asn Val Val Leu Leu Pro His Val Gly Ser Gly Thr Val Glu Thr Arg
 275 280 285
 Asn Ala Met Ala Asp Leu Val Val Gly Asn Leu Glu Ala His Phe Ser
 290 295 300
 20 Gly Lys Ser Leu Leu Thr Pro Val Val
 305 310
 (2) INFORMATION FOR SEQ ID NO:363:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..306
 (D) OTHER INFORMATION: / Ceres Seq. ID 2025189
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:
 35 Met Met Cys Pro Met Ser Ser Tyr Leu Glu Asn Glu Leu Glu Lys Arg
 1 5 10 15
 Phe Asn Leu Leu Arg Phe Trp Thr Ser Pro Glu Lys Ser Val Leu Leu
 20 25 30
 Glu Thr His Arg Asn Ser Ile Arg Ala Val Val Gly Asn Ala Ser Ala
 35 40 45
 40 Gly Ala Asp Ala Gln Leu Ile Ser Asp Leu Pro Asn Leu Glu Ile Val
 50 55 60
 Ser Ser Phe Ser Val Gly Leu Asp Lys Ile Asp Leu Gly Lys Cys Lys
 65 70 75 80
 45 Glu Lys Gly Ile Arg Val Thr Asn Thr Pro Asp Val Leu Thr Glu Asp
 85 90 95
 Val Ala Asp Leu Ala Ile Gly Leu Ile Leu Ala Leu Leu Arg Arg Leu
 100 105 110
 Cys Glu Cys Asp Arg Tyr Val Arg Ser Gly Lys Trp Lys Gln Gly Glu
 115 120 125
 50 Phe Gln Leu Thr Thr Lys Phe Ser Gly Lys Ser Val Gly Ile Ile Gly
 130 135 140
 Leu Gly Arg Ile Gly Thr Ala Ile Ala Lys Arg Ala Glu Ala Phe Ser
 145 150 155 160
 Cys Pro Ile Asn Tyr Tyr Ser Arg Thr Ile Lys Pro Asp Val Ala Tyr
 165 170 175
 55 Lys Tyr Tyr Pro Thr Val Val Asp Leu Ala Gln Asn Ser Asp Ile Leu
 180 185 190
 Val Val Ala Cys Pro Leu Thr Glu Gln Thr Arg His Ile Val Asp Arg
 195 200 205
 60 Gln Val Met Asp Ala Leu Gly Ala Lys Gly Val Leu Ile Asn Ile Gly
 210 215 220
 Arg Gly Pro His Val Asp Glu Gln Glu Leu Ile Lys Ala Leu Thr Glu

225						230						235						240
Gly	Arg	Leu	Gly	Gly	Ala	Ala	Leu	Asp	Val	Phe	Glu	Gln	Glu	Pro	His			
					245						250						255	
Val	Pro	Glu	Glu	Leu	Phe	Gly	Leu	Glu	Asn	Val	Val	Leu	Leu	Pro	His			
					260						265						270	
Val	Gly	Ser	Gly	Thr	Val	Glu	Thr	Arg	Asn	Ala	Met	Ala	Asp	Leu	Val			
					275						280						285	
Val	Gly	Asn	Leu	Glu	Ala	His	Phe	Ser	Gly	Lys	Ser	Leu	Leu	Thr	Pro			
					290						295						300	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 555 base pairs

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

MOLECULE TYPE: DNA (g

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(ix) FEATURE:
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(1X) FEATURE.

(A) NAME/KEY: -

(B) LOCATION: 1..555

(D) OTHER INFORMATION: / Ceres Seq. ID 2025372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

aaaactcact	ttcacttgca	caaagataag	gaaaccatgt	ctgtgtcagc	gatctttggt	60
accggaatcg	tcacogttgc	tgtctctccg	gttctccgcc	aatttcaagt	tccaaaattg	120
ggtaatggag	gaggattagg	gatggtgata	gagtgttcgt	cgaggccaca	gaagaaatcg	180
acggctcatc	acaggaagac	gaggccgaag	aagactcagc	cttgggacat	taagagaaaag	240
cctactgttt	acgtcctct	tctcctctt	ccggcggaat	ggagtccgtt	cactctcgct	300
tctgacgacg	gtggtgctgc	cactgctgcg	ggagatttgg	tttcaggcgc	tgcttagttg	360
gtatgagtta	tctgctgatt	tggttgtaat	ctagtttgag	aacttttggt	gttgtttact	420
gtgtttttcag	ttttctgatg	tttgttggtg	ggtttgtttg	tgtttgattg	gtgaatgaat	480
ggaccaaaatt	tgcgatttat	aaagcttcaa	cctttctcct	ctgtttttga	gtttaaaggt	540
ctcaacttta	taatt					

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..118

(D) OTHER INFORMATION: / Ceres Seq. ID 2025373

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

[illegible]

(2) INFORMATION FOR SEQ ID NO:366:

504

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 2025374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

Met Ser Val Ser Ala Ile Phe Gly Thr Gly Ile Val Thr Val Ala Ala
 1 5 10 15
 Ser Pro Val Leu Arg Gln Phe Gln Val Pro Lys Leu Gly Asn Gly Gly
 20 25 30
 Gly Leu Gly Met Val Ile Glu Cys Ser Ser Arg Pro Gln Lys Lys Ser
 35 40 45
 Thr Ala His His Arg Lys Thr Arg Pro Lys Lys Thr Gln Pro Trp Asp
 50 55 60
 Ile Lys Arg Lys Pro Thr Val Tyr Ala Pro Leu Pro Pro Leu Pro Ala
 65 70 75 80
 Glu Trp Ser Pro Phe Thr Leu Ala Ser Asp Asp Gly Gly Ala Ala Thr
 85 90 95
 Ala Ala Gly Asp Leu Val Ser Gly Ala Ala
 100 105

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..71

(D) OTHER INFORMATION: / Ceres Seq. ID 2025375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

Met Val Ile Glu Cys Ser Ser Arg Pro Gln Lys Lys Ser Thr Ala His
 1 5 10 15
 His Arg Lys Thr Arg Pro Lys Lys Thr Gln Pro Trp Asp Ile Lys Arg
 20 25 30
 Lys Pro Thr Val Tyr Ala Pro Leu Pro Pro Leu Pro Ala Glu Trp Ser
 35 40 45
 Pro Phe Thr Leu Ala Ser Asp Asp Gly Gly Ala Ala Thr Ala Ala Gly
 50 55 60
 Asp Leu Val Ser Gly Ala Ala
 65 70

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 631 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..631

(D) OTHER INFORMATION: / Ceres Seq. ID 2025471

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

atgtcgcgaa agttcctaata accgccacgt gtcagtcact tatccaacag taatccaatt 60
 attcgtcaag cctccggttt attaccgtct aaaccgaaaa gaaaaaactc ttttcggaat 120
 ctgaaaagcc ataatcagc agaaaaaaat cctaaggatc ggaaatttta taatcggatg 180

505

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aatagagtga ttagtcagtt ttccggtgaag ttgatgaagg agaagagtgt taccggtgta      240
agcggcgag atacgacttt aagatctgcc gtcaaagaat cggctctcgtc tccacagagt      300
gcgctcgctcgt cgctcgctcggg gaggaggctt aaaggagatc tggaatcgag tcgatttgggt      360
gcgggcggcga gtgagaggct gaggcaagcg gaggaatcctt tgaggacggt gatgtttctg      420
5 agctgtttggg gatcttggtta gatctgggttg agaaaataat agatgagaaa acgaaaccaa      480
aacgtttctg tttgtgtttt tgagttttgg atttttgttt tctctgtgaa tagttttttt      540
tttttttttc gttttctttg tactttgtgt tttatgtaaa tcatgtataa aatgaaaagt      600
aatcaatga agataatggt ttgtcttcac c

```

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..146

(D) OTHER INFORMATION: / Ceres Seq. ID 2025472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

```

Met Ser Arg Lys Phe Leu Lys Pro Pro Arg Val Ser His Leu Ser Asn
1      5      10      15
Ser Asn Pro Ile Arg Gln Ala Ser Gly Leu Leu Pro Ser Lys Pro
      20      25      30
25 Lys Arg Lys Asn Ser Leu Arg Asn Leu Lys Ser His Lys Ser Ala Glu
      35      40      45
Lys Asn Leu Lys Asp Arg Lys Phe Tyr Asn Arg Met Asn Arg Val Ile
      50      55      60
Ser Gln Phe Ser Gly Lys Leu Met Lys Glu Lys Ser Val Thr Gly Val
30 65      70      75      80
Ser Gly Gly Asp Thr Leu Arg Ser Ala Val Lys Glu Ser Val Ser
      85      90      95
Ser Pro Gln Ser Ala Ser Ser Ser Ser Val Arg Arg Leu Lys Gly
      100      105      110
35 Asp Leu Glu Ser Ser Arg Phe Gly Ala Ala Ala Ser Glu Arg Leu Arg
      115      120      125
Gln Ala Glu Glu Ser Leu Arg Thr Val Met Phe Leu Ser Cys Trp Gly
      130      135      140
Ser Cys
40 145

```

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..87

(D) OTHER INFORMATION: / Ceres Seq. ID 2025473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

```

Met Asn Arg Val Ile Ser Gln Phe Ser Gly Lys Leu Met Lys Glu Lys
1      5      10      15
55 Ser Val Thr Gly Val Ser Gly Gly Asp Thr Thr Leu Arg Ser Ala Val
      20      25      30
Lys Glu Ser Val Ser Ser Pro Gln Ser Ala Ser Ser Ser Ser Val
      35      40      45
Arg Arg Leu Lys Gly Asp Leu Glu Ser Ser Arg Phe Gly Ala Ala Ala
60 50      55      60
Ser Glu Arg Leu Arg Gln Ala Glu Glu Ser Leu Arg Thr Val Met Phe
65 70      75      80

```

506

Leu Ser Cys Trp Gly Ser Cys

85

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 2025474

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

```

15 Met Lys Glu Lys Ser Val Thr Gly Val Ser Gly Gly Asp Thr Thr Leu
    1             5             10             15
Arg Ser Ala Val Lys Glu Ser Val Ser Ser Pro Gln Ser Ala Ser Ser
    20             25             30
Ser Ser Ser Val Arg Arg Leu Lys Gly Asp Leu Glu Ser Ser Arg Phe
    35             40             45
Gly Ala Ala Ala Ser Glu Arg Leu Arg Gln Ala Glu Glu Ser Leu Arg
    50             55             60
Thr Val Met Phe Leu Ser Cys Trp Gly Ser Cys
    65             70             75

```

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2029 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..2029

(D) OTHER INFORMATION: / Ceres Seq. ID 2025475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

```

atgggtaaga gttggttttc agctgtgaag aaagcattaa gcccagaacc aaaacaaaag      60
aaagagcaga agccacataa gtccaagaaa tggtttggtta aatccaagaa gctagatggt      120
actaattctg gtgcagcata ttctcctcgt actgtcaaag acgcgaaact aaaggagatt      180
gaggagcaac agagcagaca tgcttactct gtggctattg caactgctgc agctgcagag      240
gcagccgttg cagctgctca agctgctgct gaagttgttc gtctctctgc attatcacgg      300
ttccccggga aatcaatgga agagatcgcc gctatcaaga ttcagacagc atttagagga      360
tatatggcaa gaagagcatt gcgtgcgttg agaggtcctg tgaggctaaa atcttttagtc      420
caggggaaat gtgtgagacg tcaagccaca tctacattgc aaagcatgca aacactagct      480
agagtacaat atcagattcg tgagagaagg ctccgattgt ctgaggataa acaggccttta      540
acacgacagc tccaacaaaa acacaataaa gactttgata agactggaga aaattggaat      600
gatagtacat tgtcgcggga gaaagttgaa gcaaacatgt tgaacaagca agtagcaaca      660
atgagaagag aaaaagcgct tgcatatgca ttcagtcacc agaatacatg gaaaaactca      720
actaaaatgg gttctcaaac attcatggac cctaacaatc cgcattgggg ttggagttgg      780
ctagaacggt ggatggctgc tcgaccaaac gaaaaccact cactcacacc agataatgct      840
gaaaaagact cttctgctag gagtgtagca agccgtgccca tgtctgagat gattccacga      900
ggcaaaaacc ttccaccaag aggaaagaca ccaaacagtc gaagagggtc aagcccgaga      960
gtgaggcaag tcccaagtga agactcaaac agcattgtga gtttccaatc agaacaacct      1020
tgcaatcgta ggcatagcac ttgtggatca attccatcaa ctagagacga tgaaagcttc      1080
accagtagtt tctctcagtc agttccaggc tacatggcac ctacacaagc cgccaaagca      1140
agagctcgat tctcaaacct tagtcctcta agctcagaga agacagcgaa aaaacggctt      1200
tccttctcgg gatctcctaa gactgtaaga cggtttttcag tagggattct agggcctttcc      1260
ttcattggtc agatcagacg acgtttttaca tcttcttctt cttcctcttc gatattcgct      1320
agtgtgtgta ttttggggaa aacttttgtga gcaaagacg agaaaatgag cggaccggta      1380
agaaaatcgc ggaatgtggc ttcaaagctt cgaggactat cgattgggat ggtaggcta      1440
aggtccttgt cacagatgag gctcgtagag aggttctctaa ccttcgtcgt gctttcgatg      1500
aggttaacac acagctccag accaaattta gtcaggaacc tgaaccata gattgggatt      1560

```

507

actataggaa gggatttga gctggcattg ttgacaagta caaggaagct tatgacagca 1620
 ttgagattcc aaagtacgtt gacaaagtta ctcctgaata caagccaaag tttgatgctt 1680
 tgttggtgga actgaaagaa gcagaacaga aatcgctcaa ggagtctgaa cggttggaga 1740
 aagaaattgc tgatgtccaa gagatcagca aaaagctcag caccatgact gcagatgagt 1800
 5 actttgagaa gcacccgga ctcaaaaaga agtttgatga cgaaatccgt aatgacaact 1860
 ggggatactg atcatgtttc tccatctccg gcttggaag aaaactctct ttctctttct 1920
 ctgttctctt actgtgattt tgtgagccaa tcataacaat aataagtaca ccattcactt 1980
 aagcagtgtt gagatcttca ttccaaggaa gataaacgca tttggtttt

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 449 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..449

(D) OTHER INFORMATION: / Ceres Seq. ID 2025476

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

Met Gly Lys Ser Trp Phe Ser Ala Val Lys Lys Ala Leu Ser Pro Glu
 1 5 10 15
 Pro Lys Gln Lys Lys Glu Gln Lys Pro His Lys Ser Lys Lys Trp Phe
 20 25 30
 25 Gly Lys Ser Lys Lys Leu Asp Val Thr Asn Ser Gly Ala Ala Tyr Ser
 35 40 45
 Pro Arg Thr Val Lys Asp Ala Lys Leu Lys Glu Ile Glu Glu Gln Gln
 50 55 60
 Ser Arg His Ala Tyr Ser Val Ala Ile Ala Thr Ala Ala Ala Glu
 65 70 75 80
 30 Ala Ala Val Ala Ala Gln Ala Ala Glu Val Val Arg Leu Ser
 85 90 95
 Ala Leu Ser Arg Phe Pro Gly Lys Ser Met Glu Glu Ile Ala Ala Ile
 100 105 110
 35 Lys Ile Gln Thr Ala Phe Arg Gly Tyr Met Ala Arg Arg Ala Leu Arg
 115 120 125
 Ala Leu Arg Gly Leu Val Arg Leu Lys Ser Leu Val Gln Gly Lys Cys
 130 135 140
 Val Arg Arg Gln Ala Thr Ser Thr Leu Gln Ser Met Gln Thr Leu Ala
 145 150 155 160
 40 Arg Val Gln Tyr Gln Ile Arg Glu Arg Arg Leu Arg Leu Ser Glu Asp
 165 170 175
 Lys Gln Ala Leu Thr Arg Gln Leu Gln Gln Lys His Asn Lys Asp Phe
 180 185 190
 45 Asp Lys Thr Gly Glu Asn Trp Asn Asp Ser Thr Leu Ser Arg Glu Lys
 195 200 205
 Val Glu Ala Asn Met Leu Asn Lys Gln Val Ala Thr Met Arg Arg Glu
 210 215 220
 Lys Ala Leu Ala Tyr Ala Phe Ser His Gln Asn Thr Trp Lys Asn Ser
 225 230 235 240
 50 Thr Lys Met Gly Ser Gln Thr Phe Met Asp Pro Asn Asn Pro His Trp
 245 250 255
 Gly Trp Ser Trp Leu Glu Arg Trp Met Ala Ala Arg Pro Asn Glu Asn
 260 265 270
 55 His Ser Leu Thr Pro Asp Asn Ala Glu Lys Asp Ser Ser Ala Arg Ser
 275 280 285
 Val Ala Ser Arg Ala Met Ser Glu Met Ile Pro Arg Gly Lys Asn Leu
 290 295 300
 Ser Pro Arg Gly Lys Thr Pro Asn Ser Arg Arg Gly Ser Ser Pro Arg
 305 310 315 320
 60 Val Arg Gln Val Pro Ser Glu Asp Ser Asn Ser Ile Val Ser Phe Gln
 325 330 335

508

Ser Glu Gln Pro Cys Asn Arg Arg His Ser Thr Cys Gly Ser Ile Pro
 340 345 350
 Ser Thr Arg Asp Asp Glu Ser Phe Thr Ser Ser Phe Ser Gln Ser Val
 355 360 365
 5 Pro Gly Tyr Met Ala Pro Thr Gln Ala Ala Lys Ala Arg Ala Arg Phe
 370 375 380
 Ser Asn Leu Ser Pro Leu Ser Ser Glu Lys Thr Ala Lys Lys Arg Leu
 385 390 395 400
 10 Ser Phe Ser Gly Ser Pro Lys Thr Val Arg Arg Phe Ser Val Gly Ile
 405 410 415
 Leu Gly Leu Ser Phe Ile Gly Gln Ile Arg Arg Arg Phe Thr Ser Ser
 420 425 430
 Ser Ser Ser Ser Ser Ile Phe Val Ser Val Cys Ile Leu Gly Lys Thr
 435 440 445
 15 Leu

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 344 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25 (A) NAME/KEY: peptide
 (B) LOCATION: 1..344
 (D) OTHER INFORMATION: / Ceres Seq. ID 2025477

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

30 Met Glu Glu Ile Ala Ala Ile Lys Ile Gln Thr Ala Phe Arg Gly Tyr
 1 5 10 15
 Met Ala Arg Arg Ala Leu Arg Ala Leu Arg Gly Leu Val Arg Leu Lys
 20 25 30
 Ser Leu Val Gln Gly Lys Cys Val Arg Arg Gln Ala Thr Ser Thr Leu
 35 35 40 45
 Gln Ser Met Gln Thr Leu Ala Arg Val Gln Tyr Gln Ile Arg Glu Arg
 50 55 60
 Arg Leu Arg Leu Ser Glu Asp Lys Gln Ala Leu Thr Arg Gln Leu Gln
 65 70 75 80
 40 Gln Lys His Asn Lys Asp Phe Asp Lys Thr Gly Glu Asn Trp Asn Asp
 85 90 95
 Ser Thr Leu Ser Arg Glu Lys Val Glu Ala Asn Met Leu Asn Lys Gln
 100 105 110
 Val Ala Thr Met Arg Arg Glu Lys Ala Leu Ala Tyr Ala Phe Ser His
 115 120 125
 45 Gln Asn Thr Trp Lys Asn Ser Thr Lys Met Gly Ser Gln Thr Phe Met
 130 135 140
 Asp Pro Asn Asn Pro His Trp Gly Trp Ser Trp Leu Glu Arg Trp Met
 145 150 155 160
 50 Ala Ala Arg Pro Asn Glu Asn His Ser Leu Thr Pro Asp Asn Ala Glu
 165 170 175
 Lys Asp Ser Ser Ala Arg Ser Val Ala Ser Arg Ala Met Ser Glu Met
 180 185 190
 Ile Pro Arg Gly Lys Asn Leu Ser Pro Arg Gly Lys Thr Pro Asn Ser
 195 200 205
 55 Arg Arg Gly Ser Ser Pro Arg Val Arg Gln Val Pro Ser Glu Asp Ser
 210 215 220
 Asn Ser Ile Val Ser Phe Gln Ser Glu Gln Pro Cys Asn Arg Arg His
 225 230 235 240
 60 Ser Thr Cys Gly Ser Ile Pro Ser Thr Arg Asp Asp Glu Ser Phe Thr
 245 250 255
 Ser Ser Phe Ser Gln Ser Val Pro Gly Tyr Met Ala Pro Thr Gln Ala
 260 265 270

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: lin

ix) FEATURE:

(B) LOCATION: 1..328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

Met 1	Ala	Arg	Arg	Ala 5	Leu	Arg	Ala	Leu	Arg 10	Gly	Leu	Val	Arg	Leu 15	Lys
Ser	Leu	Val	Gln	Gly	Lys	Cys	Val	Arg	Arg	Gln	Ala	Thr	Ser	Thr	Leu
			20					25					30		
Gln	Ser	Met	Gln	Thr	Leu	Ala	Arg	Val	Gln	Tyr	Gln	Ile	Arg	Glu	Arg
		35					40					45			
Arg	Leu	Arg	Leu	Ser	Glu	Asp	Lys	Gln	Ala	Leu	Thr	Arg	Gln	Leu	Gln
	50					55					60				
Gln	Lys	His	Asn	Lys	Asp	Phe	Asp	Lys	Thr	Gly	Glu	Asn	Trp	Asn	Asp
65					70					75					80
Ser	Thr	Leu	Ser	Arg	Glu	Lys	Val	Glu	Ala	Asn	Met	Leu	Asn	Lys	Gln
				85					90					95	
Val	Ala	Thr	Met	Arg	Arg	Glu	Lys	Ala	Leu	Ala	Tyr	Ala	Phe	Ser	His
			100					105					110		
Gln	Asn	Thr	Trp	Lys	Asn	Ser	Thr	Lys	Met	Gly	Ser	Gln	Thr	Phe	Met
		115					120					125			
Asp	Pro	Asn	Asn	Pro	His	Trp	Gly	Trp	Ser	Trp	Leu	Glu	Arg	Trp	Met
	130					135					140				
Ala	Ala	Arg	Pro	Asn	Glu	Asn	His	Ser	Leu	Thr	Pro	Asp	Asn	Ala	Glu
145					150					155					160
Lys	Asp	Ser	Ser	Ala	Arg	Ser	Val	Ala	Ser	Arg	Ala	Met	Ser	Glu	Met
				165				170						175	
Ile	Pro	Arg	Gly	Lys	Asn	Leu	Ser	Pro	Arg	Gly	Lys	Thr	Pro	Asn	Ser
			180					185					190		
Arg	Arg	Gly	Ser	Ser	Pro	Arg	Val	Arg	Gln	Val	Pro	Ser	Glu	Asp	Ser
		195					200					205			
Asn	Ser	Ile	Val	Ser	Phe	Gln	Ser	Glu	Gln	Pro	Cys	Asn	Arg	Arg	His
	210					215					220				
Ser	Thr	Cys	Gly	Ser	Ile	Pro	Ser	Thr	Arg	Asp	Asp	Glu	Ser	Phe	Thr
225					230				235						240
Ser	Ser	Phe	Ser	Gln	Ser	Val	Pro	Gly	Tyr	Met	Ala	Pro	Thr	Gln	Ala
				245					250					255	
Ala	Lys	Ala	Arg	Ala	Arg	Phe	Ser	Asn	Leu	Ser	Pro	Leu	Ser	Ser	Glu
			260					265					270		
Lys	Thr	Ala	Lys	Lys	Arg	Leu	Ser	Phe	Ser	Gly	Ser	Pro	Lys	Thr	Val
		275					280					285			
Arg	Arg	Phe	Ser	Val	Gly	Ile	Leu	Gly	Leu	Ser	Phe	Ile	Gly	Gln	Ile
	290					295					300				
Arg	Arg	Arg	Phe	Thr	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ile	Phe	Val	Ser
305					310					315					320

510

Val Cys Ile Leu Gly Lys Thr Leu

325

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..678

(D) OTHER INFORMATION: / Ceres Seq. ID 2025524

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

15	gatttttttag ggtttcaagt gaaaagagta atagcgcggc ggagccatgg ttctcaagac	60
	tgagcttttgc cgattcagtg gccagaaaat ttaccctggt agagggatca gatttatccg	120
	atcggactct caggtgtttt tgtttctcaa ctccaaatgt aagaggtatt tccacaacaa	180
	gttgaagcca tctaagcttt gctggactgc tatgtaccga aagcagcaca agaaggacgc	240
	agcacaagag gctgtgaaga gaaggagacg tgcaactaag aagccttact caaggctgat	300
20	tgtcggtgct actttggagg ttattcagaa gaagcgagca gagaagcctg aagttcgtga	360
	tgccgctaga gaagctgccc tacgtgagat caaggagaga atcaagaaga ccaaggacga	420
	gaagaaggca aagaaggtcg agtatgcac aaagcaacag aagtcacaag tgaagggaaa	480
	tatccccaag agtgctgcac ccaaggctgc taagatgggt ggtgggtggag gcagacgttg	540
	aatggagcta tagagtagcc cactcttctc tcttcactta tctttctttc ttgttttgac	600
25	attgttttgt tttgtcagcc atttttttagt tttgcaccag atctaataata ttcagtttat	660
	gaaaactttt tgtttggc	

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..164

(D) OTHER INFORMATION: / Ceres Seq. ID 2025525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

40	Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr	
	1 5 10 15	
	Pro Gly Arg Gly Ile Arg Phe Ile Arg Ser Asp Ser Gln Val Phe Leu	
	20 25 30	
	Phe Leu Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Lys Leu Lys Pro	
	35 40 45	
45	Ser Lys Leu Cys Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp	
	50 55 60	
	Ala Ala Gln Glu Ala Val Lys Arg Arg Arg Arg Ala Thr Lys Lys Pro	
	65 70 75 80	
	Tyr Ser Arg Ser Ile Val Gly Ala Thr Leu Glu Val Ile Gln Lys Lys	
50	85 90 95	
	Arg Ala Glu Lys Pro Glu Val Arg Asp Ala Ala Arg Glu Ala Ala Leu	
	100 105 110	
	Arg Glu Ile Lys Glu Arg Ile Lys Lys Thr Lys Asp Glu Lys Lys Ala	
	115 120 125	
55	Lys Lys Val Glu Tyr Ala Ser Lys Gln Gln Lys Ser Gln Val Lys Gly	
	130 135 140	
	Asn Ile Pro Lys Ser Ala Ala Pro Lys Ala Ala Lys Met Gly Gly Gly	
	145 150 155 160	
60	Gly Gly Arg Arg	

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:

511

(A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..109
 (D) OTHER INFORMATION: / Ceres Seq. ID 2025526

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:
 Met Tyr Arg Lys Gln His Lys Lys Asp Ala Ala Gln Glu Ala Val Lys
 1 5 10 15
 Arg Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
 20 25 30
 15 Ala Thr Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
 35 40 45
 Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
 50 55 60
 20 Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Val Glu Tyr Ala Ser
 65 70 75 80
 Lys Gln Gln Lys Ser Gln Val Lys Gly Asn Ile Pro Lys Ser Ala Ala
 85 90 95
 Pro Lys Ala Ala Lys Met Gly Gly Gly Gly Arg Arg
 100 105

25 (2) INFORMATION FOR SEQ ID NO:379:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1623 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1623

35 (D) OTHER INFORMATION: / Ceres Seq. ID 2025544
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:
 atggggcattt ctaagatgat tcttctgaaa ttcacatatg ttgtttcttt ctggattact 60
 tgcgtgatct tcaaaatgtc aagaacgata aaacgagcct tgttgggctc attcatcttc 120
 attcttgctt ccgctagtgt tgtggtagcc gccattgtag gagccatcga aggtcacacc 180
 40 actgacatcg gatttcttca aggtagtgtg cttggagtgg tggctggagt tatcactgcg 240
 gtccaactct ttggaccggt gctacatagt gatcaacctt tgtctaaggt ggctttactc 300
 aggagagttag tgaatgggaa agccattatg ggattggtta gaccttttgt tctcaaagca 360
 tatcaatggc aaataatagc attggataca agttacatgg agagttcaaa cttatacgat 420
 ttcaatcatg aaaaaaaggg actatcgaag agctctattc agaacatccc gatgttctac 480
 45 aaccgttcag aacatcaaac aaaatcgagt tgctcgattt gcttacagga ttgggaagaa 540
 ggggaagttag gaagaaagct agcaagatgt ggccacacat ttcatatgaa ttgcatagat 600
 gagtggttgc ttagacaaga aacttgcccc atttgaagaa gacaaaagaa gaagcacgag 660
 aatcatctgc ttaaaatcca atcgcatcga ctcagtcttc ttcttcttct tcacctacct 720
 ttctctctct ctctcgtggt ccattcgcga ttctatactt cttgtcggcg ccggagagag 780
 50 tgagatgact tggtcggttt tcagatccat aaatactcca acactcgacc tctccaccgc 840
 acttcgctcc actcgtacct cattggctgc tgctggtgtc ggctgcgcaa cattcgctgg 900
 tgtttctctc ttcagaatgt cttctagatc tctcctttc gcttccctct ctgtctctgc 960
 ttcttctgtg aagaaggaag ttgtgtctac tgagaaagca ccagctgctt tgggacctta 1020
 ctctcaggcc attaaagcca ataactctggt ttttctttca ggtgttcttg gacttatacc 1080
 55 tgagactgga aagtttgttt cggagagcgt cgaagatcag actgagcagg tactcaaaaa 1140
 catgggggag atattgaaag ctagtgggtg tgattattcc tcggtggtga agacaacaat 1200
 catgttggct gatttggctg acttcaagac agtgaacgag atatatgcca aatacttccc 1260
 agctccttct ccagcacgat cgacgtatga agttgcagct ttgcctctaa acgccaagat 1320
 cgagattgaa tgtattgcaa cactctagaa cactcaaatc aatctctacg aagggtatct 1380
 60 tggtcgggaa gatgtcaaaa caaataagag aaacaatggt ttttggggct taacctatat 1440
 ttaacctact tttcattttg ctgcactacg aaaaatgttg cggattatca accattaggt 1500
 tggttacaaa tcaaaagcct ctaatcaaga ataagttatt tagtgtcttg tccacctca 1560

512

tttgctgttg acgtatatgt attgattgta tacattattt tatttgagtg aaaccattat 1620
gct

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..249

(D) OTHER INFORMATION: / Ceres Seq. ID 2025545

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

5 Met Ser Gly Cys Leu Asp Lys Lys Leu Ala Pro Phe Glu Glu Asp Lys
1 5 10 15
Arg Arg Ser Thr Arg Ile Ile Cys Leu Lys Ser Asn Arg Ile Asp Ser
20 20 25 30
Val Phe Phe Phe Phe Phe Thr Tyr Leu Ser Leu Ser Leu Ser Trp Ser
20 35 40 45
Ile Arg Tyr Ser Ile Leu Leu Val Gly Ala Gly Glu Ser Glu Met Thr
50 55 60
Trp Ser Val Phe Arg Ser Ile Asn Thr Pro Thr Leu Asp Leu Ser Thr
65 70 75 80
25 Ala Leu Arg Ser Thr Arg Thr Pro Leu Val Ala Ala Gly Val Gly Cys
85 90 95
Ala Thr Phe Ala Gly Val Ser Leu Phe Arg Met Ser Ser Arg Ser Pro
100 105 110
30 Pro Phe Ala Ser Leu Ser Val Ser Ala Ser Ser Val Lys Lys Glu Val
115 120 125
Val Ser Thr Glu Lys Ala Pro Ala Ala Leu Gly Pro Tyr Ser Gln Ala
130 135 140
Ile Lys Ala Asn Asn Leu Val Phe Leu Ser Gly Val Leu Gly Leu Ile
145 150 155 160
35 Pro Glu Thr Gly Lys Phe Val Ser Glu Ser Val Glu Asp Gln Thr Glu
165 170 175
Gln Val Leu Lys Asn Met Gly Glu Ile Leu Lys Ala Ser Gly Ala Asp
180 185 190
Tyr Ser Ser Val Val Lys Thr Thr Ile Met Leu Ala Asp Leu Ala Asp
40 195 200 205
Phe Lys Thr Val Asn Glu Ile Tyr Ala Lys Tyr Phe Pro Ala Pro Ser
210 215 220
Pro Ala Arg Ser Thr Tyr Gln Val Ala Ala Leu Pro Leu Asn Ala Lys
225 230 235 240
45 Ile Glu Ile Glu Cys Ile Ala Thr Leu
245

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..211

(D) OTHER INFORMATION: / Ceres Seq. ID 2025546

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

60 Met Gly Ile Ser Lys Met Ile Leu Leu Lys Phe Thr Tyr Val Val Ser
1 5 10 15
Phe Trp Ile Thr Cys Val Ile Phe Lys Met Ser Arg Thr Ile Lys Arg
20 25 30

513

Ala Leu Leu Gly Ser Phe Ile Phe Ile Leu Ala Ser Ala Ser Val Val
 35 40 45
 Val Ala Ala Ile Val Gly Ala Ile Glu Gly His Thr Thr Asp Ile Gly
 50 55 60
 5 Phe Leu Gln Gly Ser Val Leu Gly Val Val Ala Gly Val Ile Thr Ala
 65 70 75 80
 Val Gln Leu Phe Gly Pro Val Leu His Ser Asp Gln Pro Leu Ser Lys
 85 90 95
 10 Val Ala Leu Leu Arg Arg Val Val Asn Gly Lys Ala Ile Met Gly Leu
 100 105 110
 Val Arg Pro Phe Val Leu Lys Ala Tyr Gln Trp Gln Ile Ile Ala Leu
 115 120 125
 Asp Thr Ser Tyr Met Glu Ser Ser Asn Leu Tyr Asp Phe Asn His Glu
 130 135 140
 15 Lys Lys Gly Leu Ser Lys Ser Ser Ile Gln Asn Ile Pro Met Phe Tyr
 145 150 155 160
 Asn Arg Ser Glu His Gln Thr Lys Ser Ser Cys Ser Ile Cys Leu Gln
 165 170 175
 20 Asp Trp Glu Glu Gly Glu Val Gly Arg Lys Leu Ala Arg Cys Gly His
 180 185 190
 Thr Phe His Met Asn Cys Ile Asp Glu Trp Leu Leu Arg Gln Glu Thr
 195 200 205
 Cys Pro Ile
 210
 25 (2) INFORMATION FOR SEQ ID NO:382:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..206
 35 (D) OTHER INFORMATION: / Ceres Seq. ID 2025547
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:
 Met Ile Leu Leu Lys Phe Thr Tyr Val Val Ser Phe Trp Ile Thr Cys
 1 5 10 15
 Val Ile Phe Lys Met Ser Arg Thr Ile Lys Arg Ala Leu Leu Gly Ser
 20 25 30
 Phe Ile Phe Ile Leu Ala Ser Ala Ser Val Val Val Ala Ala Ile Val
 35 40 45
 Gly Ala Ile Glu Gly His Thr Thr Asp Ile Gly Phe Leu Gln Gly Ser
 50 55 60
 45 Val Leu Gly Val Val Ala Gly Val Ile Thr Ala Val Gln Leu Phe Gly
 65 70 75 80
 Pro Val Leu His Ser Asp Gln Pro Leu Ser Lys Val Ala Leu Leu Arg
 85 90 95
 Arg Val Val Asn Gly Lys Ala Ile Met Gly Leu Val Arg Pro Phe Val
 100 105 110
 50 Leu Lys Ala Tyr Gln Trp Gln Ile Ala Leu Asp Thr Ser Tyr Met
 115 120 125
 Glu Ser Ser Asn Leu Tyr Asp Phe Asn His Glu Lys Lys Gly Leu Ser
 130 135 140
 55 Lys Ser Ser Ile Gln Asn Ile Pro Met Phe Tyr Asn Arg Ser Glu His
 145 150 155 160
 Gln Thr Lys Ser Ser Cys Ser Ile Cys Leu Gln Asp Trp Glu Glu Gly
 165 170 175
 Glu Val Gly Arg Lys Leu Ala Arg Cys Gly His Thr Phe His Met Asn
 180 185 190
 60 Cys Ile Asp Glu Trp Leu Leu Arg Gln Glu Thr Cys Pro Ile
 195 200 205

514

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..542

(D) OTHER INFORMATION: / Ceres Seq. ID 2026207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

```

tcaccaaaat ctcttctctc tcttccattg tcttctctta atggaaccaa ccgagaaatc      60
tatgttacta gaaactacta gtaccacgaa gatggagacc aaatacgaag atatgttacc      120
agttatggcg gagaagatgg atgttgaaga gtttgtatca gagttatgca aaggtttcag      180
tttgcttgcg gatccagaga gacatctcat cacagctgag tctctaagac gaaactcagg      240
gatacttgga attgaaggta tgagcaagga agatgctcaa ggaatggta gagaaggaga      300
cctcgatgga gatggtgctc ttaaccaaac cgaattctgc gttctcatgg ttcggttaag      360
ccctgagatg atggaagacg ccgaaacttg gttggagaaa gcactcacc aagaactatg      420
taatcacaat ctctcttcta tgccttgaat gatcgtcctc ctttcttggt tattctcttt      480
ttacttctac aaaacctata aatgtttctg aatataaaat gaagtaatga tttcttgatc      540
cc

```

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 2026208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

```

35 His Gln Asn Leu Phe Ser Leu Phe His Cys Leu Pro Leu Met Glu Pro
   1           5           10           15
Thr Glu Lys Ser Met Leu Leu Glu Thr Thr Ser Thr Thr Lys Met Glu
   20           25           30
40 Thr Lys Tyr Glu Asp Met Leu Pro Val Met Ala Glu Lys Met Asp Val
   35           40           45
Glu Glu Phe Val Ser Glu Leu Cys Lys Gly Phe Ser Leu Leu Ala Asp
   50           55           60
Pro Glu Arg His Leu Ile Thr Ala Glu Ser Leu Arg Arg Asn Ser Gly
   65           70           75           80
45 Ile Leu Gly Ile Glu Gly Met Ser Lys Glu Asp Ala Gln Gly Met Val
   85           90           95
Arg Glu Gly Asp Leu Asp Gly Asp Gly Ala Leu Asn Gln Thr Glu Phe
   100          105          110
Cys Val Leu Met Val Arg Leu Ser Pro Glu Met Met Glu Asp Ala Glu
   115          120          125
50 Thr Trp Leu Glu Lys Ala Leu Thr Gln Glu Leu Cys Asn His Asn Leu
   130          135          140
Ser Ser Met Pro
145

```

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

515

(A) NAME/KEY: peptide

(B) LOCATION: 1..135

(D) OTHER INFORMATION: / Ceres Seq. ID 2026209

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

5 Met Glu Pro Thr Glu Lys Ser Met Leu Leu Glu Thr Thr Ser Thr Thr
 1 5 10 15
 Lys Met Glu Thr Lys Tyr Glu Asp Met Leu Pro Val Met Ala Glu Lys
 20 25 30
 Met Asp Val Glu Glu Phe Val Ser Glu Leu Cys Lys Gly Phe Ser Leu
 35 40 45
 10 Leu Ala Asp Pro Glu Arg His Leu Ile Thr Ala Glu Ser Leu Arg Arg
 50 55 60
 Asn Ser Gly Ile Leu Gly Ile Glu Gly Met Ser Lys Glu Asp Ala Gln
 65 70 75 80
 15 Gly Met Val Arg Glu Gly Asp Leu Asp Gly Asp Gly Ala Leu Asn Gln
 85 90 95
 Thr Glu Phe Cys Val Leu Met Val Arg Leu Ser Pro Glu Met Met Glu
 100 105 110
 Asp Ala Glu Thr Trp Leu Glu Lys Ala Leu Thr Gln Glu Leu Cys Asn
 115 120 125
 20 His Asn Leu Ser Ser Met Pro
 130 135

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

30 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..128

(D) OTHER INFORMATION: / Ceres Seq. ID 2026210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

35 Met Leu Leu Glu Thr Thr Ser Thr Thr Lys Met Glu Thr Lys Tyr Glu
 1 5 10 15
 Asp Met Leu Pro Val Met Ala Glu Lys Met Asp Val Glu Glu Phe Val
 20 25 30
 Ser Glu Leu Cys Lys Gly Phe Ser Leu Leu Ala Asp Pro Glu Arg His
 35 40 45
 40 Leu Ile Thr Ala Glu Ser Leu Arg Arg Asn Ser Gly Ile Leu Gly Ile
 50 55 60
 Glu Gly Met Ser Lys Glu Asp Ala Gln Gly Met Val Arg Glu Gly Asp
 65 70 75 80
 45 Leu Asp Gly Asp Gly Ala Leu Asn Gln Thr Glu Phe Cys Val Leu Met
 85 90 95
 Val Arg Leu Ser Pro Glu Met Met Glu Asp Ala Glu Thr Trp Leu Glu
 100 105 110
 Lys Ala Leu Thr Gln Glu Leu Cys Asn His Asn Leu Ser Met Pro
 115 120 125
 50

(2) INFORMATION FOR SEQ ID NO:387:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 552 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..552

(D) OTHER INFORMATION: / Ceres Seq. ID 2026982

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

60

516

```

atgaagtata aaaacgtttt tcttaaatta tggatgtctt ctctttatat agtgcccact      60
tcctcattag cattctacag tctgcacact tatcacttct ttcgaaatct ctctctatcc      120
ctctcaaaaa tgaagctctc tgtgcgtttt atctccgctg ctcttctctt gttcatggta      180
ttcattgcca cagggatggg tccagtcacc gtggaggcac gcacgtgtga gtcaaaaagc      240
5 cataggttca aggggtccatg tgtgagcaca cacaactgtg caaacgtgtg ccacaacgaa      300
ggcttcggcg gaggtaaatg ccgtggattc cgtcgtcggt gctactgcac aagacactgc      360
tgatccatcc attctcatga ctcaaactct cgatccatcg tcagtgtgtt acttctttct      420
tatctaaatc ttccgtacgg taccatgtcg taccgtacat gagtggtttc tcgaataagt      480
cattgggttg tgtgtttccg gttttaatgt aatgttaa attaaatgg cttttaatat      540
10 attgtattat gg

```

(2) INFORMATION FOR SEQ ID NO:388:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 2026983

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

```

Met Lys Tyr Lys Asn Val Phe Leu Lys Leu Trp Met Ser Ser Leu Tyr
1      5      10
25 Ile Val Pro Thr Ser Ser Leu Ala Phe Tyr Ser Leu His Thr Tyr His
      20      25      30
Phe Phe Arg Asn Leu Ser Leu Ser Leu Ser Lys Met Lys Leu Ser Val
      35      40      45
30 Arg Phe Ile Ser Ala Ala Leu Leu Leu Phe Met Val Phe Ile Ala Thr
      50      55      60
Gly Met Gly Pro Val Thr Val Glu Ala Arg Thr Cys Glu Ser Lys Ser
65      70      75      80
His Arg Phe Lys Gly Pro Cys Val Ser Thr His Asn Cys Ala Asn Val
      85      90      95
35 Cys His Asn Glu Gly Phe Gly Gly Gly Lys Cys Arg Gly Phe Arg Arg
      100      105      110
Arg Cys Tyr Cys Thr Arg His Cys
      115      120

```

(2) INFORMATION FOR SEQ ID NO:389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 2026984

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

```

Met Ser Ser Leu Tyr Ile Val Pro Thr Ser Ser Leu Ala Phe Tyr Ser
1      5      10      15
Leu His Thr Tyr His Phe Phe Arg Asn Leu Ser Leu Ser Leu Ser Lys
      20      25      30
55 Met Lys Leu Ser Val Arg Phe Ile Ser Ala Ala Leu Leu Leu Phe Met
      35      40      45
Val Phe Ile Ala Thr Gly Met Gly Pro Val Thr Val Glu Ala Arg Thr
      50      55      60
Cys Glu Ser Lys Ser His Arg Phe Lys Gly Pro Cys Val Ser Thr His
60      65      70      75      80
Asn Cys Ala Asn Val Cys His Asn Glu Gly Phe Gly Gly Gly Lys Cys
      85      90      95

```

517

Arg Gly Phe Arg Arg Arg Cys Tyr Cys Thr Arg His Cys
 100 105

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..77

(D) OTHER INFORMATION: / Ceres Seq. ID 2026985

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

Met Lys Leu Ser Val Arg Phe Ile Ser Ala Ala Leu Leu Leu Phe Met
 1 5 10 15
 Val Phe Ile Ala Thr Gly Met Gly Pro Val Thr Val Glu Ala Arg Thr
 20 25 30
 Cys Glu Ser Lys Ser His Arg Phe Lys Gly Pro Cys Val Ser Thr His
 35 40 45
 Asn Cys Ala Asn Val Cys His Asn Glu Gly Phe Gly Gly Gly Lys Cys
 50 55 60
 Arg Gly Phe Arg Arg Arg Cys Tyr Cys Thr Arg His Cys
 65 70 75

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 2026986

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

Met Asp Val Phe Ser Leu Tyr Ser Ala His Phe Leu Ile Ser Ile Leu
 1 5 10 15
 Gln Ser Ala His Leu Ser Leu Leu Ser Lys Ser Leu Ser Ile Pro Leu
 20 25 30
 Lys Asn Glu Ala Leu Cys Ala Phe Tyr Leu Arg Cys Ser Ser Leu Val
 35 40 45
 His Gly Ile His Cys His Arg Asp Gly Ser Ser His Arg Gly Gly Thr
 50 55 60
 His Val
 65

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1760 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..1760

(D) OTHER INFORMATION: / Ceres Seq. ID 2027300

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

ctcgtttcat gagagaaaca aaaaatctta tctttctgac aacggtggtg gtgtgtgatg 60
 ttgtcagcca tggcaaagac agctacaacg atctctctct cttttcttct tcttctgtgt 120
 ctgtctttaa atagagtctc ttgaaacga agcagctttg tcctgttctg atatccatgg 180
 ctttaccttc gtgcttaaag actggagctt taatgtctcc ggccactgga ttaattttt 240

518

ccggcagtct tatgaagtca gacagcggct tcgcccgttcc gacaaagtta cagagtactc 300
 gaaaagggtga tcgagagaga ttgagagatcc aagctatctt cagtttccct cctgcgtttc 360
 tgacaagaaa cggctcgagct gagaaacaga aacagctcaa acaagaactt cttgaagcca 420
 5 ttgagcctct tgaacgtggt gctacggcct cgcctgatga ccagcttcgg attgatcagt 480
 tagcgcgtaa agtggagca gttaatccca ccaaggagcc tttgaagtct gatttggtca 540
 atggaaaatg ggagctcatt tatacaacct ctgcttcgat tttgcaggca aagaaaccaa 600
 gggttcttaag atcaataacc aactaccaat ctatcaatgt ggatacactt aaggtgcaaa 660
 acatggagac ttggcctttc tataactcgg taactggaga cataaaaccc ctcaattcga 720
 agaaggttgc tgggaaactc caagtgttta aaattctcgg atttattcct ataaaagcac 780
 10 ctgatagcgc ccgcggtgaa cttgagatta cctatgtgga cgaggaacta cggttatcaa 840
 gagatctttc attcatgtct catgtctggt tccatgacct ttctacattg tttctgttga 900
 tttatgaatc ttcaataaca ctacaggtta aaccaattag aagtgaagtgt gttatgggtcc 960
 ggtacaaaaga tcacaaccgg agaaggattg aagagtgggt aaagcgatgg tcagagttgg 1020
 ttggttccgt cgaaacagga agaaagagtc tctcagaaac gaccagcca ctcttataaa 1080
 15 ctccattgga aaagctttgt cctgttttga tatccatgcc tttaccttgg tgcttaaaga 1140
 ctggagtttt aacgtctccg gccgcggat ttaatcatcc atcggacagt ggcttcgccc 1200
 ttccgacgaa gttactgagt attcgaaaag gtgatcggga aagattgaga atccaagctg 1260
 ttttcagctt tcttccaaga aacggtggag ccgagaagcg gaaacagctc aaacatgaac 1320
 ttgtcgaagc cattgagcct cttgaacgtg gtgccactgc ctgcctgat gatcagcttc 1380
 20 tgattgatca gttagcacgt aaggtggaag cagtaaacc aaccaaggag cctctgaagt 1440
 ctgatttgat caatgggaaa tgggagctca tttacacaac atctgctgcg attttgcaag 1500
 caaagaaacc aaggttctta agatcggtta ctaactacca atgtatcaat atggatacac 1560
 taaaggtgca aagaatggag acttggcctt tctataactc ggtaactgga gacttgacac 1620
 cctcactc aaagacgggt gctgtgaaac ttcaagtgtt taaaattctc ggctttattc 1680
 25 cggtaaaagc acctgatggt actgcacgcg gtgaactaga gattacctat gtggacgagg 1740
 aactacgca caaactttga

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 527 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

35 (A) NAME/KEY: peptide
 (B) LOCATION: 1..527
 (D) OTHER INFORMATION: / Ceres Seq. ID 2027301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

40 Met Ala Leu Pro Ser Cys Leu Lys Thr Gly Ala Leu Met Ser Pro Ala
 1 5 10 15
 Thr Gly Phe Asn Phe Ser Gly Ser Leu Met Lys Ser Asp Ser Gly Phe
 20 25 30
 Ala Val Pro Thr Lys Leu Gln Ser Thr Arg Lys Gly Asp Arg Glu Arg
 35 40 45
 45 Leu Arg Val Gln Ala Ile Phe Ser Phe Pro Pro Ala Phe Leu Thr Arg
 50 55 60
 Asn Gly Arg Ala Glu Lys Gln Lys Gln Leu Lys Gln Glu Leu Leu Glu
 65 70 75 80
 Ala Ile Glu Pro Leu Glu Arg Gly Ala Thr Ala Ser Pro Asp Asp Gln
 85 90 95
 50 Leu Arg Ile Asp Gln Leu Ala Arg Lys Val Glu Ala Val Asn Pro Thr
 100 105 110
 Lys Glu Pro Leu Lys Ser Asp Leu Val Asn Gly Lys Trp Glu Leu Ile
 115 120 125
 55 Tyr Thr Thr Ser Ala Ser Ile Leu Gln Ala Lys Lys Pro Arg Phe Leu
 130 135 140
 Arg Ser Ile Thr Asn Tyr Gln Ser Ile Asn Val Asp Thr Leu Lys Val
 145 150 155 160
 60 Gln Asn Met Glu Thr Trp Pro Phe Tyr Asn Ser Val Thr Gly Asp Ile
 165 170 175
 Lys Pro Leu Asn Ser Lys Lys Val Ala Val Lys Leu Gln Val Phe Lys
 180 185 190

519

	Ile	Leu	Gly	Phe	Ile	Pro	Ile	Lys	Ala	Pro	Asp	Ser	Ala	Arg	Gly	Glu
			195					200					205			
	Leu	Glu	Ile	Thr	Tyr	Val	Asp	Glu	Glu	Leu	Arg	Leu	Ser	Arg	Asp	Leu
		210					215					220				
5	Ser	Phe	Met	Ser	His	Val	Trp	Phe	His	Asp	Leu	Ser	Thr	Leu	Phe	Leu
		225				230					235					240
	Leu	Ile	Tyr	Glu	Ser	Ser	Ile	Thr	Leu	Gln	Val	Lys	Pro	Ile	Arg	Ser
					245					250					255	
10	Glu	Leu	Val	Met	Val	Arg	Tyr	Lys	Asp	His	Asn	Arg	Arg	Arg	Ile	Glu
				260					265					270		
	Glu	Trp	Ser	Lys	Arg	Trp	Ser	Glu	Leu	Val	Gly	Ser	Val	Glu	Thr	Gly
			275					280					285			
	Arg	Lys	Ser	Leu	Ser	Glu	Thr	Thr	Gln	Pro	Leu	Phe	Lys	Thr	Pro	Leu
		290					295					300				
15	Glu	Lys	Leu	Cys	Pro	Val	Leu	Ile	Ser	Met	Ala	Leu	Pro	Trp	Cys	Leu
		305				310					315					320
	Lys	Thr	Gly	Val	Leu	Thr	Ser	Pro	Ala	Ala	Gly	Phe	Asn	His	Pro	Ser
					325					330					335	
20	Asp	Ser	Gly	Phe	Ala	Val	Pro	Thr	Lys	Leu	Leu	Ser	Ile	Arg	Lys	Gly
				340					345					350		
	Asp	Arg	Glu	Arg	Leu	Arg	Ile	Gln	Ala	Val	Phe	Ser	Phe	Pro	Pro	Arg
			355					360					365			
	Asn	Gly	Gly	Ala	Glu	Lys	Arg	Lys	Gln	Leu	Lys	His	Glu	Leu	Val	Glu
		370					375					380				
25	Ala	Ile	Glu	Pro	Leu	Glu	Arg	Gly	Ala	Thr	Ala	Ser	Pro	Asp	Asp	Gln
		385				390					395					400
	Leu	Leu	Ile	Asp	Gln	Leu	Ala	Arg	Lys	Val	Glu	Ala	Val	Asn	Pro	Thr
				405						410				415		
30	Lys	Glu	Pro	Leu	Lys	Ser	Asp	Leu	Ile	Asn	Gly	Lys	Trp	Glu	Leu	Ile
				420					425					430		
	Tyr	Thr	Thr	Ser	Ala	Ala	Ile	Leu	Gln	Ala	Lys	Lys	Pro	Arg	Phe	Leu
			435					440					445			
	Arg	Ser	Leu	Thr	Asn	Tyr	Gln	Cys	Ile	Asn	Met	Asp	Thr	Leu	Lys	Val
		450					455					460				
35	Gln	Arg	Met	Glu	Thr	Trp	Pro	Phe	Tyr	Asn	Ser	Val	Thr	Gly	Asp	Leu
		465				470					475					480
	Thr	Pro	Leu	Asn	Ser	Lys	Thr	Val	Ala	Val	Lys	Leu	Gln	Val	Phe	Lys
				485						490					495	
40	Ile	Leu	Gly	Phe	Ile	Pro	Val	Lys	Ala	Pro	Asp	Gly	Thr	Ala	Arg	Gly
			500						505					510		
	Glu	Leu	Glu	Ile	Thr	Tyr	Val	Asp	Glu	Glu	Leu	Arg	Asp	Lys	Leu	
		515					520					525				

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 515 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

50 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..515

(D) OTHER INFORMATION: / Ceres Seq. ID 2027302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

55 Met Ser Pro Ala Thr Gly Phe Asn Phe Ser Gly Ser Leu Met Lys Ser
 1 5 10 15
 Asp Ser Gly Phe Ala Val Pro Thr Lys Leu Gln Ser Thr Arg Lys Gly
 20 25 30
 Asp Arg Glu Arg Leu Arg Val Gln Ala Ile Phe Ser Phe Pro Pro Ala
 35 40 45
 Phe Leu Thr Arg Asn Gly Arg Ala Glu Lys Gln Lys Gln Leu Lys Gln
 50 55 60

520

	Glu	Leu	Leu	Glu	Ala	Ile	Glu	Pro	Leu	Glu	Arg	Gly	Ala	Thr	Ala	Ser
	65					70					75					80
	Pro	Asp	Asp	Gln	Leu	Arg	Ile	Asp	Gln	Leu	Ala	Arg	Lys	Val	Glu	Ala
					85					90					95	
5	Val	Asn	Pro	Thr	Lys	Glu	Pro	Leu	Lys	Ser	Asp	Leu	Val	Asn	Gly	Lys
				100					105					110		
	Trp	Glu	Leu	Ile	Tyr	Thr	Thr	Ser	Ala	Ser	Ile	Leu	Gln	Ala	Lys	Lys
				115				120					125			
10	Pro	Arg	Phe	Leu	Arg	Ser	Ile	Thr	Asn	Tyr	Gln	Ser	Ile	Asn	Val	Asp
		130					135					140				
	Thr	Leu	Lys	Val	Gln	Asn	Met	Glu	Thr	Trp	Pro	Phe	Tyr	Asn	Ser	Val
		145				150					155					160
	Thr	Gly	Asp	Ile	Lys	Pro	Leu	Asn	Ser	Lys	Lys	Val	Ala	Val	Lys	Leu
					165					170					175	
15	Gln	Val	Phe	Lys	Ile	Leu	Gly	Phe	Ile	Pro	Ile	Lys	Ala	Pro	Asp	Ser
				180				185						190		
	Ala	Arg	Gly	Glu	Leu	Glu	Ile	Thr	Tyr	Val	Asp	Glu	Glu	Leu	Arg	Leu
				195				200					205			
20	Ser	Arg	Asp	Leu	Ser	Phe	Met	Ser	His	Val	Trp	Phe	His	Asp	Leu	Ser
		210					215					220				
	Thr	Leu	Phe	Leu	Leu	Ile	Tyr	Glu	Ser	Ser	Ile	Thr	Leu	Gln	Val	Lys
		225				230					235					240
	Pro	Ile	Arg	Ser	Glu	Leu	Val	Met	Val	Arg	Tyr	Lys	Asp	His	Asn	Arg
					245					250					255	
25	Arg	Arg	Ile	Glu	Glu	Trp	Ser	Lys	Arg	Trp	Ser	Glu	Leu	Val	Gly	Ser
				260				265						270		
	Val	Glu	Thr	Gly	Arg	Lys	Ser	Leu	Ser	Glu	Thr	Thr	Gln	Pro	Leu	Phe
				275				280					285			
30	Lys	Thr	Pro	Leu	Glu	Lys	Leu	Cys	Pro	Val	Leu	Ile	Ser	Met	Ala	Leu
		290					295					300				
	Pro	Trp	Cys	Leu	Lys	Thr	Gly	Val	Leu	Thr	Ser	Pro	Ala	Ala	Gly	Phe
		305				310					315					320
	Asn	His	Pro	Ser	Asp	Ser	Gly	Phe	Ala	Val	Pro	Thr	Lys	Leu	Leu	Ser
					325					330					335	
35	Ile	Arg	Lys	Gly	Asp	Arg	Glu	Arg	Leu	Arg	Ile	Gln	Ala	Val	Phe	Ser
				340				345						350		
	Phe	Pro	Pro	Arg	Asn	Gly	Gly	Ala	Glu	Lys	Arg	Lys	Gln	Leu	Lys	His
				355				360					365			
40	Glu	Leu	Val	Glu	Ala	Ile	Glu	Pro	Leu	Glu	Arg	Gly	Ala	Thr	Ala	Ser
		370					375					380				
	Pro	Asp	Asp	Gln	Leu	Leu	Ile	Asp	Gln	Leu	Ala	Arg	Lys	Val	Glu	Ala
						390				395						400
	Val	Asn	Pro	Thr	Lys	Glu	Pro	Leu	Lys	Ser	Asp	Leu	Ile	Asn	Gly	Lys
					405					410					415	
45	Trp	Glu	Leu	Ile	Tyr	Thr	Thr	Ser	Ala	Ala	Ile	Leu	Gln	Ala	Lys	Lys
				420				425						430		
	Pro	Arg	Phe	Leu	Arg	Ser	Leu	Thr	Asn	Tyr	Gln	Cys	Ile	Asn	Met	Asp
				435				440					445			
50	Thr	Leu	Lys	Val	Gln	Arg	Met	Glu	Thr	Trp	Pro	Phe	Tyr	Asn	Ser	Val
		450					455					460				
	Thr	Gly	Asp	Leu	Thr	Pro	Leu	Asn	Ser	Lys	Thr	Val	Ala	Val	Lys	Leu
		465				470					475					480
	Gln	Val	Phe	Lys	Ile	Leu	Gly	Phe	Ile	Pro	Val	Lys	Ala	Pro	Asp	Gly
					485					490					495	
55	Thr	Ala	Arg	Gly	Glu	Leu	Glu	Ile	Thr	Tyr	Val	Asp	Glu	Glu	Leu	Arg
				500					505					510		
	Asp	Lys	Leu													
				515												

(2) INFORMATION FOR SEQ ID NO:395:

- 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 502 amino acids
 (B) TYPE: amino acid

521

(C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

5 (A) NAME/KEY: peptide
 (B) LOCATION: 1..502
 (D) OTHER INFORMATION: / Ceres Seq. ID 2027303
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

10	Met	Lys	Ser	Asp	Ser	Gly	Phe	Ala	Val	Pro	Thr	Lys	Leu	Gln	Ser	Thr
	1				5					10				15		
	Arg	Lys	Gly	Asp	Arg	Glu	Arg	Leu	Arg	Val	Gln	Ala	Ile	Phe	Ser	Phe
				20				25						30		
	Pro	Pro	Ala	Phe	Leu	Thr	Arg	Asn	Gly	Arg	Ala	Glu	Lys	Gln	Lys	Gln
			35					40					45			
15	Leu	Lys	Gln	Glu	Leu	Leu	Glu	Ala	Ile	Glu	Pro	Leu	Glu	Arg	Gly	Ala
		50					55					60				
	Thr	Ala	Ser	Pro	Asp	Asp	Gln	Leu	Arg	Ile	Asp	Gln	Leu	Ala	Arg	Lys
	65					70				75						80
	Val	Glu	Ala	Val	Asn	Pro	Thr	Lys	Glu	Pro	Leu	Lys	Ser	Asp	Leu	Val
20					85					90					95	
	Asn	Gly	Lys	Trp	Glu	Leu	Ile	Tyr	Thr	Thr	Ser	Ala	Ser	Ile	Leu	Gln
				100					105					110		
	Ala	Lys	Lys	Pro	Arg	Phe	Leu	Arg	Ser	Ile	Thr	Asn	Tyr	Gln	Ser	Ile
			115					120					125			
25	Asn	Val	Asp	Thr	Leu	Lys	Val	Gln	Asn	Met	Glu	Thr	Trp	Pro	Phe	Tyr
		130					135					140				
	Asn	Ser	Val	Thr	Gly	Asp	Ile	Lys	Pro	Leu	Asn	Ser	Lys	Lys	Val	Ala
	145					150					155					160
	Val	Lys	Leu	Gln	Val	Phe	Lys	Ile	Leu	Gly	Phe	Ile	Pro	Ile	Lys	Ala
30					165					170					175	
	Pro	Asp	Ser	Ala	Arg	Gly	Glu	Leu	Glu	Ile	Thr	Tyr	Val	Asp	Glu	Glu
				180					185					190		
	Leu	Arg	Leu	Ser	Arg	Asp	Leu	Ser	Phe	Met	Ser	His	Val	Trp	Phe	His
		195					200						205			
35	Asp	Leu	Ser	Thr	Leu	Phe	Leu	Leu	Ile	Tyr	Glu	Ser	Ser	Ile	Thr	Leu
		210					215					220				
	Gln	Val	Lys	Pro	Ile	Arg	Ser	Glu	Leu	Val	Met	Val	Arg	Tyr	Lys	Asp
	225					230					235					240
	His	Asn	Arg	Arg	Arg	Ile	Glu	Glu	Trp	Ser	Lys	Arg	Trp	Ser	Glu	Leu
40					245					250					255	
	Val	Gly	Ser	Val	Glu	Thr	Gly	Arg	Lys	Ser	Leu	Ser	Glu	Thr	Thr	Gln
				260					265					270		
	Pro	Leu	Phe	Lys	Thr	Pro	Leu	Glu	Lys	Leu	Cys	Pro	Val	Leu	Ile	Ser
		275						280					285			
45	Met	Ala	Leu	Pro	Trp	Cys	Leu	Lys	Thr	Gly	Val	Leu	Thr	Ser	Pro	Ala
		290					295					300				
	Ala	Gly	Phe	Asn	His	Pro	Ser	Asp	Ser	Gly	Phe	Ala	Val	Pro	Thr	Lys
	305					310					315					320
	Leu	Leu	Ser	Ile	Arg	Lys	Gly	Asp	Arg	Glu	Arg	Leu	Arg	Ile	Gln	Ala
50					325					330					335	
	Val	Phe	Ser	Phe	Pro	Pro	Arg	Asn	Gly	Gly	Ala	Glu	Lys	Arg	Lys	Gln
				340					345					350		
	Leu	Lys	His	Glu	Leu	Val	Glu	Ala	Ile	Glu	Pro	Leu	Glu	Arg	Gly	Ala
			355					360					365			
55	Thr	Ala	Ser	Pro	Asp	Asp	Gln	Leu	Leu	Ile	Asp	Gln	Leu	Ala	Arg	Lys
		370					375					380				
	Val	Glu	Ala	Val	Asn	Pro	Thr	Lys	Glu	Pro	Leu	Lys	Ser	Asp	Leu	Ile
	385					390					395					400
	Asn	Gly	Lys	Trp	Glu	Leu	Ile	Tyr	Thr	Thr	Ser	Ala	Ala	Ile	Leu	Gln
60					405					410					415	
	Ala	Lys	Lys	Pro	Arg	Phe	Leu	Arg	Ser	Leu	Thr	Asn	Tyr	Gln	Cys	Ile
				420					425					430		

522

Asn Met Asp Thr Leu Lys Val Gln Arg Met Glu Thr Trp Pro Phe Tyr
 435 440 445
 Asn Ser Val Thr Gly Asp Leu Thr Pro Leu Asn Ser Lys Thr Val Ala
 450 455 460
 5 Val Lys Leu Gln Val Phe Lys Ile Leu Gly Phe Ile Pro Val Lys Ala
 465 470 475 480
 Pro Asp Gly Thr Ala Arg Gly Glu Leu Glu Ile Thr Tyr Val Asp Glu
 485 490 495
 Glu Leu Arg Asp Lys Leu
 500
 10 (2) INFORMATION FOR SEQ ID NO:396:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 539 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 20 (B) LOCATION: 1..539
 (D) OTHER INFORMATION: / Ceres Seq. ID 2027375
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:
 actgtgttcg ataataatgt cgacaggaga agcgatacca agagtgcgcg tcgtcgtttt 60
 cattctcaac ggaaactcaa tcttattagg tcgccgccgt tcctcaatcg gcaactccac 120
 25 tttcgctctt cccggtggcc acctcgaatt cggagagagc tttgaagaat gtgcagcgag 180
 agaagtaatg gaggaaacag gtctaaagat tgaaaagatg aagcttttga ctgttacaaa 240
 caatgtcttc aaagaagcac caacgccatc acactacgtc tctgtttcga tacgtgcggt 300
 gttggtggat ccaagtcaag aaccgaagaa tatggaacca gagaagtgtg aaggatggga 360
 ttggtatgat tgggagaatc taccaaagcc tttgttttgg ccacttgaga aattgtttgg 420
 30 aagtggtttc aatcctttca ctcatggtgg tggagactaa tagatgtaag agttaatgat 480
 tgatttggga ttgaatgttg cacaaattgg gcatttggtc tagtggtatg atctygctt
 (2) INFORMATION FOR SEQ ID NO:397:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 amino acids
 35 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 40 (B) LOCATION: 1..152
 (D) OTHER INFORMATION: / Ceres Seq. ID 2027376
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:
 Leu Cys Ser Ile Ile Met Ser Thr Gly Glu Ala Ile Pro Arg Val Ala
 45 1 5 10 15
 Val Val Val Phe Ile Leu Asn Gly Asn Ser Ile Leu Leu Gly Arg Arg
 20 25 30
 Arg Ser Ser Ile Gly Asn Ser Thr Phe Ala Leu Pro Gly Gly His Leu
 35 40 45
 50 Glu Phe Gly Glu Ser Phe Glu Cys Ala Ala Arg Glu Val Met Glu
 50 55 60
 Glu Thr Gly Leu Lys Ile Glu Lys Met Lys Leu Leu Thr Val Thr Asn
 65 70 75 80
 Asn Val Phe Lys Glu Ala Pro Thr Pro Ser His Tyr Val Ser Val Ser
 85 90 95
 55 Ile Arg Ala Val Leu Val Asp Pro Ser Gln Glu Pro Lys Asn Met Glu
 100 105 110
 Pro Glu Lys Cys Glu Gly Trp Asp Trp Tyr Asp Trp Glu Asn Leu Pro
 115 120 125
 60 Lys Pro Leu Phe Trp Pro Leu Glu Lys Leu Phe Gly Ser Gly Phe Asn
 130 135 140
 Pro Phe Thr His Gly Gly Gly Asp

523

145

150

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 147 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..147

(D) OTHER INFORMATION: / Ceres Seq. ID 2027377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

Met Ser Thr Gly Glu Ala Ile Pro Arg Val Ala Val Val Val Phe Ile
 1 5 10 15
 Leu Asn Gly Asn Ser Ile Leu Leu Gly Arg Arg Arg Ser Ser Ile Gly
 20 25 30
 Asn Ser Thr Phe Ala Leu Pro Gly Gly His Leu Glu Phe Gly Glu Ser
 35 40 45
 Phe Glu Glu Cys Ala Ala Arg Glu Val Met Glu Glu Thr Gly Leu Lys
 50 55 60
 Ile Glu Lys Met Lys Leu Leu Thr Val Thr Asn Asn Val Phe Lys Glu
 65 70 75 80
 Ala Pro Thr Pro Ser His Tyr Val Ser Val Ser Ile Arg Ala Val Leu
 85 90 95
 Val Asp Pro Ser Gln Glu Pro Lys Asn Met Glu Pro Glu Lys Cys Glu
 100 105 110
 Gly Trp Asp Trp Tyr Asp Trp Glu Asn Leu Pro Lys Pro Leu Phe Trp
 115 120 125
 Pro Leu Glu Lys Leu Phe Gly Ser Gly Phe Asn Pro Phe Thr His Gly
 130 135 140
 Gly Gly Asp

145

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..90

(D) OTHER INFORMATION: / Ceres Seq. ID 2027378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

Met Glu Glu Thr Gly Leu Lys Ile Glu Lys Met Lys Leu Leu Thr Val
 1 5 10 15
 Thr Asn Asn Val Phe Lys Glu Ala Pro Thr Pro Ser His Tyr Val Ser
 20 25 30
 Val Ser Ile Arg Ala Val Leu Val Asp Pro Ser Gln Glu Pro Lys Asn
 35 40 45
 Met Glu Pro Glu Lys Cys Glu Gly Trp Asp Trp Tyr Asp Trp Glu Asn
 50 55 60
 Leu Pro Lys Pro Leu Phe Trp Pro Leu Glu Lys Leu Phe Gly Ser Gly
 65 70 75 80
 Phe Asn Pro Phe Thr His Gly Gly Gly Asp
 85 90

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3983 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

60

524

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..3983

(D) OTHER INFORMATION: / Ceres Seq. ID 2028729

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

	atgaacacga	cgccgtttca	ctcggatcct	ccgccgtcga	ggatccagcg	taagctcggt	60
	gtcgaagttg	ttgaagctcg	taatattctc	cctaaagatg	gtcaaggaag	ctctagcgct	120
10	tacgtcgttg	tgcatttcga	tgtcagaag	aaacgaacct	ccactaagtt	ccgtgacct	180
	aaccctatatt	ggaacgagat	gcttgatttc	gccgtctccg	atcccaaaaa	catggattac	240
	gacgagctcg	atatcgaggt	ttataacgat	aaaagatttg	gtaacggagg	tggccggaag	300
	aatcatttttc	tccgtagggg	taagatctat	ggaagccagt	tctcgcgaa	aggtgaagaa	360
	ggtcttgtgt	atttcccttt	ggagaagaag	agtgtgttca	gctggattcg	cggcgagatt	420
15	ggactcaaaa	tctactatta	cgacgaagcc	gccgacgaag	acacggcggg	tggaggtgga	480
	ggacagcaac	aacaacagca	acagcaacaa	tttcatccgc	cgcaacaaga	agccgatgaa	540
	caacaacacc	agcaacaatt	tcatcctccg	ccgcagcaga	tgatgaatat	accaccggag	600
	aaacctaattg	tagttgtggt	tgaagaaggt	agggttttcg	aatcggctca	gagtcagcgc	660
	tatacagaga	cacatcagca	acctccggtg	gttattgttg	aagaatcacc	accgcagcat	720
20	gtaatgcaag	gtccaaatga	taaccatcct	caccgaaatg	ataaccatcc	tcaacggcca	780
	ccgtctccgc	cgccacctcc	atcggctggg	gaagtacatt	attatccacc	ggaagtgagg	840
	aagatgcaag	taggaagacc	tcccggcgga	gatagaatta	gggttacgaa	gagaccaccg	900
	aatggagatt	attcacctag	ggttatcaat	agcaaaactg	gaggaggaga	gacgacgatg	960
	gagaagaaga	ctcatcatcc	ttacaatctt	gttgagccaa	tgcagtatct	cttcggttcg	1020
25	attgtgaagg	cgcggtggtt	accacctaac	gagagcgctg	atgttaaggt	acggacgtcg	1080
	aaccatttcg	tcaggtctaa	accggccgtt	aaccggcccg	gcgaatcggg	tgattcaccg	1140
	gagtggaatc	agggttttgc	tcttggtcat	aaccggtctg	attccgctgt	aactgggtgcg	1200
	actcttgaga	tctctgcttg	ggatgcttcg	tccgagaggt	ttctcgagg	agtttgtttt	1260
	gatctctctg	aggttccggt	tcgtgacctg	ccgcatagtc	cgcttgctcc	tcagtgggtat	1320
30	cggtcgaag	gctccggcgc	ggatcagaac	tctgggagaa	tttccggtga	cattcagctc	1380
	tctgtttgga	ttggtactca	ggtagatgag	gcatttccgg	aggcttgagg	ctctgatgct	1440
	ccgcatgtag	ctcacacgcg	ttctaagggt	tatcaatcgc	cgaaactttg	gtacttgaga	1500
	gtgacggttc	ttgaggcaca	ggatttacac	atagctccta	atctcccggc	gttgactgcg	1560
	cctgagattc	gtgtgaaagc	tcaattaggg	tttcagtcgg	cgcgtaaca	aagaggctca	1620
35	atgaataaac	acagtgggtc	gtttcatttg	catgaggata	tgatctttgt	tgctggagag	1680
	ccgttggaag	attgcttggt	tctgatgggt	gaagaccgga	cgactaaaga	agcaacactt	1740
	ctaggacatg	ccatgatccc	agtgagctcc	atcgagcagc	gaattgatga	gcgttttgtg	1800
	ccgtcgaaat	ggcacactct	ggaaggagaa	ggtggagggt	gaggtggagg	aggaggacct	1860
	ggaggtgggt	gtggtgggtg	accttattgt	ggaaggatta	gccttagact	ttgtctcgaa	1920
40	ggtgggtatc	atgtgcttga	agaggcgcg	catgtatgca	gcgatttccg	tccgacggct	1980
	aagcagctat	ggaaaccgcc	gattggaata	cttgagtttg	ggattcttgg	agctcgtggg	2040
	ttgttgccga	tgaaggcgaa	aaacggaggg	aaaggttcca	ctgatgctta	ttgtgttget	2100
	aagtacggga	agaaatgggt	caggactcga	accataacag	acagttttga	cccagggtgg	2160
	cacgagcagt	atacgtggca	ggtttatgta	ccttgacacg	tgctaactgt	tggagtcttc	2220
45	gacaattgga	ggatgttctc	tgcgcctccc	gatgatagac	ctgacacacg	gattgggaag	2280
	atacggatcc	gggtgtcgac	gttagagagc	aacaaagtgt	acaccaattc	atatactctg	2340
	ttggttttgt	tacctagcgg	tatgaaaaaa	atgggtgaaa	ttgaagtggc	agtcgggttt	2400
	gcatgcccg	ctctgctgcc	tgatgtttgt	gcagcttatg	gacagccgct	tctgcctcgg	2460
	atgcactaca	taaggcctct	agggtgtagc	caacaagatg	cattaagagg	ggccgccacg	2520
50	aaaatggtag	cagcttggtt	ggctcgagca	gaaccaccat	tgggaccaga	ggtagttcga	2580
	tatatgttag	atgcagattc	gcatgcatgg	agcatgagga	aaagcaaagc	gaattgggtac	2640
	agaattgttg	gtgttttagc	ttgggcagtg	ggtttagcta	agtggttgga	taatatcagg	2700
	cgggtgagga	atccagtgc	gacgggtgcta	gtccatatct	tatatcttgt	tctgttttgt	2760
	taccttgatt	tggtagtccc	gactgcattc	ttgtacgtgg	tgatgatcgg	agtttgggtac	2820
55	taccggttta	gaccaagat	accggctggg	atggatatcc	gcttatcaca	agctgaaacc	2880
	gtcgatcctg	atgagctaga	tgaagaattc	gacaccatac	caagctcaag	gcgaccagaa	2940
	gtaatccgag	ctaggtacga	ccgattaagg	atcttagcag	tgagggttca	gaccattcta	3000
	ggagattttg	cagcgcaagg	agaacggatt	caagcggttg	ttagctggag	agatccgaga	3060
	gcgacaaaagc	tgttcatagc	aatctgtttg	gtaatcacia	tagttctgta	tgcagttcct	3120
60	gcgaaaatgg	tggcgggtggc	tctaggaggt	tcagatagtg	tgccaacggc	gaaacaagac	3180
	acgaaagaat	ctctaaagaa	atcattttca	tcgcttcgct	tcgatttttc	ttcaatggct	3240
	gtcgtcggcg	ctccaatatc	gtctccggcg	gctcagctgc	agacacaatt	tctctccaat	3300

525

5 cccattctcc cccgctttcg ccggtctttc tccaccggaa aatcaccagc aactttctcc 3360
 gtcgtagcta tggctcccca gaaaaaggtg aacaaatatg atgccaagtg gaagaaacaa 3420
 tggtagcgag ctggattgtt tttcgaaggg agtgagcaaa taaacgttga tgttttcaag 3480
 aagctggaga agcgaagagt gttgagcaac gttgagaaat ctggcctgct gtcaaaagca 3540
 gaggggttgg gactcacatt gtcattctctt gagaagctta aagtcttctc caaagcagag 3600
 gaccttggtc ttctcagtct ccttgagaac ttagctggaa catcgctgct ggtcttagcc 3660
 tcggctgcat taccagctct cacggctgct attgtagccg tgggtgtgat cccggatgac 3720
 tcaactactc tagtggttgc tcaggcggtt ttggccggtg ctcttgcgct tacaggggtt 3780
 gttttgttgg ttggttctgt tgttttggat ggacttcaag aagctgactg attctttctc 3840
 10 tgtaaaccga acataaacc atgtcttgtc caattgattt ttgtcagttg ctgatttata 3900
 gctgtatggt tcagttgttt atggttagtc caagacataa gctgagtgat agaaagaagc 3960
 ttataataa ttaaacaat att

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1276 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (ix) FEATURE:

(A) NAME/KEY: peptide
 (B) LOCATION: 1..1276

(D) OTHER INFORMATION: / Ceres Seq. ID 2028730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

25 Met Asn Thr Thr Pro Phe His Ser Asp Pro Pro Pro Ser Arg Ile Gln
 1 5 10 15
 Arg Lys Leu Val Glu Val Val Glu Ala Arg Asn Ile Leu Pro Lys
 20 25 30
 Asp Gly Gln Gly Ser Ser Ser Ala Tyr Val Val Val Asp Phe Asp Ala
 30 35 40 45
 Gln Lys Lys Arg Thr Ser Thr Lys Phe Arg Asp Leu Asn Pro Ile Trp
 50 55 60
 Asn Glu Met Leu Asp Phe Ala Val Ser Asp Pro Lys Asn Met Asp Tyr
 65 70 75 80
 35 Asp Glu Leu Asp Ile Glu Val Tyr Asn Asp Lys Arg Phe Gly Asn Gly
 85 90 95
 Gly Gly Arg Lys Asn His Phe Leu Gly Arg Val Lys Ile Tyr Gly Ser
 100 105 110
 Gln Phe Ser Arg Arg Gly Glu Glu Gly Leu Val Tyr Phe Pro Leu Glu
 40 115 120 125
 Lys Lys Ser Val Phe Ser Trp Ile Arg Gly Glu Ile Gly Leu Lys Ile
 130 135 140
 Tyr Tyr Tyr Asp Glu Ala Ala Asp Glu Asp Thr Ala Gly Gly Gly Gly
 145 150 155 160
 45 Gly Gln Gln Gln Gln Gln Gln Gln Gln Phe His Pro Pro Gln Gln
 165 170 175
 Glu Ala Asp Glu Gln Gln His Gln Gln Gln Phe His Pro Pro Pro Gln
 180 185 190
 Gln Met Met Asn Ile Pro Pro Glu Lys Pro Asn Val Val Val Val Glu
 50 195 200 205
 Glu Gly Arg Val Phe Glu Ser Ala Gln Ser Gln Arg Tyr Thr Glu Thr
 210 215 220
 His Gln Gln Pro Pro Val Val Ile Val Glu Glu Ser Pro Pro Gln His
 225 230 235 240
 55 Val Met Gln Gly Pro Asn Asp Asn His Pro His Arg Asn Asp Asn His
 245 250 255
 Pro Gln Arg Pro Pro Ser Pro Pro Pro Pro Pro Ser Ala Gly Glu Val
 260 265 270
 His Tyr Tyr Pro Pro Glu Val Arg Lys Met Gln Val Gly Arg Pro Pro
 60 275 280 285
 Gly Gly Asp Arg Ile Arg Val Thr Lys Arg Pro Pro Asn Gly Asp Tyr
 290 295 300

526																
	Ser	Pro	Arg	Val	Ile	Asn	Ser	Lys	Thr	Gly	Gly	Gly	Glu	Thr	Thr	Met
	305					310					315					320
	Glu	Lys	Lys	Thr	His	His	Pro	Tyr	Asn	Leu	Val	Glu	Pro	Met	Gln	Tyr
					325					330					335	
5	Leu	Phe	Val	Arg	Ile	Val	Lys	Ala	Arg	Gly	Leu	Pro	Pro	Asn	Glu	Ser
				340					345					350		
	Ala	Tyr	Val	Lys	Val	Arg	Thr	Ser	Asn	His	Phe	Val	Arg	Ser	Lys	Pro
			355					360					365			
10	Ala	Val	Asn	Arg	Pro	Gly	Glu	Ser	Val	Asp	Ser	Pro	Glu	Trp	Asn	Gln
		370					375					380				
	Val	Phe	Ala	Leu	Gly	His	Asn	Arg	Ser	Asp	Ser	Ala	Val	Thr	Gly	Ala
	385					390					395					400
	Thr	Leu	Glu	Ile	Ser	Ala	Trp	Asp	Ala	Ser	Ser	Glu	Ser	Phe	Leu	Gly
					405				410						415	
15	Gly	Val	Cys	Phe	Asp	Leu	Ser	Glu	Val	Pro	Val	Arg	Asp	Pro	Pro	Asp
				420					425					430		
	Ser	Pro	Leu	Ala	Pro	Gln	Trp	Tyr	Arg	Leu	Glu	Gly	Ser	Gly	Ala	Asp
			435					440					445			
20	Gln	Asn	Ser	Gly	Arg	Ile	Ser	Gly	Asp	Ile	Gln	Leu	Ser	Val	Trp	Ile
		450					455					460				
	Gly	Thr	Gln	Val	Asp	Glu	Ala	Phe	Pro	Glu	Ala	Trp	Ser	Ser	Asp	Ala
	465					470					475					480
	Pro	His	Val	Ala	His	Thr	Arg	Ser	Lys	Val	Tyr	Gln	Ser	Pro	Lys	Leu
					485					490					495	
25	Trp	Tyr	Leu	Arg	Val	Thr	Val	Leu	Glu	Ala	Gln	Asp	Leu	His	Ile	Ala
				500					505					510		
	Pro	Asn	Leu	Pro	Pro	Leu	Thr	Ala	Pro	Glu	Ile	Arg	Val	Lys	Ala	Gln
			515					520					525			
30	Leu	Gly	Phe	Gln	Ser	Ala	Arg	Thr	Arg	Arg	Gly	Ser	Met	Asn	Asn	His
		530					535					540				
	Ser	Gly	Ser	Phe	His	Trp	His	Glu	Asp	Met	Ile	Phe	Val	Ala	Gly	Glu
	545					550					555					560
	Pro	Leu	Glu	Asp	Cys	Leu	Val	Leu	Met	Val	Glu	Asp	Arg	Thr	Thr	Lys
					565					570					575	
35	Glu	Ala	Thr	Leu	Leu	Gly	His	Ala	Met	Ile	Pro	Val	Ser	Ser	Ile	Glu
				580					585					590		
	Gln	Arg	Ile	Asp	Glu	Arg	Phe	Val	Pro	Ser	Lys	Trp	His	Thr	Leu	Glu
			595					600					605			
40	Gly	Glu	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Pro	Gly	Gly	Gly	Gly
		610					615						620			
	Gly	Gly	Gly	Pro	Tyr	Cys	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Cys	Leu	Glu
	625					630					635					640
	Gly	Gly	Tyr	His	Val	Leu	Glu	Glu	Ala	Ala	His	Val	Cys	Ser	Asp	Phe
					645					650					655	
45	Arg	Pro	Thr	Ala	Lys	Gln	Leu	Trp	Lys	Pro	Pro	Ile	Gly	Ile	Leu	Glu
				660					665					670		
	Leu	Gly	Ile	Leu	Gly	Ala	Arg	Gly	Leu	Leu	Pro	Met	Lys	Ala	Lys	Asn
			675					680					685			
50	Gly	Gly	Lys	Gly	Ser	Thr	Asp	Ala	Tyr	Cys	Val	Ala	Lys	Tyr	Gly	Lys
		690					695					700				
	Lys	Trp	Val	Arg	Thr	Arg	Thr	Ile	Thr	Asp	Ser	Phe	Asp	Pro	Arg	Trp
	705					710					715					720
	His	Glu	Gln	Tyr	Thr	Trp	Gln	Val	Tyr	Asp	Pro	Cys	Thr	Val	Leu	Thr
					725					730					735	
55	Val	Gly	Val	Phe	Asp	Asn	Trp	Arg	Met	Phe	Ser	Asp	Ala	Ser	Asp	Asp
				740					745					750		
	Arg	Pro	Asp	Thr	Arg	Ile	Gly	Lys	Ile	Arg	Ile	Arg	Val	Ser	Thr	Leu
			755					760					765			
60	Glu	Ser	Asn	Lys	Val	Tyr	Thr	Asn	Ser	Tyr	Pro	Leu	Leu	Val	Leu	Leu
		770					775					780				
	Pro	Ser	Gly	Met	Lys	Lys	Met	Gly	Glu	Ile	Glu	Val	Ala	Val	Arg	Phe
	785					790					795					800

527

	Ala	Cys	Pro	Ser	Leu	Leu	Pro	Asp	Val	Cys	Ala	Ala	Tyr	Gly	Gln	Pro	
					805					810					815		
	Leu	Leu	Pro	Arg	Met	His	Tyr	Ile	Arg	Pro	Leu	Gly	Val	Ala	Gln	Gln	
				820					825					830			
5	Asp	Ala	Leu	Arg	Gly	Ala	Ala	Thr	Lys	Met	Val	Ala	Ala	Trp	Leu	Ala	
		835						840					845				
	Arg	Ala	Glu	Pro	Pro	Leu	Gly	Pro	Glu	Val	Val	Arg	Tyr	Met	Leu	Asp	
		850					855					860					
10	Ala	Asp	Ser	His	Ala	Trp	Ser	Met	Arg	Lys	Ser	Lys	Ala	Asn	Trp	Tyr	
	865					870					875					880	
	Arg	Ile	Val	Gly	Val	Leu	Ala	Trp	Ala	Val	Gly	Leu	Ala	Lys	Trp	Leu	
				885						890					895		
	Asp	Asn	Ile	Arg	Arg	Trp	Arg	Asn	Pro	Val	Thr	Thr	Val	Leu	Val	His	
				900					905					910			
15	Ile	Leu	Tyr	Leu	Val	Leu	Val	Trp	Tyr	Pro	Asp	Leu	Val	Val	Pro	Thr	
		915						920					925				
	Ala	Phe	Leu	Tyr	Val	Val	Met	Ile	Gly	Val	Trp	Tyr	Tyr	Arg	Phe	Arg	
		930					935					940					
20	Pro	Lys	Ile	Pro	Ala	Gly	Met	Asp	Ile	Arg	Leu	Ser	Gln	Ala	Glu	Thr	
	945					950					955					960	
	Val	Asp	Pro	Asp	Glu	Leu	Asp	Glu	Glu	Phe	Asp	Thr	Ile	Pro	Ser	Ser	
					965					970					975		
	Arg	Arg	Pro	Glu	Val	Ile	Arg	Ala	Arg	Tyr	Asp	Arg	Leu	Arg	Ile	Leu	
				980					985					990			
25	Ala	Val	Arg	Val	Gln	Thr	Ile	Leu	Gly	Asp	Phe	Ala	Ala	Gln	Gly	Glu	
		995						1000					1005				
	Arg	Ile	Gln	Ala	Leu	Val	Ser	Trp	Arg	Asp	Pro	Arg	Ala	Thr	Lys	Leu	
		1010					1015					1020					
30	Phe	Ile	Ala	Ile	Cys	Leu	Val	Ile	Thr	Ile	Val	Leu	Tyr	Ala	Val	Pro	
	1025					1030					1035					1040	
	Ala	Lys	Met	Val	Ala	Val	Ala	Leu	Gly	Val	Ser	Asp	Ser	Val	Pro	Thr	
					1045					1050					1055		
	Ala	Lys	Gln	Asp	Thr	Lys	Glu	Ser	Leu	Lys	Lys	Ser	Phe	Ser	Ser	Leu	
				1060					1065					1070			
35	Arg	Phe	Asp	Phe	Ser	Ser	Met	Ala	Val	Val	Gly	Ala	Pro	Ile	Ser	Ser	
		1075						1080					1085				
	Pro	Ala	Ala	Gln	Leu	Gln	Thr	Gln	Phe	Leu	Ser	Asn	Pro	Ile	Leu	Pro	
		1090					1095					1100					
40	Arg	Phe	Arg	Arg	Ser	Phe	Ser	Thr	Gly	Lys	Ser	Pro	Ala	Thr	Phe	Ser	
	1105					1110					1115					1120	
	Val	Val	Ala	Met	Ala	Pro	Gln	Lys	Lys	Val	Asn	Lys	Tyr	Asp	Ala	Lys	
					1125					1130					1135		
	Trp	Lys	Lys	Gln	Trp	Tyr	Gly	Ala	Gly	Leu	Phe	Phe	Glu	Gly	Ser	Glu	
				1140					1145					1150			
45	Gln	Ile	Asn	Val	Asp	Val	Phe	Lys	Lys	Leu	Glu	Lys	Arg	Lys	Val	Leu	
		1155						1160					1165				
	Ser	Asn	Val	Glu	Lys	Ser	Gly	Leu	Leu	Ser	Lys	Ala	Glu	Gly	Leu	Gly	
		1170					1175					1180					
50	Leu	Thr	Leu	Ser	Ser	Leu	Glu	Lys	Leu	Lys	Val	Phe	Ser	Lys	Ala	Glu	
	1185					1190					1195					1200	
	Asp	Leu	Gly	Leu	Leu	Ser	Leu	Leu	Glu	Asn	Leu	Ala	Gly	Thr	Ser	Pro	
					1205					1210					1215		
	Ala	Val	Leu	Ala	Ser	Ala	Ala	Leu	Pro	Ala	Leu	Thr	Ala	Ala	Ile	Val	
					1220				1225					1230			
55	Ala	Val	Val	Leu	Ile	Pro	Asp	Asp	Ser	Thr	Thr	Leu	Val	Val	Ala	Gln	
		1235						1240					1245				
	Ala	Val	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Thr	Gly	Val	Val	Leu	Leu	Val	
		1250					1255					1260					
60	Gly	Ser	Val	Val	Leu	Asp	Gly	Leu	Gln	Glu	Ala	Asp					
	1265					1270					1275						

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

528

(A) LENGTH: 1210 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..1210

(D) OTHER INFORMATION: / Ceres Seq. ID 2028731

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

Met	Leu	Asp	Phe	Ala	Val	Ser	Asp	Pro	Lys	Asn	Met	Asp	Tyr	Asp	Glu	1	5	10	15
Leu	Asp	Ile	Glu	Val	Tyr	Asn	Asp	Lys	Arg	Phe	Gly	Asn	Gly	Gly	Gly	20	25	30	
Arg	Lys	Asn	His	Phe	Leu	Gly	Arg	Val	Lys	Ile	Tyr	Gly	Ser	Gln	Phe	35	40	45	
Ser	Arg	Arg	Gly	Glu	Glu	Gly	Leu	Val	Tyr	Phe	Pro	Leu	Glu	Lys	Lys	50	55	60	
Ser	Val	Phe	Ser	Trp	Ile	Arg	Gly	Glu	Ile	Gly	Leu	Lys	Ile	Tyr	Tyr	65	70	75	80
Tyr	Asp	Glu	Ala	Ala	Asp	Glu	Asp	Thr	Ala	Gly	Gly	Gly	Gly	Gly	Gln	85	90	95	
Gln	Gln	Gln	Gln	Gln	Gln	Gln	Gln	Phe	His	Pro	Pro	Gln	Gln	Glu	Ala	100	105	110	
Asp	Glu	Gln	Gln	His	Gln	Gln	Gln	Phe	His	Pro	Pro	Pro	Gln	Gln	Met	115	120	125	
Met	Asn	Ile	Pro	Pro	Glu	Lys	Pro	Asn	Val	Val	Val	Val	Glu	Glu	Gly	130	135	140	
Arg	Val	Phe	Glu	Ser	Ala	Gln	Ser	Gln	Arg	Tyr	Thr	Glu	Thr	His	Gln	145	150	155	160
Gln	Pro	Pro	Val	Val	Ile	Val	Glu	Glu	Ser	Pro	Pro	Gln	His	Val	Met	165	170	175	
Gln	Gly	Pro	Asn	Asp	Asn	His	Pro	His	Arg	Asn	Asp	Asn	His	Pro	Gln	180	185	190	
Arg	Pro	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Ser	Ala	Gly	Glu	Val	His	Tyr	195	200	205	
Tyr	Pro	Pro	Glu	Val	Arg	Lys	Met	Gln	Val	Gly	Arg	Pro	Pro	Gly	Gly	210	215	220	
Asp	Arg	Ile	Arg	Val	Thr	Lys	Arg	Pro	Pro	Asn	Gly	Asp	Tyr	Ser	Pro	225	230	235	240
Arg	Val	Ile	Asn	Ser	Lys	Thr	Gly	Gly	Gly	Glu	Thr	Thr	Met	Glu	Lys	245	250	255	
Lys	Thr	His	His	Pro	Tyr	Asn	Leu	Val	Glu	Pro	Met	Gln	Tyr	Leu	Phe	260	265	270	
Val	Arg	Ile	Val	Lys	Ala	Arg	Gly	Leu	Pro	Pro	Asn	Glu	Ser	Ala	Tyr	275	280	285	
Val	Lys	Val	Arg	Thr	Ser	Asn	His	Phe	Val	Arg	Ser	Lys	Pro	Ala	Val	290	295	300	
Asn	Arg	Pro	Gly	Glu	Ser	Val	Asp	Ser	Pro	Glu	Trp	Asn	Gln	Val	Phe	305	310	315	320
Ala	Leu	Gly	His	Asn	Arg	Ser	Asp	Ser	Ala	Val	Thr	Gly	Ala	Thr	Leu	325	330	335	
Glu	Ile	Ser	Ala	Trp	Asp	Ala	Ser	Ser	Glu	Ser	Phe	Leu	Gly	Gly	Val	340	345	350	
Cys	Phe	Asp	Leu	Ser	Glu	Val	Pro	Val	Arg	Asp	Pro	Pro	Asp	Ser	Pro	355	360	365	
Leu	Ala	Pro	Gln	Trp	Tyr	Arg	Leu	Glu	Gly	Ser	Gly	Ala	Asp	Gln	Asn	370	375	380	
Ser	Gly	Arg	Ile	Ser	Gly	Asp	Ile	Gln	Leu	Ser	Val	Trp	Ile	Gly	Thr	385	390	395	400
Gln	Val	Asp	Glu	Ala	Phe	Pro	Glu	Ala	Trp	Ser	Ser	Asp	Ala	Pro	His	405	410	415	

529																
	Val	Ala	His	Thr	Arg	Ser	Lys	Val	Tyr	Gln	Ser	Pro	Lys	Leu	Trp	Tyr
				420					425					430		
	Leu	Arg	Val	Thr	Val	Leu	Glu	Ala	Gln	Asp	Leu	His	Ile	Ala	Pro	Asn
			435					440					445			
5	Leu	Pro	Pro	Leu	Thr	Ala	Pro	Glu	Ile	Arg	Val	Lys	Ala	Gln	Leu	Gly
		450					455					460				
	Phe	Gln	Ser	Ala	Arg	Thr	Arg	Arg	Gly	Ser	Met	Asn	Asn	His	Ser	Gly
	465					470					475					480
10	Ser	Phe	His	Trp	His	Glu	Asp	Met	Ile	Phe	Val	Ala	Gly	Glu	Pro	Leu
					485					490					495	
	Glu	Asp	Cys	Leu	Val	Leu	Met	Val	Glu	Asp	Arg	Thr	Thr	Lys	Glu	Ala
				500					505					510		
	Thr	Leu	Leu	Gly	His	Ala	Met	Ile	Pro	Val	Ser	Ser	Ile	Glu	Gln	Arg
			515					520					525			
15	Ile	Asp	Glu	Arg	Phe	Val	Pro	Ser	Lys	Trp	His	Thr	Leu	Glu	Gly	Glu
		530					535					540				
	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Pro	Gly	Gly	Gly	Gly	Gly	Gly
	545					550					555					560
20	Gly	Pro	Tyr	Cys	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Cys	Leu	Glu	Gly	Gly
					565					570					575	
	Tyr	His	Val	Leu	Glu	Glu	Ala	Ala	His	Val	Cys	Ser	Asp	Phe	Arg	Pro
				580					585					590		
	Thr	Ala	Lys	Gln	Leu	Trp	Lys	Pro	Pro	Ile	Gly	Ile	Leu	Glu	Leu	Gly
			595					600					605			
25	Ile	Leu	Gly	Ala	Arg	Gly	Leu	Leu	Pro	Met	Lys	Ala	Lys	Asn	Gly	Gly
		610					615					620				
	Lys	Gly	Ser	Thr	Asp	Ala	Tyr	Cys	Val	Ala	Lys	Tyr	Gly	Lys	Lys	Trp
	625					630					635					640
30	Val	Arg	Thr	Arg	Thr	Ile	Thr	Asp	Ser	Phe	Asp	Pro	Arg	Trp	His	Glu
					645					650					655	
	Gln	Tyr	Thr	Trp	Gln	Val	Tyr	Asp	Pro	Cys	Thr	Val	Leu	Thr	Val	Gly
				660					665					670		
	Val	Phe	Asp	Asn	Trp	Arg	Met	Phe	Ser	Asp	Ala	Ser	Asp	Asp	Arg	Pro
			675					680					685			
35	Asp	Thr	Arg	Ile	Gly	Lys	Ile	Arg	Ile	Arg	Val	Ser	Thr	Leu	Glu	Ser
		690					695					700				
	Asn	Lys	Val	Tyr	Thr	Asn	Ser	Tyr	Pro	Leu	Leu	Val	Leu	Leu	Pro	Ser
	705					710					715					720
40	Gly	Met	Lys	Lys	Met	Gly	Glu	Ile	Glu	Val	Ala	Val	Arg	Phe	Ala	Cys
					725					730					735	
	Pro	Ser	Leu	Leu	Pro	Asp	Val	Cys	Ala	Ala	Tyr	Gly	Gln	Pro	Leu	Leu
				740					745					750		
	Pro	Arg	Met	His	Tyr	Ile	Arg	Pro	Leu	Gly	Val	Ala	Gln	Gln	Asp	Ala
			755					760					765			
45	Leu	Arg	Gly	Ala	Ala	Thr	Lys	Met	Val	Ala	Ala	Trp	Leu	Ala	Arg	Ala
		770					775					780				
	Glu	Pro	Pro	Leu	Gly	Pro	Glu	Val	Val	Arg	Tyr	Met	Leu	Asp	Ala	Asp
	785					790					795					800
50	Ser	His	Ala	Trp	Ser	Met	Arg	Lys	Ser	Lys	Ala	Asn	Trp	Tyr	Arg	Ile
					805					810					815	
	Val	Gly	Val	Leu	Ala	Trp	Ala	Val	Gly	Leu	Ala	Lys	Trp	Leu	Asp	Asn
				820					825					830		
	Ile	Arg	Arg	Trp	Arg	Asn	Pro	Val	Thr	Thr	Val	Leu	Val	His	Ile	Leu
			835				840						845			
55	Tyr	Leu	Val	Leu	Val	Trp	Tyr	Pro	Asp	Leu	Val	Val	Pro	Thr	Ala	Phe
		850					855					860				
	Leu	Tyr	Val	Val	Met	Ile	Gly	Val	Trp	Tyr	Tyr	Arg	Phe	Arg	Pro	Lys
	865					870					875					880
60	Ile	Pro	Ala	Gly	Met	Asp	Ile	Arg	Leu	Ser	Gln	Ala	Glu	Thr	Val	Asp
					885					890					895	
	Pro	Asp	Glu	Leu	Asp	Glu	Glu	Phe	Asp	Thr	Ile	Pro	Ser	Ser	Arg	Arg
				900					905						910	

530

	Pro	Glu	Val	Ile	Arg	Ala	Arg	Tyr	Asp	Arg	Leu	Arg	Ile	Leu	Ala	Val	
			915					920					925				
	Arg	Val	Gln	Thr	Ile	Leu	Gly	Asp	Phe	Ala	Ala	Gln	Gly	Glu	Arg	Ile	
			930				935					940					
5	Gln	Ala	Leu	Val	Ser	Trp	Arg	Asp	Pro	Arg	Ala	Thr	Lys	Leu	Phe	Ile	
						950					955					960	
	Ala	Ile	Cys	Leu	Val	Ile	Thr	Ile	Val	Leu	Tyr	Ala	Val	Pro	Ala	Lys	
					965					970					975		
	Met	Val	Ala	Val	Ala	Leu	Gly	Val	Ser	Asp	Ser	Val	Pro	Thr	Ala	Lys	
10				980					985					990			
	Gln	Asp	Thr	Lys	Glu	Ser	Leu	Lys	Lys	Ser	Phe	Ser	Ser	Leu	Arg	Phe	
			995					1000					1005				
	Asp	Phe	Ser	Ser	Met	Ala	Val	Val	Gly	Ala	Pro	Ile	Ser	Ser	Pro	Ala	
			1010				1015					1020					
15	Ala	Gln	Leu	Gln	Thr	Gln	Phe	Leu	Ser	Asn	Pro	Ile	Leu	Pro	Arg	Phe	
						1030					1035					1040	
	Arg	Arg	Ser	Phe	Ser	Thr	Gly	Lys	Ser	Pro	Ala	Thr	Phe	Ser	Val	Val	
					1045					1050					1055		
	Ala	Met	Ala	Pro	Gln	Lys	Lys	Val	Asn	Lys	Tyr	Asp	Ala	Lys	Trp	Lys	
20				1060					1065					1070			
	Lys	Gln	Trp	Tyr	Gly	Ala	Gly	Leu	Phe	Phe	Glu	Gly	Ser	Glu	Gln	Ile	
			1075				1080					1085					
	Asn	Val	Asp	Val	Phe	Lys	Lys	Leu	Glu	Lys	Arg	Lys	Val	Leu	Ser	Asn	
			1090				1095					1100					
25	Val	Glu	Lys	Ser	Gly	Leu	Leu	Ser	Lys	Ala	Glu	Gly	Leu	Gly	Leu	Thr	
					1110						1115					1120	
	Leu	Ser	Ser	Leu	Glu	Lys	Leu	Lys	Val	Phe	Ser	Lys	Ala	Glu	Asp	Leu	
					1125					1130					1135		
	Gly	Leu	Leu	Ser	Leu	Leu	Glu	Asn	Leu	Ala	Gly	Thr	Ser	Pro	Ala	Val	
30				1140					1145					1150			
	Leu	Ala	Ser	Ala	Ala	Leu	Pro	Ala	Leu	Thr	Ala	Ala	Ile	Val	Ala	Val	
			1155					1160					1165				
	Val	Leu	Ile	Pro	Asp	Asp	Ser	Thr	Thr	Leu	Val	Val	Ala	Gln	Ala	Val	
			1170				1175					1180					
35	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Thr	Gly	Val	Val	Leu	Leu	Val	Gly	Ser	
			1185				1190				1195					1200	
	Val	Val	Leu	Asp	Gly	Leu	Gln	Glu	Ala	Asp							
				1205						1210							

(2) INFORMATION FOR SEQ ID NO:403:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1199 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
- (A) NAME/KEY: peptide
 - (B) LOCATION: 1..1199
 - (D) OTHER INFORMATION: / Ceres Seq. ID 2028732
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:
- | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Asp | Tyr | Asp | Glu | Leu | Asp | Ile | Glu | Val | Tyr | Asn | Asp | Lys | Arg | Phe | | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | | |
| Gly | Asn | Gly | Gly | Gly | Arg | Lys | Asn | His | Phe | Leu | Gly | Arg | Val | Lys | Ile | | |
| | | 20 | | | | | 25 | | | | | 30 | | | | | |
| 55 | Tyr | Gly | Ser | Gln | Phe | Ser | Arg | Arg | Gly | Glu | Glu | Gly | Leu | Val | Tyr | Phe | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Pro | Leu | Glu | Lys | Lys | Ser | Val | Phe | Ser | Trp | Ile | Arg | Gly | Glu | Ile | Gly | | |
| | 50 | | | | | 55 | | | | 60 | | | | | | | |
| Leu | Lys | Ile | Tyr | Tyr | Tyr | Asp | Glu | Ala | Ala | Asp | Glu | Asp | Thr | Ala | Gly | | |
| 60 | | | | | 70 | | | | | 75 | | | | | 80 | | |
| Gly | Gly | Gly | Gly | Gln | Gln | Gln | Gln | Gln | Gln | Gln | Gln | Gln | Gln | Phe | His | Pro | |
| | | | | 85 | | | | | 90 | | | | | | 95 | | |

531																
	Pro	Gln	Gln	Glu	Ala	Asp	Glu	Gln	Gln	His	Gln	Gln	Gln	Phe	His	Pro
				100					105					110		
	Pro	Pro	Gln	Gln	Met	Met	Asn	Ile	Pro	Pro	Glu	Lys	Pro	Asn	Val	Val
			115					120					125			
5	Val	Val	Glu	Glu	Gly	Arg	Val	Phe	Glu	Ser	Ala	Gln	Ser	Gln	Arg	Tyr
		130					135					140				
	Thr	Glu	Thr	His	Gln	Gln	Pro	Pro	Val	Val	Ile	Val	Glu	Glu	Ser	Pro
	145					150					155					160
10	Pro	Gln	His	Val	Met	Gln	Gly	Pro	Asn	Asp	Asn	His	Pro	His	Arg	Asn
				165					170						175	
	Asp	Asn	His	Pro	Gln	Arg	Pro	Pro	Ser	Pro	Pro	Pro	Pro	Pro	Ser	Ala
				180					185						190	
	Gly	Glu	Val	His	Tyr	Tyr	Pro	Pro	Glu	Val	Arg	Lys	Met	Gln	Val	Gly
			195					200					205			
15	Arg	Pro	Pro	Gly	Gly	Asp	Arg	Ile	Arg	Val	Thr	Lys	Arg	Pro	Pro	Asn
		210				215						220				
	Gly	Asp	Tyr	Ser	Pro	Arg	Val	Ile	Asn	Ser	Lys	Thr	Gly	Gly	Gly	Glu
	225					230					235					240
20	Thr	Thr	Met	Glu	Lys	Lys	Thr	His	His	Pro	Tyr	Asn	Leu	Val	Glu	Pro
				245						250					255	
	Met	Gln	Tyr	Leu	Phe	Val	Arg	Ile	Val	Lys	Ala	Arg	Gly	Leu	Pro	Pro
				260					265					270		
	Asn	Glu	Ser	Ala	Tyr	Val	Lys	Val	Arg	Thr	Ser	Asn	His	Phe	Val	Arg
			275					280					285			
25	Ser	Lys	Pro	Ala	Val	Asn	Arg	Pro	Gly	Glu	Ser	Val	Asp	Ser	Pro	Glu
		290				295						300				
	Trp	Asn	Gln	Val	Phe	Ala	Leu	Gly	His	Asn	Arg	Ser	Asp	Ser	Ala	Val
	305					310					315					320
30	Thr	Gly	Ala	Thr	Leu	Glu	Ile	Ser	Ala	Trp	Asp	Ala	Ser	Ser	Glu	Ser
				325						330					335	
	Phe	Leu	Gly	Gly	Val	Cys	Phe	Asp	Leu	Ser	Glu	Val	Pro	Val	Arg	Asp
			340						345					350		
	Pro	Pro	Asp	Ser	Pro	Leu	Ala	Pro	Gln	Trp	Tyr	Arg	Leu	Glu	Gly	Ser
			355					360					365			
35	Gly	Ala	Asp	Gln	Asn	Ser	Gly	Arg	Ile	Ser	Gly	Asp	Ile	Gln	Leu	Ser
		370					375					380				
	Val	Trp	Ile	Gly	Thr	Gln	Val	Asp	Glu	Ala	Phe	Pro	Glu	Ala	Trp	Ser
	385					390					395					400
40	Ser	Asp	Ala	Pro	His	Val	Ala	His	Thr	Arg	Ser	Lys	Val	Tyr	Gln	Ser
				405						410					415	
	Pro	Lys	Leu	Trp	Tyr	Leu	Arg	Val	Thr	Val	Leu	Glu	Ala	Gln	Asp	Leu
			420						425					430		
	His	Ile	Ala	Pro	Asn	Leu	Pro	Pro	Leu	Thr	Ala	Pro	Glu	Ile	Arg	Val
			435					440					445			
45	Lys	Ala	Gln	Leu	Gly	Phe	Gln	Ser	Ala	Arg	Thr	Arg	Arg	Gly	Ser	Met
		450					455					460				
	Asn	Asn	His	Ser	Gly	Ser	Phe	His	Trp	His	Glu	Asp	Met	Ile	Phe	Val
	465					470					475					480
50	Ala	Gly	Glu	Pro	Leu	Glu	Asp	Cys	Leu	Val	Leu	Met	Val	Glu	Asp	Arg
				485						490				495		
	Thr	Thr	Lys	Glu	Ala	Thr	Leu	Leu	Gly	His	Ala	Met	Ile	Pro	Val	Ser
			500						505					510		
	Ser	Ile	Glu	Gln	Arg	Ile	Asp	Glu	Arg	Phe	Val	Pro	Ser	Lys	Trp	His
			515					520					525			
55	Thr	Leu	Glu	Gly	Glu	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Pro	Gly
		530					535						540			
	Gly	Gly	Gly	Gly	Gly	Gly	Pro	Tyr	Cys	Gly	Arg	Ile	Ser	Leu	Arg	Leu
	545					550					555					560
60	Cys	Leu	Glu	Gly	Gly	Tyr	His	Val	Leu	Glu	Glu	Ala	Ala	His	Val	Cys
				565						570					575	
	Ser	Asp	Phe	Arg	Pro	Thr	Ala	Lys	Gln	Leu	Trp	Lys	Pro	Pro	Ile	Gly
				580					585					590		

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	Ile	Leu	Glu	Leu	Gly	Ile	Leu	Gly	Ala	Arg	Gly	Leu	Leu	Pro	Met	Lys	
			595					600					605				
	Ala	Lys	Asn	Gly	Gly	Lys	Gly	Ser	Thr	Asp	Ala	Tyr	Cys	Val	Ala	Lys	
		610					615					620					
5	Tyr	Gly	Lys	Lys	Trp	Val	Arg	Thr	Arg	Thr	Ile	Thr	Asp	Ser	Phe	Asp	
	625					630					635					640	
	Pro	Arg	Trp	His	Glu	Gln	Tyr	Thr	Trp	Gln	Val	Tyr	Asp	Pro	Cys	Thr	
					645					650					655		
10	Val	Leu	Thr	Val	Gly	Val	Phe	Asp	Asn	Trp	Arg	Met	Phe	Ser	Asp	Ala	
				660					665						670		
	Ser	Asp	Asp	Arg	Pro	Asp	Thr	Arg	Ile	Gly	Lys	Ile	Arg	Ile	Arg	Val	
			675					680					685				
	Ser	Thr	Leu	Glu	Ser	Asn	Lys	Val	Tyr	Thr	Asn	Ser	Tyr	Pro	Leu	Leu	
			690				695					700					
15	Val	Leu	Leu	Pro	Ser	Gly	Met	Lys	Lys	Met	Gly	Glu	Ile	Glu	Val	Ala	
	705					710					715					720	
	Val	Arg	Phe	Ala	Cys	Pro	Ser	Leu	Leu	Pro	Asp	Val	Cys	Ala	Ala	Tyr	
					725					730					735		
20	Gly	Gln	Pro	Leu	Leu	Pro	Arg	Met	His	Tyr	Ile	Arg	Pro	Leu	Gly	Val	
				740					745					750			
	Ala	Gln	Gln	Asp	Ala	Leu	Arg	Gly	Ala	Ala	Thr	Lys	Met	Val	Ala	Ala	
			755					760					765				
	Trp	Leu	Ala	Arg	Ala	Glu	Pro	Pro	Leu	Gly	Pro	Glu	Val	Val	Arg	Tyr	
		770					775					780					
25	Met	Leu	Asp	Ala	Asp	Ser	His	Ala	Trp	Ser	Met	Arg	Lys	Ser	Lys	Ala	
	785					790					795					800	
	Asn	Trp	Tyr	Arg	Ile	Val	Gly	Val	Leu	Ala	Trp	Ala	Val	Gly	Leu	Ala	
					805					810					815		
30	Lys	Trp	Leu	Asp	Asn	Ile	Arg	Arg	Trp	Arg	Asn	Pro	Val	Thr	Thr	Val	
				820					825					830			
	Leu	Val	His	Ile	Leu	Tyr	Leu	Val	Leu	Val	Trp	Tyr	Pro	Asp	Leu	Val	
			835					840					845				
	Val	Pro	Thr	Ala	Phe	Leu	Tyr	Val	Val	Met	Ile	Gly	Val	Trp	Tyr	Tyr	
		850					855					860					
35	Arg	Phe	Arg	Pro	Lys	Ile	Pro	Ala	Gly	Met	Asp	Ile	Arg	Leu	Ser	Gln	
	865					870					875					880	
	Ala	Glu	Thr	Val	Asp	Pro	Asp	Glu	Leu	Asp	Glu	Glu	Phe	Asp	Thr	Ile	
					885					890					895		
40	Pro	Ser	Ser	Arg	Arg	Pro	Glu	Val	Ile	Arg	Ala	Arg	Tyr	Asp	Arg	Leu	
				900					905					910			
	Arg	Ile	Leu	Ala	Val	Arg	Val	Gln	Thr	Ile	Leu	Gly	Asp	Phe	Ala	Ala	
			915					920					925				
	Gln	Gly	Glu	Arg	Ile	Gln	Ala	Leu	Val	Ser	Trp	Arg	Asp	Pro	Arg	Ala	
		930					935					940					
45	Thr	Lys	Leu	Phe	Ile	Ala	Ile	Cys	Leu	Val	Ile	Thr	Ile	Val	Leu	Tyr	
	945					950					955					960	
	Ala	Val	Pro	Ala	Lys	Met	Val	Ala	Val	Ala	Leu	Gly	Val	Ser	Asp	Ser	
					965					970					975		
50	Val	Pro	Thr	Ala	Lys	Gln	Asp	Thr	Lys	Glu	Ser	Leu	Lys	Lys	Ser	Phe	
				980					985					990			
	Ser	Ser	Leu	Arg	Phe	Asp	Phe	Ser	Ser	Met	Ala	Val	Val	Gly	Ala	Pro	
			995					1000					1005				
	Ile	Ser	Ser	Pro	Ala	Ala	Gln	Leu	Gln	Thr	Gln	Phe	Leu	Ser	Asn	Pro	
		1010					1015					1020					
55	Ile	Leu	Pro	Arg	Phe	Arg	Arg	Ser	Phe	Ser	Thr	Gly	Lys	Ser	Pro	Ala	
	1025					1030					1035					1040	
	Thr	Phe	Ser	Val	Val	Ala	Met	Ala	Pro	Gln	Lys	Lys	Val	Asn	Lys	Tyr	
					1045					1050					1055		
60	Asp	Ala	Lys	Trp	Lys	Lys	Gln	Trp	Tyr	Gly	Ala	Gly	Leu	Phe	Phe	Glu	
				1060					1065					1070			
	Gly	Ser	Glu	Gln	Ile	Asn	Val	Asp	Val	Phe	Lys	Lys	Leu	Glu	Lys	Arg	
				1075				1080						1085			

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Lys Val Leu Ser Asn Val Glu Lys Ser Gly Leu Leu Ser Lys Ala Glu
 1090 1095 1100
 Gly Leu Gly Leu Thr Leu Ser Ser Leu Glu Lys Leu Lys Val Phe Ser
 1105 1110 1115 1120
 5 Lys Ala Glu Asp Leu Gly Leu Leu Ser Leu Leu Glu Asn Leu Ala Gly
 1125 1130 1135
 Thr Ser Pro Ala Val Leu Ala Ser Ala Ala Leu Pro Ala Leu Thr Ala
 1140 1145 1150
 10 Ala Ile Val Ala Val Val Leu Ile Pro Asp Asp Ser Thr Thr Leu Val
 1155 1160 1165
 Val Ala Gln Ala Val Leu Ala Gly Ala Leu Ala Leu Thr Gly Val Val
 1170 1175 1180
 Leu Leu Val Gly Ser Val Val Leu Asp Gly Leu Gln Glu Ala Asp
 1185 1190 1195
 15 (2) INFORMATION FOR SEQ ID NO:404:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..528
 25 (D) OTHER INFORMATION: / Ceres Seq. ID 2029079
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:
 aaaaaactca ctttcacttg cacaaagata aggaaaccat gtctgtgtca gcgatcctttg 60
 gtaccggaat cgtcaccgtc gctgcttctc cggttctccg ccaatttcaa gttccaaaat 120
 tgggtaatgg aggtggatta gggatggtga ttgagtgttc gtcgaggcca cagaagaaat 180
 30 cgacagctca tcacaggaag acgaggccga agaagactca gccttgggac attaagagaa 240
 agcctactgt gtatgtctct cttctctctc ttccggcgga atggagtcgc tttactcttg 300
 cttccaacga cggtggtgcc gccgttgctg cttctctctc cggagatttg gtttcaggct 360
 ctgcctagtt atatgagcta tctggtggtt tggttgtaat ctagtttgag agcttttggt 420
 ggtggttggt tctgttaatg tttttcagtt ttctgctgtc tgttttcttat tatccggttt 480
 35 atgtttggct ggtgaatgaa tgtcaatgga ccaaactgca attttttt
 (2) INFORMATION FOR SEQ ID NO:405:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 amino acids
 (B) TYPE: amino acid
 40 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 45 (B) LOCATION: 1..121
 (D) OTHER INFORMATION: / Ceres Seq. ID 2029080
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:
 Lys Thr His Phe His Leu His Lys Asp Lys Glu Thr Met Ser Val Ser
 1 5 10 15
 50 Ala Ile Phe Gly Thr Gly Ile Val Thr Val Ala Ala Ser Pro Val Leu
 20 25 30
 Arg Gln Phe Gln Val Pro Lys Leu Gly Asn Gly Gly Gly Leu Gly Met
 35 40 45
 Val Ile Glu Cys Ser Ser Arg Pro Gln Lys Lys Ser Thr Ala His His
 50 55 60
 Arg Lys Thr Arg Pro Lys Lys Thr Gln Pro Trp Asp Ile Lys Arg Lys
 65 70 75 80
 Pro Thr Val Tyr Ala Pro Leu Pro Pro Leu Pro Ala Glu Trp Ser Pro
 85 90 95
 60 Phe Thr Leu Ala Ser Asn Asp Gly Gly Ala Ala Val Ala Ala Ser Pro
 100 105 110
 Ala Gly Asp Leu Val Ser Gly Ser Ala

534

115 120
(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..109
(D) OTHER INFORMATION: / Ceres Seq. ID 2029081

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

Met Ser Val Ser Ala Ile Phe Gly Thr Gly Ile Val Thr Val Ala Ala
1 5 10 15
Ser Pro Val Leu Arg Gln Phe Gln Val Pro Lys Leu Gly Asn Gly Gly
20 25 30
Gly Leu Gly Met Val Ile Glu Cys Ser Ser Arg Pro Gln Lys Lys Ser
35 40 45
Thr Ala His His Arg Lys Thr Arg Pro Lys Lys Thr Gln Pro Trp Asp
50 55 60
Ile Lys Arg Lys Pro Thr Val Tyr Ala Pro Leu Pro Pro Leu Pro Ala
65 70 75 80
Glu Trp Ser Pro Phe Thr Leu Ala Ser Asn Asp Gly Gly Ala Ala Val
85 90 95
Ala Ala Ser Pro Ala Gly Asp Leu Val Ser Gly Ser Ala
100 105

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..74
(D) OTHER INFORMATION: / Ceres Seq. ID 2029082

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

Met Val Ile Glu Cys Ser Ser Arg Pro Gln Lys Lys Ser Thr Ala His
1 5 10 15
His Arg Lys Thr Arg Pro Lys Lys Thr Gln Pro Trp Asp Ile Lys Arg
20 25 30
Lys Pro Thr Val Tyr Ala Pro Leu Pro Pro Leu Pro Ala Glu Trp Ser
35 40 45
Pro Phe Thr Leu Ala Ser Asn Asp Gly Gly Ala Ala Val Ala Ala Ser
50 55 60
Pro Ala Gly Asp Leu Val Ser Gly Ser Ala
65 70

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..787
(D) OTHER INFORMATION: / Ceres Seq. ID 2029225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

agggattcta gggctttcct tcattgggtca gatcagacga cgttttacat cttcttcttc

60

535

5 ttcctcttcg atattcgta gtgtgtgtat tttggggaaa actttgtgag caaagagcga 120
 gaaaatgagc ggagccggtg agaaaatcgc ggatgtggct ttcaaagctt caaggactat 180
 cgattgggat ggtatggcta aggtccttgt cacagatgag gctcgtagag agttctctaa 240
 ccttcgtcgt gctttcgatg aggttaacac acagctccag accaaattta gtcaggaacc 300
 tgaacctata gattgggatt actataggaa gggatttgga gctggcattg ttgacaagta 360
 caaggaagct tatgacagca ttgagattcc aaagtacgtt gacaaagtta ctctgaata 420
 caagccaaag tttgatgctt tggttggtgga actgaaagaa gcagaacaga aatcgctcaa 480
 ggagtctgaa cggttggaga aagaaattgc tgatgtccaa gagatcagca aaaagctcag 540
 caccatgact gcagatgagt actttgagaa gcacccggaa ctcaaaaaga agtttgatga 600
 10 cgaaatccgt aatgacaact ggggatactg atcatgtttc tccatctccg gcttggaaag 660
 aaaactctct ttctctttct ctgttctctt actgtgattt tgtgagccaa tcataacaat 720
 aataagtaca ccattcactt aagcagtgtt gagatcttca ttccaaggaa gataaacgca 780
 tttgggtt

(2) INFORMATION FOR SEQ ID NO:409:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..168

(D) OTHER INFORMATION: / Ceres Seq. ID 2029226

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

Met Ser Gly Ala Gly Lys Lys Ile Ala Asp Val Ala Phe Lys Ala Ser
 1 5 10 15
 Arg Thr Ile Asp Trp Asp Gly Met Ala Lys Val Leu Val Thr Asp Glu
 20 25 30
 30 Ala Arg Arg Glu Phe Ser Asn Leu Arg Arg Ala Phe Asp Glu Val Asn
 35 40 45
 Thr Gln Leu Gln Thr Lys Phe Ser Gln Glu Pro Glu Pro Ile Asp Trp
 50 55 60
 Asp Tyr Tyr Arg Lys Gly Ile Gly Ala Gly Ile Val Asp Lys Tyr Lys
 35 65 70 75 80
 Glu Ala Tyr Asp Ser Ile Glu Ile Pro Lys Tyr Val Asp Lys Val Thr
 85 90 95
 Pro Glu Tyr Lys Pro Lys Phe Asp Ala Leu Leu Val Glu Leu Lys Glu
 100 105 110
 40 Ala Glu Gln Lys Ser Leu Lys Glu Ser Glu Arg Leu Glu Lys Glu Ile
 115 120 125
 Ala Asp Val Gln Glu Ile Ser Lys Lys Leu Ser Thr Met Thr Ala Asp
 130 135 140
 Glu Tyr Phe Glu Lys His Pro Glu Leu Lys Lys Lys Phe Asp Asp Glu
 45 145 150 155 160
 Ile Arg Asn Asp Asn Trp Gly Tyr
 165

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

55 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..145

(D) OTHER INFORMATION: / Ceres Seq. ID 2029227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

60 Met Ala Lys Val Leu Val Thr Asp Glu Ala Arg Arg Glu Phe Ser Asn
 1 5 10 15
 Leu Arg Arg Ala Phe Asp Glu Val Asn Thr Gln Leu Gln Thr Lys Phe

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20 25 30
 Ser Gln Glu Pro Glu Pro Ile Asp Trp Asp Tyr Tyr Arg Lys Gly Ile
 35 40 45
 Gly Ala Gly Ile Val Asp Lys Tyr Lys Glu Ala Tyr Asp Ser Ile Glu
 5 50 55 60
 Ile Pro Lys Tyr Val Asp Lys Val Thr Pro Glu Tyr Lys Pro Lys Phe
 65 70 75 80
 Asp Ala Leu Leu Val Glu Leu Lys Glu Ala Glu Gln Lys Ser Leu Lys
 85 90 95
 10 Glu Ser Glu Arg Leu Glu Lys Glu Ile Ala Asp Val Gln Glu Ile Ser
 100 105 110
 Lys Lys Leu Ser Thr Met Thr Ala Asp Glu Tyr Phe Glu Lys His Pro
 115 120 125
 15 Glu Leu Lys Lys Lys Phe Asp Asp Glu Ile Arg Asn Asp Asn Trp Gly
 130 135 140
 Tyr
 145

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1587 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1587

(D) OTHER INFORMATION: / Ceres Seq. ID 2029422

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

30 gtagtctctc tttttataac cacttctcga aaactgaaac ctttgtagag agaaccata 60
 gttcgataaa acattctttt tgcaactgag acttggaac ttggttttac tcaaagtaag 120
 atttcttctt gttgatgggtg ataagttcaa tatgatgaaa agtttggtta gtgcggttg 180
 aggaagacg gcgagggcat gtgatagctg cgtgaagagg cgggcacgtt ggtattgcgc 240
 agctgatgat gcctttcttt gccatgcttg tgacgggttc gtccactcgg caaacctct 300
 35 tgctcgtagg cagcagagag ttcgcttgaa atcggttagc gccggaaagt atcgccatgc 360
 ctgcgcgcct caccaagcca cgtggcatca gggatttaca cgtaaagctc ggacccacg 420
 tggaggcaag aagagccaca cgtggtttt tcatgatctt gtgccggaga tgagcacgga 480
 ggatcaagcg gagagttacg aggtggaaga gcagctcata tttagaggtgc cgggtgatga 540
 ctcatggtt gagagcaat gctttaacca atccctggag aaacagaatg agtttccaat 600
 40 gatgccctta agtttcaaga gtagtgacga agaagatgac gacaacgctg agagttgtct 660
 gaatggtttg ttccaaccg acatggaact agctcagttc acagctgacg tggagactct 720
 actcgggtga ggggatcgag agtttcattc catagaagaa ctagggttag gtgagatgtt 780
 aaagatcgaa aaagaggagg tggaggaaga gggagttgtg acaagagaag tgcgatgaca 840
 agatgaaggt gatgagacat cccatttga aataagcttt gactacgagt acacacacaa 900
 45 gaccacattc gatgaaggag aagaagatga gaaagaagac gtgatgaaga atgtgatgga 960
 gatgggagt aatgagatga gtggtgggat taaagaagag aagaaggaga aggctcttat 1020
 gcttagattg gactatgaat cagtcatttc cacttgggga ggccaaggga tcccatggac 1080
 cgcccggtg ccatctgaaa tagacctga catggtttgt ttccaaccc ataccatggg 1140
 tgaaagtga gcagaggctc atcatcaca ccacttccgc ggcctagggt tacacctagg 1200
 50 agatgctggg gatggaggaa gagaggctag ggtttcaaga taccgagaga aaaggaggac 1260
 aaggttggtc tccaagaaga taaggtacga ggtacgtaaa ttgaatgcag agaaaaggcc 1320
 tcgcatgaaa ggaaggttcg tcaagagatc ttcaattggt gttgctcact aaagaactta 1380
 attaattatg gatattaaat tactttgctc tcacttctgt tttttgttg tatagttttg 1440
 gtgattgta gctttctttt tctgcattca tagagaattt tgcacgtttt tgtgagctac 1500
 55 gtatgtacat aaatatatca ccaaaaaatg tgactatctt graagcactg atttatatag 1560
 tcgatataac gtgaattttg attgctg

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 406 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

537

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..406

(D) OTHER INFORMATION: / Ceres Seq. ID 2029423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

5 Met Met Lys Ser Leu Ala Ser Ala Val Gly Lys Thr Ala Arg Ala
 1 5 10 15
 10 Cys Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr Cys Ala Ala Asp
 20 25 30
 Asp Ala Phe Leu Cys His Ala Cys Asp Gly Ser Val His Ser Ala Asn
 35 40 45
 Pro Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys Ser Ala Ser Ala
 50 55 60
 15 Gly Lys Tyr Arg His Ala Ser Pro Pro His Gln Ala Thr Trp His Gln
 65 70 75 80
 Gly Phe Thr Arg Lys Ala Arg Thr Pro Arg Gly Gly Lys Lys Ser His
 85 90 95
 20 Thr Met Val Phe His Asp Leu Val Pro Glu Met Ser Thr Glu Asp Gln
 100 105 110
 Ala Glu Ser Tyr Glu Val Glu Glu Gln Leu Ile Phe Glu Val Pro Val
 115 120 125
 Met Asn Ser Met Val Glu Glu Gln Cys Phe Asn Gln Ser Leu Glu Lys
 130 135 140
 25 Gln Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu
 145 150 155 160
 Glu Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr
 165 170 175
 30 Asp Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly
 180 185 190
 Gly Gly Asp Arg Glu Phe His Ser Ile Glu Glu Leu Gly Leu Gly Glu
 195 200 205
 Met Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Gly Val Val Thr
 210 215 220
 35 Arg Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe Glu
 225 230 235 240
 Ile Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu Gly
 245 250 255
 40 Glu Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met Gly
 260 265 270
 Val Asn Glu Met Ser Gly Gly Ile Lys Glu Glu Lys Lys Glu Lys Ala
 275 280 285
 Leu Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly Gly
 290 295 300
 45 Gln Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu Asp
 305 310 315 320
 Met Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu Ala
 325 330 335
 50 His His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp Ala
 340 345 350
 Gly Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys Arg
 355 360 365
 Arg Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys Leu
 370 375 380
 55 Asn Ala Glu Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg Ser
 385 390 395 400
 Ser Ile Gly Val Ala His
 405

(2) INFORMATION FOR SEQ ID NO:413:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid

538

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..405

(D) OTHER INFORMATION: / Ceres Seq. ID 2029424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

5 Met Lys Ser Leu Ala Ser Ala Val Gly Gly Lys Thr Ala Arg Ala Cys
 10 1 5 10 15
 Asp Ser Cys Val Lys Arg Arg Ala Arg Trp Tyr Cys Ala Ala Asp Asp
 20 20 25 30
 Ala Phe Leu Cys His Ala Cys Asp Gly Ser Val His Ser Ala Asn Pro
 35 35 40 45
 15 Leu Ala Arg Arg His Glu Arg Val Arg Leu Lys Ser Ala Ser Ala Gly
 50 50 55 60
 Lys Tyr Arg His Ala Ser Pro Pro His Gln Ala Thr Trp His Gln Gly
 65 65 70 75 80
 20 Phe Thr Arg Lys Ala Arg Thr Pro Arg Gly Gly Lys Lys Ser His Thr
 85 90 95
 Met Val Phe His Asp Leu Val Pro Glu Met Ser Thr Glu Asp Gln Ala
 100 105 110
 Glu Ser Tyr Glu Val Glu Glu Gln Leu Ile Phe Glu Val Pro Val Met
 115 120 125
 25 Asn Ser Met Val Glu Glu Gln Cys Phe Asn Gln Ser Leu Glu Lys Gln
 130 135 140
 Asn Glu Phe Pro Met Met Pro Leu Ser Phe Lys Ser Ser Asp Glu Glu
 145 150 155 160
 30 Asp Asp Asp Asn Ala Glu Ser Cys Leu Asn Gly Leu Phe Pro Thr Asp
 165 170 175
 Met Glu Leu Ala Gln Phe Thr Ala Asp Val Glu Thr Leu Leu Gly Gly
 180 185 190
 Gly Asp Arg Glu Phe His Ser Ile Glu Glu Leu Gly Leu Gly Glu Met
 195 200 205
 35 Leu Lys Ile Glu Lys Glu Glu Val Glu Glu Glu Gly Val Val Thr Arg
 210 215 220
 Glu Val His Asp Gln Asp Glu Gly Asp Glu Thr Ser Pro Phe Glu Ile
 225 230 235 240
 40 Ser Phe Asp Tyr Glu Tyr Thr His Lys Thr Thr Phe Asp Glu Gly Glu
 245 250 255
 Glu Asp Glu Lys Glu Asp Val Met Lys Asn Val Met Glu Met Gly Val
 260 265 270
 Asn Glu Met Ser Gly Gly Ile Lys Glu Glu Lys Lys Glu Lys Ala Leu
 275 280 285
 45 Met Leu Arg Leu Asp Tyr Glu Ser Val Ile Ser Thr Trp Gly Gly Gln
 290 295 300
 Gly Ile Pro Trp Thr Ala Arg Val Pro Ser Glu Ile Asp Leu Asp Met
 305 310 315 320
 50 Val Cys Phe Pro Thr His Thr Met Gly Glu Ser Gly Ala Glu Ala His
 325 330 335
 His His Asn His Phe Arg Gly Leu Gly Leu His Leu Gly Asp Ala Gly
 340 345 350
 Asp Gly Gly Arg Glu Ala Arg Val Ser Arg Tyr Arg Glu Lys Arg Arg
 355 360 365
 55 Thr Arg Leu Phe Ser Lys Lys Ile Arg Tyr Glu Val Arg Lys Leu Asn
 370 375 380
 Ala Glu Lys Arg Pro Arg Met Lys Gly Arg Phe Val Lys Arg Ser Ser
 385 390 395 400
 60 Ile Gly Val Ala His
 405

(2) INFORMATION FOR SEQ ID NO:414:

(i) SEQUENCE CHARACTERISTICS:

539

(A) LENGTH: 309 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..309

(D) OTHER INFORMATION: / Ceres Seq. ID 2029425

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

Met	Val	Phe	His	Asp	Leu	Val	Pro	Glu	Met	Ser	Thr	Glu	Asp	Gln	Ala
1				5					10					15	
Glu	Ser	Tyr	Glu	Val	Glu	Glu	Gln	Leu	Ile	Phe	Glu	Val	Pro	Val	Met
			20					25					30		
Asn	Ser	Met	Val	Glu	Glu	Gln	Cys	Phe	Asn	Gln	Ser	Leu	Glu	Lys	Gln
		35					40					45			
Asn	Glu	Phe	Pro	Met	Met	Pro	Leu	Ser	Phe	Lys	Ser	Ser	Asp	Glu	Glu
	50					55					60				
Asp	Asp	Asp	Asn	Ala	Glu	Ser	Cys	Leu	Asn	Gly	Leu	Phe	Pro	Thr	Asp
65					70					75				80	
Met	Glu	Leu	Ala	Gln	Phe	Thr	Ala	Asp	Val	Glu	Thr	Leu	Leu	Gly	Gly
			85						90					95	
Gly	Asp	Arg	Glu	Phe	His	Ser	Ile	Glu	Glu	Leu	Gly	Leu	Gly	Glu	Met
			100					105					110		
Leu	Lys	Ile	Glu	Lys	Glu	Glu	Val	Glu	Glu	Gly	Val	Val	Thr	Arg	
		115					120					125			
Glu	Val	His	Asp	Gln	Asp	Glu	Gly	Asp	Glu	Thr	Ser	Pro	Phe	Glu	Ile
	130					135					140				
Ser	Phe	Asp	Tyr	Glu	Tyr	Thr	His	Lys	Thr	Thr	Phe	Asp	Glu	Gly	Glu
145					150					155				160	
Glu	Asp	Glu	Lys	Glu	Asp	Val	Met	Lys	Asn	Val	Met	Glu	Met	Gly	Val
			165					170						175	
Asn	Glu	Met	Ser	Gly	Gly	Ile	Lys	Glu	Glu	Lys	Lys	Glu	Lys	Ala	Leu
		180						185					190		
Met	Leu	Arg	Leu	Asp	Tyr	Glu	Ser	Val	Ile	Ser	Thr	Trp	Gly	Gly	Gln
		195					200					205			
Gly	Ile	Pro	Trp	Thr	Ala	Arg	Val	Pro	Ser	Glu	Ile	Asp	Leu	Asp	Met
	210					215					220				
Val	Cys	Phe	Pro	Thr	His	Thr	Met	Gly	Glu	Ser	Gly	Ala	Glu	Ala	His
225					230					235				240	
His	His	Asn	His	Phe	Arg	Gly	Leu	Gly	Leu	His	Leu	Gly	Asp	Ala	Gly
			245					250						255	
Asp	Gly	Gly	Arg	Glu	Ala	Arg	Val	Ser	Arg	Tyr	Arg	Glu	Lys	Arg	Arg
		260					265						270		
Thr	Arg	Leu	Phe	Ser	Lys	Lys	Ile	Arg	Tyr	Glu	Val	Arg	Lys	Leu	Asn
		275					280					285			
Ala	Glu	Lys	Arg	Pro	Arg	Met	Lys	Gly	Arg	Phe	Val	Lys	Arg	Ser	Ser
	290					295					300				
Ile	Gly	Val	Ala	His											

50 305

(2) INFORMATION FOR SEQ ID NO:415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1300 base pairs

(B) TYPE: nucleic acid

55 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1300

(D) OTHER INFORMATION: / Ceres Seq. ID 2029806

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

540

ctcaagtttc ttgcaattac ctacttacaa caaagcaact cgactcgaac aaacacatcc 60
 atggctcctt ctgcgcaacc tcttcctgtg agtgtttcgg atgaaaaata tgcgaatgtc 120
 aagtgggaag agttggcatt caagtttgrt cgtacggatt atatgtatgt tgcgaagtgc 180
 aatcatggag agagttttca agagggggaag attcttcctt ttgctgattt gcaacttaac 240
 5 ccttgcgctg ctgttcttca gtatggccag ggtttatatg aaggactgaa agcttacagg 300
 acagaagatg gtcggattct gctattccga ccagaccaa acggtctccg ccttcaagcc 360
 ggagctgaca gactctatat gccttatcct tcggtcgatc aattcgtctc cgccatcaaa 420
 caagttgctc ttgccaacaa gaaatggatt cctcctccgg ggaaaggaac attgtatatt 480
 aggctatct tgtttgggag tgggtccgatt cttggttcat ttcccattcc tgagaccacc 540
 10 ttcacagctt ttgcctgtcc tgttgagcgt tatcataagg ataactctgg tttgaatctg 600
 aaaatcgaag atcagtttccg tcgagctttt cctagtggaa ctggtggtgt gaagagcatc 660
 aaaaactatt gtccgtgttg gataccattg gcagaggcga aaaaacaagg tttctctgat 720
 attttgtttt tggatgctgc aactggcaaa aacattgaag aacttttccg agctaattgt 780
 tttatgctca agggcaatgt tgtatcgaca ccaacaattg caggaaactat tttgcccggg 840
 15 gtcactcgaa actgcgtaat ggaatttgtt cgtgatttcg gctaccaggc cgaggaaact 900
 acgattcctc tagtggactt tctcgatgct gacgaagcct tctgtactgg cactgcttcc 960
 attgtgacta gtattgcac cgtaacctt aaagacaaaa agaccggatt caaaacaggg 1020
 gaagaaacat tggctgcgaa gctatacgag acgttaagt ataccagac gggtcgggtc 1080
 gaggatacca agggatggac ggtggagatt gaccgccagg gctgaaagt gaaactgtaa 1140
 20 cttgatgcta aatatgtgtg tgtgtgtata caaaacttat gtaagaaaca tctgaagatg 1200
 tctctgatct ttgtgattgt gatgatcat catgtcctat cgttgcgatg tattttataa 1260
 atgttcgtct gtaagttatt taataactat ggctttttgc

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..374

(D) OTHER INFORMATION: / Ceres Seq. ID 2029807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

35 Leu Lys Phe Leu Ala Ile Thr Tyr Leu Gln Gln Ser Asn Ser Thr Arg
 1 5 10 15
 Thr Asn Thr Ser Met Ala Pro Ser Ala Gln Pro Leu Pro Val Ser Val
 20 25 30
 40 Ser Asp Glu Lys Tyr Ala Asn Val Lys Trp Glu Glu Leu Ala Phe Lys
 35 40 45
 Phe Val Arg Thr Asp Tyr Met Tyr Val Ala Lys Cys Asn His Gly Glu
 50 55 60
 Ser Phe Gln Glu Gly Lys Ile Leu Pro Phe Ala Asp Leu Gln Leu Asn
 65 70 75 80
 45 Pro Cys Ala Ala Val Leu Gln Tyr Gly Gln Gly Leu Tyr Glu Gly Leu
 85 90 95
 Lys Ala Tyr Arg Thr Glu Asp Gly Arg Ile Leu Leu Phe Arg Pro Asp
 100 105 110
 50 Gln Asn Gly Leu Arg Leu Gln Ala Gly Ala Asp Arg Leu Tyr Met Pro
 115 120 125
 Tyr Pro Ser Val Asp Gln Phe Val Ser Ala Ile Lys Gln Val Ala Leu
 130 135 140
 Ala Asn Lys Lys Trp Ile Pro Pro Pro Gly Lys Gly Thr Leu Tyr Ile
 145 150 155 160
 55 Arg Pro Ile Leu Phe Gly Ser Gly Pro Ile Leu Gly Ser Phe Pro Ile
 165 170 175
 Pro Glu Thr Thr Phe Thr Ala Phe Ala Cys Pro Val Gly Arg Tyr His
 180 185 190
 60 Lys Asp Asn Ser Gly Leu Asn Leu Lys Ile Glu Asp Gln Phe Arg Arg
 195 200 205
 Ala Phe Pro Ser Gly Thr Gly Gly Val Lys Ser Ile Thr Asn Tyr Cys
 210 215 220

541

Pro Val Trp Ile Pro Leu Ala Glu Ala Lys Lys Gln Gly Phe Ser Asp
 225 230 235 240
 Ile Leu Phe Leu Asp Ala Ala Thr Gly Lys Asn Ile Glu Glu Leu Phe
 245 250 255
 5 Ala Ala Asn Val Phe Met Leu Lys Gly Asn Val Val Ser Thr Pro Thr
 260 265 270
 Ile Ala Gly Thr Ile Leu Pro Gly Val Thr Arg Asn Cys Val Met Glu
 275 280 285
 10 Leu Cys Arg Asp Phe Gly Tyr Gln Val Glu Glu Arg Thr Ile Pro Leu
 290 295 300
 Val Asp Phe Leu Asp Ala Asp Glu Ala Phe Cys Thr Gly Thr Ala Ser
 305 310 315 320
 Ile Val Thr Ser Ile Ala Ser Val Thr Phe Lys Asp Lys Lys Thr Gly
 325 330 335
 15 Phe Lys Thr Gly Glu Glu Thr Leu Ala Ala Lys Leu Tyr Glu Thr Leu
 340 345 350
 Ser Asp Ile Gln Thr Gly Arg Val Glu Asp Thr Lys Gly Trp Thr Val
 355 360 365
 Glu Ile Asp Arg Gln Gly
 20 370
 (2) INFORMATION FOR SEQ ID NO:417:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 amino acids
 (B) TYPE: amino acid
 25 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 30 (B) LOCATION: 1..354
 (D) OTHER INFORMATION: / Ceres Seq. ID 2029808
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:
 Met Ala Pro Ser Ala Gln Pro Leu Pro Val Ser Val Ser Asp Glu Lys
 1 5 10 15
 35 Tyr Ala Asn Val Lys Trp Glu Glu Leu Ala Phe Lys Phe Val Arg Thr
 20 25 30
 Asp Tyr Met Tyr Val Ala Lys Cys Asn His Gly Glu Ser Phe Gln Glu
 35 40
 Gly Lys Ile Leu Pro Phe Ala Asp Leu Gln Leu Asn Pro Cys Ala Ala
 50 55 60
 Val Leu Gln Tyr Gly Gln Gly Leu Tyr Glu Gly Leu Lys Ala Tyr Arg
 65 70 75 80
 Thr Glu Asp Gly Arg Ile Leu Leu Phe Arg Pro Asp Gln Asn Gly Leu
 85 90 95
 45 Arg Leu Gln Ala Gly Ala Asp Arg Leu Tyr Met Pro Tyr Pro Ser Val
 100 105 110
 Asp Gln Phe Val Ser Ala Ile Lys Gln Val Ala Leu Ala Asn Lys Lys
 115 120 125
 Trp Ile Pro Pro Pro Gly Lys Gly Thr Leu Tyr Ile Arg Pro Ile Leu
 50 130 135 140
 Phe Gly Ser Gly Pro Ile Leu Gly Ser Phe Pro Ile Pro Glu Thr Thr
 145 150 155 160
 Phe Thr Ala Phe Ala Cys Pro Val Gly Arg Tyr His Lys Asp Asn Ser
 165 170 175
 55 Gly Leu Asn Leu Lys Ile Glu Asp Gln Phe Arg Arg Ala Phe Pro Ser
 180 185 190
 Gly Thr Gly Gly Val Lys Ser Ile Thr Asn Tyr Cys Pro Val Trp Ile
 195 200 205
 Pro Leu Ala Glu Ala Lys Lys Gln Gly Phe Ser Asp Ile Leu Phe Leu
 60 210 215 220
 Asp Ala Ala Thr Gly Lys Asn Ile Glu Glu Leu Phe Ala Ala Asn Val
 225 230 235 240

542

[illegible]

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..320

(D) OTHER INFORMATION: / Ceres Seq. ID 2029809

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

30	Met 1	Tyr	Val	Ala	Lys 5	Cys	Asn	His	Gly	Glu 10	Ser	Phe	Gln	Glu	Gly 15	Lys
	Ile	Leu	Pro	Phe 20	Ala	Asp	Leu	Gln	Leu 25	Asn	Pro	Cys	Ala	Ala 30	Val	Leu
	Gln	Tyr	Gly 35	Gln	Gly	Leu	Tyr	Glu 40	Gly	Leu	Lys	Ala	Tyr 45	Arg	Thr	Glu
35	Asp 50	Gly	Arg	Ile	Leu	Leu	Phe 55	Arg	Pro	Asp	Gln	Asn 60	Gly	Leu	Arg	Leu
	Gln 65	Ala	Gly	Ala	Asp 70	Arg	Leu	Tyr	Met	Pro	Tyr 75	Pro	Ser	Val	Asp 80	Gln
40	Phe	Val	Ser	Ala	Ile 85	Lys	Gln	Val	Ala 90	Leu	Ala	Asn	Lys	Lys 95	Trp	Ile
	Pro	Pro	Pro	Gly 100	Lys	Gly	Thr	Leu	Tyr 105	Ile	Arg	Pro	Ile	Leu 110	Phe	Gly
	Ser	Gly	Pro 115	Ile	Leu	Gly	Ser	Phe 120	Pro	Ile	Pro	Glu	Thr 125	Thr	Phe	Thr
45	Ala 130	Phe	Ala	Cys	Pro	Val	Gly 135	Arg	Tyr	His	Lys	Asp 140	Asn	Ser	Gly	Leu
	Asn 145	Leu	Lys	Ile	Glu	Asp 150	Gln	Phe	Arg	Arg	Ala	Phe 155	Pro	Ser	Gly 160	Thr
50	Gly	Gly	Val	Lys	Ser 165	Ile	Thr	Asn	Tyr	Cys 170	Pro	Val	Trp	Ile	Pro 175	Leu
	Ala	Glu	Ala	Lys 180	Lys	Gln	Gly	Phe	Ser 185	Asp	Ile	Leu	Phe	Leu 190	Asp	Ala
	Ala	Thr	Gly 195	Lys	Asn	Ile	Glu	Glu 200	Leu	Phe	Ala	Ala 205	Asn	Val	Phe	Met
55	Leu 210	Lys	Gly	Asn	Val	Val	Ser 215	Thr	Pro	Thr	Ile	Ala 220	Gly	Thr	Ile	Leu
	Pro 225	Gly	Val	Thr	Arg	Asn 230	Cys	Val	Met	Glu	Leu	Cys 235	Arg	Asp	Phe	Gly 240
	Tyr	Gln	Val	Glu	Glu 245	Arg	Thr	Ile	Pro	Leu	Val	Asp	Phe	Leu	Asp 255	Ala
60	Asp	Glu	Ala	Phe 260	Cys	Thr	Gly	Thr	Ala 265	Ser	Ile	Val	Thr	Ser 270	Ile	Ala

543

Ser Val Thr Phe Lys Asp Lys Lys Thr Gly Phe Lys Thr Gly Glu Glu
 275 280 285
 Thr Leu Ala Ala Lys Leu Tyr Glu Thr Leu Ser Asp Ile Gln Thr Gly
 290 295 300
 Arg Val Glu Asp Thr Lys Gly Trp Thr Val Glu Ile Asp Arg Gln Gly
 305 310 315 320

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 987 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..987
- (D) OTHER INFORMATION: / Ceres Seq. ID 2030038

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

```

atatctgaaa gactcaaaaa cctatcgtca tttatcttca acaggcggaa taacggagat      60
ggccgccatt acagctctca ctctccgttc tctgtttat ctcccatcat ctgccacaag      120
ccctagattc catggcttca ccaatcaacc accaccagct cgtctcttct tctctcttaa      180
ccccctccct tctctatcaa tccaaaaccc taaatccatc cgaatttccg catccgcttc      240
gccgataaca acaccaatcc tccagacgga gaagtcaaca gtcgggtcat cgacactcac      300
cgggtccact cggctctctc ctactctcgc ggctttagca atcgctgtaa ccagagtcct      360
agctcagaaa ctctctctcg caatccagac ttcaagtccc gtaatcgccg acgggttacg      420
attctctctc agtaccgccg gacctgtctt ctccgcgtct ctccgggata gtcctccggg      480
atacttgaac acgccgctga cggttggtgc ggtggggata aagaagtggc tagacattta      540
cagtggggta ttgctggtta gggttttgct gagttgggtc cctaatatcc cttgggaaag      600
acagcctttg tctgccatta gagatctctg tgatccttac ttgaatctct tcagaaacat      660
cattctctct atcttcgata cgcttgatgt tagtccattg ctgcttttcg cggttcttgg      720
tacacttgga tcgattgttc atggcagcac tgggtagaaa ttggaagact tgagctaatt      780
gttttggtga aacgttcaat tgggaaattt ctgcaacttg tttccctaga ttagggaaaa      840
atcagaattt gatgctgtgt tggatgctcg atgagagttg tgagctt at cgtttttgtt      900
gttctctttt tgactttgat tctgaataat gagatttttg gttgttgtaa atctcctaatt      960
tacaatgtca gactaccgtt tattgat

```

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..251
- (D) OTHER INFORMATION: / Ceres Seq. ID 2030039

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

Tyr Leu Lys Asp Ser Lys Thr Tyr Arg His Leu Ser Ser Thr Gly Gly
 1 5 10 15
 Ile Thr Glu Met Ala Ala Ile Thr Ala Leu Thr Leu Arg Ser Pro Val
 20 25 30
 Tyr Leu Pro Ser Ser Ala Thr Ser Pro Arg Phe His Gly Phe Thr Asn
 35 40 45
 Gln Pro Pro Pro Ala Arg Leu Phe Phe Pro Leu Asn Pro Phe Pro Ser
 50 55 60
 Leu Ser Ile Gln Asn Pro Lys Ser Ile Arg Ile Ser Ala Ser Ala Ser
 65 70 75 80
 Pro Ile Thr Thr Pro Ile Leu Gln Thr Glu Lys Ser Thr Ala Arg Ser
 85 90 95
 Ser Thr Leu Thr Gly Ser Thr Arg Ser Leu Ala Thr Leu Ala Ala Leu
 100 105 110
 Ala Ile Ala Val Thr Arg Val Leu Ala Gln Lys Leu Ser Leu Ala Ile

544

115 120 125
 Gln Thr Ser Ser Pro Val Ile Ala Asp Gly Leu Arg Phe Ser Leu Ser
 130 135 140
 Thr Ala Gly Pro Val Phe Phe Ala Ser Leu Arg Asp Arg Pro Pro Gly
 145 150 155 160
 Tyr Leu Asn Thr Pro Leu Thr Val Val Ala Val Gly Ile Lys Lys Trp
 165 170 175
 Leu Asp Ile Tyr Ser Gly Val Leu Met Val Arg Val Leu Leu Ser Trp
 180 185 190
 10 Phe Pro Asn Ile Pro Trp Glu Arg Gln Pro Leu Ser Ala Ile Arg Asp
 195 200 205
 Leu Cys Asp Pro Tyr Leu Asn Leu Phe Arg Asn Ile Ile Pro Pro Ile
 210 215 220
 Phe Asp Thr Leu Asp Val Ser Pro Leu Leu Ala Phe Ala Val Leu Gly
 15 225 230 235 240
 Thr Leu Gly Ser Ile Val His Gly Ser Thr Gly
 245 250

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..232

(D) OTHER INFORMATION: / Ceres Seq. ID 2030040

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

30 Met Ala Ala Ile Thr Ala Leu Thr Leu Arg Ser Pro Val Tyr Leu Pro
 1 5 10 15
 Ser Ser Ala Thr Ser Pro Arg Phe His Gly Phe Thr Asn Gln Pro Pro
 20 25 30
 35 Pro Ala Arg Leu Phe Phe Pro Leu Asn Pro Phe Pro Ser Leu Ser Ile
 35 40 45
 Gln Asn Pro Lys Ser Ile Arg Ile Ser Ala Ser Ala Ser Pro Ile Thr
 50 55 60
 Thr Pro Ile Leu Gln Thr Glu Lys Ser Thr Ala Arg Ser Ser Thr Leu
 65 70 75 80
 40 Thr Gly Ser Thr Arg Ser Leu Ala Thr Leu Ala Ala Leu Ala Ile Ala
 85 90 95
 Val Thr Arg Val Leu Ala Gln Lys Leu Ser Leu Ala Ile Gln Thr Ser
 100 105 110
 45 Ser Pro Val Ile Ala Asp Gly Leu Arg Phe Ser Leu Ser Thr Ala Gly
 115 120 125
 Pro Val Phe Phe Ala Ser Leu Arg Asp Arg Pro Pro Gly Tyr Leu Asn
 130 135 140
 Thr Pro Leu Thr Val Val Ala Val Gly Ile Lys Lys Trp Leu Asp Ile
 145 150 155 160
 50 Tyr Ser Gly Val Leu Met Val Arg Val Leu Leu Ser Trp Phe Pro Asn
 165 170 175
 Ile Pro Trp Glu Arg Gln Pro Leu Ser Ala Ile Arg Asp Leu Cys Asp
 180 185 190
 Pro Tyr Leu Asn Leu Phe Arg Asn Ile Ile Pro Pro Ile Phe Asp Thr
 195 200 205
 55 Leu Asp Val Ser Pro Leu Leu Ala Phe Ala Val Leu Gly Thr Leu Gly
 210 215 220
 Ser Ile Val His Gly Ser Thr Gly
 225 230

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 755 base pairs

545

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 5 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..755
 (D) OTHER INFORMATION: / Ceres Seq. ID 2031778
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

10	ccgcagaaaa	ccctattgct	cccctttgct	caagctcagt	gcctctttgc	agcgaaagct	60
	caaccaacaa	gacgatgatt	atctcagaga	acaatcgag	agagatctgc	aaataccttt	120
	tcaaagaggg	agtatgcttt	gctaagaagg	atttcaatct	cccaaagcat	ccgttgattg	180
	atgtaccaaaa	cctgcaagtg	attaagctca	tgcagagttt	caagtccaag	gagtacgtta	240
	gggagacatt	tgcgtggatg	cattattatt	ggtttctgac	taatgaagga	attgagttct	300
15	tgagaactta	tcttaacctt	ccttccgatg	ttgtccctgc	tactttgaag	aagctcgcta	360
	agcccgggtg	tcgctccctt	ggtggcccac	ctggatgatc	ccaaagagga	ccacctcgct	420
	ctgatggaga	ccgtcccaga	tttggtgacc	gtgatggata	ccgtggaggc	ccacgtgggtg	480
	gtgatgagaa	gggtggagct	ccagctgatt	tccagccgtc	tttccaagga	ggtggtggta	540
	ggcctggttt	tggccgtggt	gcaggcgggt	acagtgcagc	agcaccatct	ggttcagggt	600
20	tcccttgaaa	aatttgttgt	catattgcga	cgatggaagg	acagttttgt	ttttgttct	660
	agttctgttt	gtgtaatgca	aatctggaat	ctataatcta	tctattacct	tcaccttggt	720
	ttaaacgaac	aaatcctgta	gtttcaggat	tagtg			

(2) INFORMATION FOR SEQ ID NO:423:
 (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 201 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 30 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..201
 (D) OTHER INFORMATION: / Ceres Seq. ID 2031779
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

35	Ala	Glu	Asn	Pro	Ile	Ala	Pro	Leu	Cys	Ser	Ser	Ser	Val	Pro	Leu	Cys
	1			5					10						15	
	Ser	Glu	Ser	Ser	Thr	Asn	Lys	Thr	Met	Ile	Ile	Ser	Glu	Asn	Asn	Arg
				20					25					30		
	Arg	Glu	Ile	Cys	Lys	Tyr	Leu	Phe	Lys	Glu	Gly	Val	Cys	Phe	Ala	Lys
40			35					40					45			
	Lys	Asp	Phe	Asn	Leu	Pro	Lys	His	Pro	Leu	Ile	Asp	Val	Pro	Asn	Leu
		50					55					60				
	Gln	Val	Ile	Lys	Leu	Met	Gln	Ser	Phe	Lys	Ser	Lys	Glu	Tyr	Val	Arg
				70							75				80	
45	Glu	Thr	Phe	Ala	Trp	Met	His	Tyr	Tyr	Trp	Phe	Leu	Thr	Asn	Glu	Gly
				85						90				95		
	Ile	Glu	Phe	Leu	Arg	Thr	Tyr	Leu	Asn	Leu	Pro	Ser	Asp	Val	Val	Pro
				100					105					110		
	Ala	Thr	Leu	Lys	Lys	Ser	Ala	Lys	Pro	Gly	Gly	Arg	Pro	Phe	Gly	Gly
50				115					120				125			
	Pro	Pro	Gly	Asp	Arg	Gln	Arg	Gly	Pro	Pro	Arg	Ser	Asp	Gly	Asp	Arg
				130				135				140				
	Pro	Arg	Phe	Gly	Asp	Arg	Asp	Gly	Tyr	Arg	Gly	Gly	Pro	Arg	Gly	Gly
				145			150				155				160	
55	Asp	Glu	Lys	Gly	Gly	Ala	Pro	Ala	Asp	Phe	Gln	Pro	Ser	Phe	Gln	Gly
				165					170						175	
	Gly	Gly	Gly	Arg	Pro	Gly	Phe	Gly	Arg	Gly	Ala	Gly	Gly	Tyr	Ser	Ala
				180				185						190		
	Ala	Ala	Pro	Ser	Gly	Ser	Gly	Phe	Pro							
60				195				200								

(2) INFORMATION FOR SEQ ID NO:424:
 (i) SEQUENCE CHARACTERISTICS:

546

(A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..177
 (D) OTHER INFORMATION: / Ceres Seq. ID 2031780

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

Met	Ile	Ile	Ser	Glu	Asn	Asn	Arg	Arg	Glu	Ile	Cys	Lys	Tyr	Leu	Phe
1				5					10					15	
Lys	Glu	Gly	Val	Cys	Phe	Ala	Lys	Lys	Asp	Phe	Asn	Leu	Pro	Lys	His
			20					25				30			
15	Pro	Leu	Ile	Asp	Val	Pro	Asn	Leu	Gln	Val	Ile	Lys	Leu	Met	Gln
			35				40					45			
Phe	Lys	Ser	Lys	Glu	Tyr	Val	Arg	Glu	Thr	Phe	Ala	Trp	Met	His	Tyr
	50					55				60					
20	Tyr	Trp	Phe	Leu	Thr	Asn	Glu	Gly	Ile	Glu	Phe	Leu	Arg	Thr	Tyr
	65					70				75					80
Asn	Leu	Pro	Ser	Asp	Val	Val	Pro	Ala	Thr	Leu	Lys	Lys	Ser	Ala	Lys
				85					90					95	
Pro	Gly	Gly	Arg	Pro	Phe	Gly	Gly	Pro	Pro	Gly	Asp	Arg	Gln	Arg	Gly
			100					105					110		
25	Pro	Pro	Arg	Ser	Asp	Gly	Asp	Arg	Pro	Arg	Phe	Gly	Asp	Arg	Gly
			115				120					125			
Tyr	Arg	Gly	Gly	Pro	Arg	Gly	Gly	Asp	Glu	Lys	Gly	Gly	Ala	Pro	Ala
	130					135					140				
30	Asp	Phe	Gln	Pro	Ser	Phe	Gln	Gly	Gly	Gly	Gly	Arg	Pro	Gly	Phe
	145					150					155				160
Arg	Gly	Ala	Gly	Gly	Tyr	Ser	Ala	Ala	Ala	Pro	Ser	Gly	Ser	Gly	Phe
				165					170					175	
	Pro														

35 (2) INFORMATION FOR SEQ ID NO:425:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..132
 (D) OTHER INFORMATION: / Ceres Seq. ID 2031781

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

Met	Gln	Ser	Phe	Lys	Ser	Lys	Glu	Tyr	Val	Arg	Glu	Thr	Phe	Ala	Trp
1				5					10					15	
Met	His	Tyr	Tyr	Trp	Phe	Leu	Thr	Asn	Glu	Gly	Ile	Glu	Phe	Leu	Arg
			20					25					30		
50	Thr	Tyr	Leu	Asn	Leu	Pro	Ser	Asp	Val	Val	Pro	Ala	Thr	Leu	Lys
			35				40					45			
Ser	Ala	Lys	Pro	Gly	Gly	Arg	Pro	Phe	Gly	Gly	Pro	Pro	Gly	Asp	Arg
	50					55					60				
55	Gln	Arg	Gly	Pro	Pro	Arg	Ser	Asp	Gly	Asp	Arg	Pro	Arg	Phe	Gly
	65					70					75				80
Arg	Asp	Gly	Tyr	Arg	Gly	Gly	Pro	Arg	Gly	Gly	Asp	Glu	Lys	Gly	Gly
				85					90					95	
Ala	Pro	Ala	Asp	Phe	Gln	Pro	Ser	Phe	Gln	Gly	Gly	Gly	Gly	Arg	Pro
			100					105					110		
60	Gly	Phe	Gly	Arg	Gly	Ala	Gly	Gly	Tyr	Ser	Ala	Ala	Ala	Pro	Ser
			115					120					125		

547

Ser Gly Phe Pro

130

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..538
 (D) OTHER INFORMATION: / Ceres Seq. ID 2032723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

```

15 aaagcaataa aaaacaaaaa tggcggtttac tccgaagatc atcacatgcc tcattgtcct      60
   tacgatctac atggcatccc caacagagtc aaccatccag tgtgggacag tgacgagcac      120
   actggcacag tgcctgacct acttgaccaa cagtgggtcca ttgccatcac aatgctgcgt      180
   gggagtcaag tcattgtacc aattggctca gaccacaccg gaccgtaaac aagtatgtga      240
   gtgccttaaa ctagcgggta aagaaatcaa gggcctcaac accgaccttg tggccgcact      300
20 tccctaccact tgtggtgttt caattcccta ccccatcagt tttagcacca attgcgacag      360
   tatatcgact gccgtgtgaa agaggctagt gatcagatgt acgactaatc aaacttgcca      420
   gcttttaacc taattaaata aaagtattct gcttatattt cccattttat gattttatct      480
   tcttatctat gtaaccacac gatttcatat gctaataatg acaacggatc tttctctc

```

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..119
 (D) OTHER INFORMATION: / Ceres Seq. ID 2032724

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

```

35 Met Ala Phe Thr Pro Lys Ile Ile Thr Cys Leu Ile Val Leu Thr Ile
   1           5           10           15
   Tyr Met Ala Ser Pro Thr Glu Ser Thr Ile Gln Cys Gly Thr Val Thr
           20           25           30
40 Ser Thr Leu Ala Gln Cys Leu Thr Tyr Leu Thr Asn Ser Gly Pro Leu
   35           40           45
   Pro Ser Gln Cys Cys Val Gly Val Lys Ser Leu Tyr Gln Leu Ala Gln
   50           55           60
   Thr Thr Pro Asp Arg Lys Gln Val Cys Glu Cys Leu Lys Leu Ala Gly
45 65           70           75           80
   Lys Glu Ile Lys Gly Leu Asn Thr Asp Leu Val Ala Ala Leu Pro Thr
           85           90           95
   Thr Cys Gly Val Ser Ile Pro Tyr Pro Ile Ser Phe Ser Thr Asn Cys
           100          105          110
50 Asp Ser Ile Ser Thr Ala Val
   115

```

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: / Ceres Seq. ID 2032725

548

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

Met Ala Ser Pro Thr Glu Ser Thr Ile Gln Cys Gly Thr Val Thr Ser
 1 5 10 15
 Thr Leu Ala Gln Cys Leu Thr Tyr Leu Thr Asn Ser Gly Pro Leu Pro
 20 25 30
 Ser Gln Cys Cys Val Gly Val Lys Ser Leu Tyr Gln Leu Ala Gln Thr
 35 40 45
 Thr Pro Asp Arg Lys Gln Val Cys Glu Cys Leu Lys Leu Ala Gly Lys
 50 55 60
 Glu Ile Lys Gly Leu Asn Thr Asp Leu Val Ala Ala Leu Pro Thr Thr
 65 70 75 80
 Cys Gly Val Ser Ile Pro Tyr Pro Ile Ser Phe Ser Thr Asn Cys Asp
 85 90 95
 Ser Ile Ser Thr Ala Val
 100

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 2032726

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

Lys Ala Ile Lys Asn Lys Asn Gly Val Tyr Ser Glu Asp His His Met
 1 5 10 15
 Pro His Cys Pro Tyr Asp Leu His Gly Ile Pro Asn Arg Val Asn His
 20 25 30
 Pro Val Trp Asp Ser Asp Glu His Thr Gly Thr Val Pro Asp Leu Leu
 35 40 45
 Asp Gln Gln Trp Ser Ile Ala Ile Thr Met Leu Arg Gly Ser Gln Val
 50 55 60
 Ile Val Pro Ile Gly Ser Asp His Thr Gly Pro
 65 70 75

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..198

(D) OTHER INFORMATION: / Ceres Seq. ID 2035536

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

atgtcggttg tatggttgga agcgatgttg cctctcggaa tcatcggttg gatgctctgt 60
 atcatgggca attctcagta ctacatccac aaagcttatt atggccgtcc taagcacatc 120
 ggccacgatg aatgggatgt tgctatggaa agacgcgaca agaaagtcgt cgagaaagct 180
 gcagctcctt cctcatga

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

549

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 2035537

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

5 Met Ser Leu Val Trp Leu Glu Ala Met Leu Pro Leu Gly Ile Ile Gly
 1 5 10 15
 Gly Met Leu Cys Ile Met Gly Asn Ser Gln Tyr Tyr Ile His Lys Ala
 20 25 30
 Tyr His Gly Arg Pro Lys His Ile Gly His Asp Glu Trp Asp Val Ala
 35 40 45
 10 Met Glu Arg Arg Asp Lys Lys Val Val Glu Lys Ala Ala Ala Pro Ser
 50 55 60

Ser
 65

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 2035538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

25 Cys Arg Trp Tyr Gly Trp Lys Arg Cys Cys Leu Ser Glu Ser Ser Val
 1 5 10 15
 Gly Cys Ser Val Ser Trp Ala Ile Leu Ser Thr Thr Ser Thr Lys Leu
 20 25 30
 30 Ile Met Ala Val Leu Ser Thr Ser Ala Thr Met Asn Gly Met Leu Leu
 35 40 45
 Trp Lys Asp Ala Thr Arg Lys Ser Ser Arg Lys Leu Gln Leu Leu Pro
 50 55 60

His
 65

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 2035539

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

50 Met Leu Pro Leu Gly Ile Ile Gly Gly Met Leu Cys Ile Met Gly Asn
 1 5 10 15
 Ser Gln Tyr Tyr Ile His Lys Ala Tyr His Gly Arg Pro Lys His Ile
 20 25 30
 Gly His Asp Glu Trp Asp Val Ala Met Glu Arg Arg Asp Lys Lys Val
 35 40 45
 55 Val Glu Lys Ala Ala Ala Pro Ser Ser
 50 55

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 573 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

550

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..573

(D) OTHER INFORMATION: / Ceres Seq. ID 2035575

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

```

atggagactt ctatgaggta taccagcaat tccaagtcta tgaagattca tgccaaagag      60
aagggtccgg tgaactcaaa aaccatttta cagcttcatg gagagttaga tactggaact      120
ggggctccga gttacttctg tgcgatgatt agacactttt ttcttgaggc ttcaacaggc      180
cttggggtag gattgcatta tgataagcgc caaaagcttc ggtgtcttgt acgcggaaaa      240
10 aaagagtttc ctgtaagagc tgataagcgt gtaaccttta atattaaagg gcggtgtgat      300
attgatcagg acttaaatca gaagaacccc aaaggagcag cagaatttgc ctggaacata      360
atggatttca aggaagatca ggatgtacgg atcaaagttg gctacgaaat gtttgataag      420
gtcccttata tgcagattag agaaaacaat tggactctca acgcgaacat gaagggaaaa      480
15 tggaaacttgc ggtatgacct gtaactgcat ttttttcaat catcatctga gaaatgtatt      540
gataccactg ctgatgaaca cattttaatt cta

```

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..167

(D) OTHER INFORMATION: / Ceres Seq. ID 2035576

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

```

Met Glu Thr Ser Met Arg Tyr Thr Ser Asn Ser Lys Ser Met Lys Ile
1      5      10      15
30 His Ala Lys Glu Lys Val Pro Val Asn Ser Lys Thr His Leu Gln Leu
      20      25      30
His Gly Glu Leu Asp Thr Gly Thr Gly Ala Pro Ser Tyr Phe Cys Ala
      35      40      45
35 Met Ile Arg His Phe Phe Pro Glu Ala Ser Thr Gly Leu Gly Val Gly
      50      55      60
Leu His Tyr Asp Lys Arg Gln Lys Leu Arg Cys Leu Val Arg Gly Lys
65      70      75      80
Lys Glu Phe Pro Val Arg Ala Asp Lys Arg Val Thr Phe Asn Ile Lys
      85      90      95
40 Gly Arg Cys Asp Ile Asp Gln Asp Leu Asn Gln Lys Asn Pro Lys Gly
      100      105      110
Ala Ala Glu Phe Ala Trp Asn Ile Met Asp Phe Lys Glu Asp Gln Asp
      115      120      125
45 Val Arg Ile Lys Val Gly Tyr Glu Met Phe Asp Lys Val Pro Tyr Met
      130      135      140
Gln Ile Arg Glu Asn Asn Trp Thr Leu Asn Ala Asn Met Lys Gly Lys
145      150      155      160
Trp Asn Leu Arg Tyr Asp Leu
      165

```

50 (2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..163

(D) OTHER INFORMATION: / Ceres Seq. ID 2035577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

```

Met Arg Tyr Thr Ser Asn Ser Lys Ser Met Lys Ile His Ala Lys Glu

```

551

	1		5		10		15
	Lys	Val	Pro	Val	Asn	Ser	Leu
			20		25		30
5	Asp	Thr	Gly	Thr	Gly	Ala	Pro
		35		40		45	
	Phe	Phe	Pro	Glu	Ala	Ser	Thr
		50		55		60	
	Lys	Arg	Gln	Lys	Leu	Arg	Cys
		65		70		75	
10	Val	Arg	Ala	Asp	Lys	Arg	Val
			85		90		95
	Ile	Asp	Gln	Asp	Leu	Asn	Gln
			100		105		110
	Ala	Trp	Asn	Ile	Met	Asp	Phe
15			115		120		125
	Val	Gly	Tyr	Glu	Met	Phe	Asp
		130		135		140	
	Asn	Asn	Trp	Thr	Leu	Asn	Ala
		145		150		155	
20	Tyr	Asp	Leu				

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..154

(D) OTHER INFORMATION: / Ceres Seq. ID 2035578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

35	Met	Lys	Ile	His	Ala	Lys	Glu	Lys	Val	Pro	Val	Asn	Ser	Lys	Thr	His
				5					10						15	
	Leu	Gln	Leu	His	Gly	Glu	Leu	Asp	Thr	Gly	Thr	Gly	Ala	Pro	Ser	Tyr
			20					25					30			
	Phe	Cys	Ala	Met	Ile	Arg	His	Phe	Phe	Pro	Glu	Ala	Ser	Thr	Gly	Leu
		35				40						45				
40	Gly	Val	Gly	Leu	His	Tyr	Asp	Lys	Arg	Gln	Lys	Leu	Arg	Cys	Leu	Val
		50				55						60				
	Arg	Gly	Lys	Lys	Glu	Phe	Pro	Val	Arg	Ala	Asp	Lys	Arg	Val	Thr	Phe
		65			70					75					80	
	Asn	Ile	Lys	Gly	Arg	Cys	Asp	Ile	Asp	Gln	Asp	Leu	Asn	Gln	Lys	Asn
45				85					90					95		
	Pro	Lys	Gly	Ala	Ala	Glu	Phe	Ala	Trp	Asn	Ile	Met	Asp	Phe	Lys	Glu
			100					105						110		
	Asp	Gln	Asp	Val	Arg	Ile	Lys	Val	Gly	Tyr	Glu	Met	Phe	Asp	Lys	Val
		115				120						125				
50	Pro	Tyr	Met	Gln	Ile	Arg	Glu	Asn	Asn	Trp	Thr	Leu	Asn	Ala	Asn	Met
		130				135						140				
	Lys	Gly	Lys	Trp	Asn	Leu	Arg	Tyr	Asp	Leu						
		145			150											

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 750 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

552

(B) LOCATION: 1..750

(D) OTHER INFORMATION: / Ceres Seq. ID 2036457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

```

5  atgacgactc agatcagcaa gaagagaaag tttgtagcgg acggtgtgtt ctacgctgaa      60
   ttgaatgagg ttcttacaag agagctagca gaggatgggt actctgggtg tgagggttagg      120
   gttactccta tgaggactga gattatcatc agagctacac gtactcagaa tgttctcggg      180
   gagaagggga ggagaattag ggaattgact tcccttggtc agaagagatt caagtttcca      240
   gttgacagtg ttgagcttta tgccgagaag gttaacaaca gaggtctctg tgccatcgct      300
   caggctgagt ctttacgtta caagcttctt ggtgggtctg ctgttcgtag ggcttgctat      360
10  ggtgtgttga ggtttgttat ggagagtgga gctaagggat gcgaggttat cgtgagtgga      420
   aagcttctgt ctgccagagc caagtctatg aagttcaaag atggctacat ggtgtcatct      480
   ggtcaaccaa ctaaggaata catagactct gcagtgaagc atgttttgct tagacaagggt      540
   gtgttgggaa tcaagggtgaa ggttatgctt gattgggacc ctaaggggcat atcaggacca      600
   aagacaccat tgcctgatgt tgtgatcatt cattctccta aagaagaaga ggccatctat      660
15  gcacctgctc aggttgctgc cccggctgct ctgtagcagc atgcaccact cacagccgta      720
   gattaccctg cgatgatccc agtcgcctaa

```

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

```

20  (A) LENGTH: 249 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS:
     (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```

25  (A) NAME/KEY: peptide
     (B) LOCATION: 1..249

```

(D) OTHER INFORMATION: / Ceres Seq. ID 2036458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

```

30  Met Thr Thr Gln Ile Ser Lys Lys Arg Lys Phe Val Ala Asp Gly Val
    1      5      10      15
    Phe Tyr Ala Glu Leu Asn Glu Val Leu Thr Arg Glu Leu Ala Glu Asp
        20      25      30
    Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Met Arg Thr Glu Ile
        35      40      45
35  Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu Gly Glu Lys Gly Arg
    50      55      60
    Arg Ile Arg Glu Leu Thr Ser Leu Val Gln Lys Arg Phe Lys Phe Pro
    65      70      75      80
    Val Asp Ser Val Glu Leu Tyr Ala Glu Lys Val Asn Asn Arg Gly Leu
    80      85      90      95
40  Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly
    100      105      110
    Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu Arg Phe Val Met Glu
    115      120      125
45  Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser Gly Lys Leu Arg Ala
    130      135      140
    Ala Arg Ala Lys Ser Met Lys Phe Lys Asp Gly Tyr Met Val Ser Ser
    145      150      155      160
    Gly Gln Pro Thr Lys Glu Tyr Ile Asp Ser Ala Val Arg His Val Leu
    165      170      175
50  Leu Arg Gln Gly Val Leu Gly Ile Lys Val Lys Val Met Leu Asp Trp
    180      185      190
    Asp Pro Lys Gly Ile Ser Gly Pro Lys Thr Pro Leu Pro Asp Val Val
    195      200      205
55  Ile Ile His Ser Pro Lys Glu Glu Glu Ala Ile Tyr Ala Pro Ala Gln
    210      215      220
    Val Ala Ala Pro Ala Ala Leu Val Ala Asp Ala Pro Leu Thr Ala Val
    225      230      235      240
    Asp Tyr Pro Ala Met Ile Pro Val Ala
    245
60

```

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

553

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 2036459

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

```

Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu
1      5      10      15
Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser Leu Val Gln Lys
20      25      30
Arg Phe Lys Phe Pro Val Asp Ser Val Glu Leu Tyr Ala Glu Lys Val
35      40      45
Asn Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr
50      55      60
Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu
65      70      75      80
Arg Phe Val Met Glu Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser
85      90      95
Gly Lys Leu Arg Ala Ala Arg Ala Lys Ser Met Lys Phe Lys Asp Gly
100      105      110
Tyr Met Val Ser Ser Gly Gln Pro Thr Lys Glu Tyr Ile Asp Ser Ala
115      120      125
Val Arg His Val Leu Leu Arg Gln Gly Val Leu Gly Ile Lys Val Lys
130      135      140
Val Met Leu Asp Trp Asp Pro Lys Gly Ile Ser Gly Pro Lys Thr Pro
145      150      155      160
Leu Pro Asp Val Val Ile Ile His Ser Pro Lys Glu Glu Glu Ala Ile
165      170      175
Tyr Ala Pro Ala Gln Val Ala Ala Pro Ala Ala Leu Val Ala Asp Ala
180      185      190
Pro Leu Thr Ala Val Asp Tyr Pro Ala Met Ile Pro Val Ala
195      200      205

```

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 549 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..549

(D) OTHER INFORMATION: / Ceres Seq. ID 2036585

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

```

atggtttctca agacggagct ttgtcgtttc agtggacaga agattttaccc aggaagagga      60
attaggttta tccgatctga ttctcaggtt ttcttggttc ttaactcaaa atgtaagagg      120
tacttccata acaagttgaa gccatccaag cttgcatgga ctgccatgta cagaaagcaa      180
cacaagaagg atgcagcaca agaggctgtg aagagaagga gacgtgccac caagaagcca      240
tactcaaggt ccattgttg tgctaccttg gaagtaattc agaagaagag agctgagaag      300
cctgaagttc gtgatgcagc caggaagct gctctgcgtg agatcaagga aagaatcaaa      360
aagaccaaag agtaaaagaa ggctaagaag gtggaatttg cttctaagca acagaaggtc      420
aaggctaatt tccccaaagc tgctgctgca tccaagggtc ctaagggtgt ggtggcaaac      480
gctgaagagc ttaaagccat cttttctcac tctgcgtctt ttctgctagt agctactttt      540
agtagttga

```

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 amino acids

(B) TYPE: amino acid

554

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..182

(D) OTHER INFORMATION: / Ceres Seq. ID 2036586

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

5 Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr
 10 1 5 10 15
 Pro Gly Arg Gly Ile Arg Phe Ile Arg Ser Asp Ser Gln Val Phe Leu
 20 20 25 30
 Phe Leu Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Lys Leu Lys Pro
 35 40 45
 15 Ser Lys Leu Ala Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp
 50 55 60
 Ala Ala Gln Glu Ala Val Lys Arg Arg Arg Arg Ala Thr Lys Lys Pro
 65 70 75 80
 Tyr Ser Arg Ser Ile Val Gly Ala Thr Leu Glu Val Ile Gln Lys Lys
 85 90 95
 20 Arg Ala Glu Lys Pro Glu Val Arg Asp Ala Ala Arg Glu Ala Ala Leu
 100 105 110
 Arg Glu Ile Lys Glu Arg Ile Lys Lys Thr Lys Asp Glu Lys Lys Ala
 115 120 125
 25 Lys Lys Val Glu Phe Ala Ser Lys Gln Gln Lys Val Lys Ala Asn Phe
 130 135 140
 Pro Lys Ala Ala Ala Ala Ser Lys Gly Pro Lys Val Val Val Ala Asn
 145 150 155 160
 30 Ala Glu Glu Leu Lys Ala Ile Phe Ser His Ser Ala Ser Phe Leu Leu
 165 170 175
 Val Ala Thr Phe Ser Ser
 180

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..127

(D) OTHER INFORMATION: / Ceres Seq. ID 2036587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

45 Met Tyr Arg Lys Gln His Lys Lys Asp Ala Ala Gln Glu Ala Val Lys
 1 5 10 15
 Arg Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
 20 25 30
 50 Ala Thr Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
 35 40 45
 Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
 50 55 60
 Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Val Glu Phe Ala Ser
 65 70 75 80
 55 Lys Gln Gln Lys Val Lys Ala Asn Phe Pro Lys Ala Ala Ala Ala Ser
 85 90 95
 Lys Gly Pro Lys Val Val Val Ala Asn Ala Glu Glu Leu Lys Ala Ile
 100 105 110
 60 Phe Ser His Ser Ala Ser Phe Leu Leu Val Ala Thr Phe Ser Ser
 115 120 125

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

555

- (A) LENGTH: 486 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..486
 (D) OTHER INFORMATION: / Ceres Seq. ID 2039554
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:
- | | | | | | | |
|---------------|------------|------------|------------|------------|-------------|-----|
| atggctgtcg | tccggcgtcc | aatatcgtct | cgggcggctc | agctgcagac | acaattttctc | 60 |
| tccaatccca | ttctcccccg | ctttcgccgg | tctttctcca | ccggaaaatc | accagcaact | 120 |
| ttctccgtcg | tagctatggc | tccccagaaa | aaggtgaaca | aatatgatgc | caagtggaag | 180 |
| aaacaatggg | acggagctgg | attgtttttc | gaagggagtg | agcaaataaa | cgttgatgtt | 240 |
| 15 ttcaagaagc | tggagaagcg | aaaagtgttg | agcaacgttg | agaaatctgg | cctgctgtca | 300 |
| aaagcagagg | ggttgggact | cacattgtca | tctcttgaga | agcttaaagt | cttctccaaa | 360 |
| gcagaggacc | ttggtcttct | cagtctcctt | gagaacttag | ctggaacatc | gcctgcgggc | 420 |
| ttagcctcgg | ctgcattacc | agctctcacg | agctgctatt | gtagccgtgg | tgttgatccc | 480 |
| ggatga | | | | | | |
- 20 (2) INFORMATION FOR SEQ ID NO:445:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 2039555
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:
- | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Val | Val | Gly | Ala | Pro | Ile | Ser | Ser | Pro | Ala | Ala | Gln | Leu | Gln |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Thr | Gln | Phe | Leu | Ser | Asn | Pro | Ile | Leu | Pro | Arg | Phe | Arg | Arg | Ser | Phe |
| 35 | | | 20 | | | | | 25 | | | | | 30 | | |
| Ser | Thr | Gly | Lys | Ser | Pro | Ala | Thr | Phe | Ser | Val | Val | Ala | Met | Ala | Pro |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| Gln | Lys | Lys | Val | Asn | Lys | Tyr | Asp | Ala | Lys | Trp | Lys | Lys | Gln | Trp | Tyr |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| 40 | Gly | Ala | Gly | Leu | Phe | Phe | Glu | Gly | Ser | Glu | Gln | Ile | Asn | Val | Asp |
| | 65 | | | | 70 | | | | | 75 | | | | 80 | |
| Phe | Lys | Lys | Leu | Glu | Lys | Arg | Lys | Val | Leu | Ser | Asn | Val | Glu | Lys | Ser |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Gly | Leu | Leu | Ser | Lys | Ala | Glu | Gly | Leu | Gly | Leu | Thr | Leu | Ser | Ser | Leu |
| | | | 100 | | | | 105 | | | | | 110 | | | |
| Glu | Lys | Leu | Lys | Val | Phe | Ser | Lys | Ala | Glu | Asp | Leu | Gly | Leu | Leu | Ser |
| | 115 | | | | | 120 | | | | | 125 | | | | |
| Leu | Leu | Glu | Asn | Leu | Ala | Gly | Thr | Ser | Pro | Ala | Val | Leu | Ala | Ser | Ala |
| | 130 | | | | 135 | | | | | 140 | | | | | |
| 50 | Ala | Leu | Pro | Ala | Leu | Thr | Ser | Cys | Tyr | Cys | Ser | Arg | Gly | Val | Asp |
| | 145 | | | | 150 | | | | | 155 | | | | 160 | |
| Gly | | | | | | | | | | | | | | | |
- (2) INFORMATION FOR SEQ ID NO:446:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 60 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide

556

(B) LOCATION: 1..116

(D) OTHER INFORMATION: / Ceres Seq. ID 2039556

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

5 Met Ala Pro Gln Lys Lys Val Asn Lys Tyr Asp Ala Lys Trp Lys Lys
 1 5 10 15
 Gln Trp Tyr Gly Ala Gly Leu Phe Phe Glu Gly Ser Glu Gln Ile Asn
 20 25 30
 Val Asp Val Phe Lys Lys Leu Glu Lys Arg Lys Val Leu Ser Asn Val
 35 40 45
 10 Glu Lys Ser Gly Leu Leu Ser Lys Ala Glu Gly Leu Gly Leu Thr Leu
 50 55 60
 Ser Ser Leu Glu Lys Leu Lys Val Phe Ser Lys Ala Glu Asp Leu Gly
 65 70 75 80
 Leu Leu Ser Leu Leu Glu Asn Leu Ala Gly Thr Ser Pro Ala Val Leu
 85 90 95
 15 Ala Ser Ala Ala Leu Pro Ala Leu Thr Ser Cys Tyr Cys Ser Arg Gly
 100 105 110
 Val Asp Pro Gly
 115

20 (2) INFORMATION FOR SEQ ID NO:447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..378

30 (D) OTHER INFORMATION: / Ceres Seq. ID 2044283

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

atggcggaatt tgatgatgag attaccaatt agcttgagaa gcttctctgt ttcagcttct 60
 tcatccaacg gttcgccgcc ggtgatcgga ggatctagcg gcggtgtagg accgatgatt 120
 gtggaattac cggttgagaa gatacgaaga ccgttgatgc gaaccagatc caacgatcag 180
 35 aacaaagtga aagagcttat ggatagtatc cgtcaaatacg gtcttcaagt tccgattgat 240
 gtgattgaag ttgatggaac ttactatggg ttctcgggat gtcacagata cgaggcgcat 300
 cagaagctag ggcttccaac tatacgttgc aaaatccgta aaggaacaaa ggaaacatta 360
 aggcattcatc ttcgctga

40 (2) INFORMATION FOR SEQ ID NO:448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..125

(D) OTHER INFORMATION: / Ceres Seq. ID 2044284

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

Met Ala Asn Leu Met Met Arg Leu Pro Ile Ser Leu Arg Ser Phe Ser
 1 5 10 15
 Val Ser Ala Ser Ser Ser Asn Gly Ser Pro Pro Val Ile Gly Gly Ser
 20 25 30
 55 Ser Gly Gly Val Gly Pro Met Ile Val Glu Leu Pro Leu Glu Lys Ile
 35 40 45
 Arg Arg Pro Leu Met Arg Thr Arg Ser Asn Asp Gln Asn Lys Val Lys
 50 55 60
 Glu Leu Met Asp Ser Ile Arg Gln Ile Gly Leu Gln Val Pro Ile Asp
 65 70 75 80
 60 Val Ile Glu Val Asp Gly Thr Tyr Tyr Gly Phe Ser Gly Cys His Arg
 85 90 95

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Tyr Glu Ala His Gln Lys Leu Gly Leu Pro Thr Ile Arg Cys Lys Ile
 100 105 110
 Arg Lys Gly Thr Lys Glu Thr Leu Arg His His Leu Arg
 115 120 125

5 (2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

10 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..121

15 (D) OTHER INFORMATION: / Ceres Seq. ID 2044285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

Met Met Arg Leu Pro Ile Ser Leu Arg Ser Phe Ser Val Ser Ala Ser
 1 5 10 15
 Ser Ser Asn Gly Ser Pro Pro Val Ile Gly Gly Ser Ser Gly Gly Val
 20 20 25 30
 Gly Pro Met Ile Val Glu Leu Pro Leu Glu Lys Ile Arg Arg Pro Leu
 35 40 45
 Met Arg Thr Arg Ser Asn Asp Gln Asn Lys Val Lys Glu Leu Met Asp
 50 55 60
 Ser Ile Arg Gln Ile Gly Leu Gln Val Pro Ile Asp Val Ile Glu Val
 25 65 70 75 80
 Asp Gly Thr Tyr Tyr Gly Phe Ser Gly Cys His Arg Tyr Glu Ala His
 85 90 95
 Gln Lys Leu Gly Leu Pro Thr Ile Arg Cys Lys Ile Arg Lys Gly Thr
 30 100 105 110
 Lys Glu Thr Leu Arg His His Leu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 2044286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

Met Arg Leu Pro Ile Ser Leu Arg Ser Phe Ser Val Ser Ala Ser Ser
 1 5 10 15
 Ser Asn Gly Ser Pro Pro Val Ile Gly Gly Ser Ser Gly Gly Val Gly
 20 25 30
 Pro Met Ile Val Glu Leu Pro Leu Glu Lys Ile Arg Arg Pro Leu Met
 35 40 45
 Arg Thr Arg Ser Asn Asp Gln Asn Lys Val Lys Glu Leu Met Asp Ser
 50 55 60
 Ile Arg Gln Ile Gly Leu Gln Val Pro Ile Asp Val Ile Glu Val Asp
 65 70 75 80
 Gly Thr Tyr Tyr Gly Phe Ser Gly Cys His Arg Tyr Glu Ala His Gln
 85 90 95
 Lys Leu Gly Leu Pro Thr Ile Arg Cys Lys Ile Arg Lys Gly Thr Lys
 100 105 110
 Glu Thr Leu Arg His His Leu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

558

(A) LENGTH: 1236 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1236

(D) OTHER INFORMATION: / Ceres Seq. ID 2048114

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

atgagaagac	ctagtcaa	gatgaggctt	ctattaacat	cctttttcgg	tgttattggt	60
ggtttcctta	tgggtattac	ttttccaacc	ttgacttta	ctaagatgaa	tcttccatcc	120
acattgtttc	cctcgattga	tcttgcatac	attgaggata	aatactctga	catatcaaga	180
caaagactat	ttggttcttg	gtcttcgaca	aaaggcctca	aactcaagaa	tgacatccct	240
gaccctccat	ataactataa	tgacactaag	ggtgatgata	gaacgttcga	gctattgcag	300
atatgggttt	cgactaacc	ccgtgggtgt	gagaggctac	caccagatat	agtcacgcct	360
gaatcagatt	tttacctccg	tcgactgttg	ggcgacccta	atgaggattt	aacagtcaag	420
cagcggtatc	tagtaacatt	tacggttggc	tatgatcaga	ggaaaaatat	agacactgtg	480
ttgaagaagt	tctcagataa	cttctctata	atgctgtttc	actacgatgg	ccgggcaagc	540
gaatgggaag	agtttgaatg	gtccaagcga	gccattcatg	tgagcattcg	gaaacaaaca	600
aaatggtggt	acgctaagcg	atcttctcat	cctgacatag	ttgcccccta	tgaatatatc	660
ttcatatggg	atgaggatct	tggcgtggaa	cactttgatt	cggaaaaata	tctggcgggtg	720
gtgaagaagc	atggttttga	aatctcacag	cctggattag	agccatatga	agggctcaca	780
tgggagatga	ccaagaaaag	agacgacact	gaagtccaca	agcatgctga	ggaaaggaat	840
gggtggtgca	ctgatcccaa	tttaccctct	tgtgcagcgt	ttgtggagat	tatggctcct	900
gttttctccc	gcaaggcatg	gcgctgtgtg	tggcatatga	ttcagaacga	tttgattcat	960
ggatgggggtc	tggaactttgc	cgttcggaaa	tgtgttcaga	acgcacacga	gaaaattgga	1020
gttgtagatg	ctcaatggat	tatacatcaa	ggtgttccat	cattagggaa	tcaaggacaa	1080
ccagagcaag	ggaacaacc	atgggaagg	gtgagagaac	gatgcaggag	agagtggaca	1140
atgtttcaag	acagattgga	tgatgctgaa	aaagcttatt	ttgaagcatc	tgctcacaag	1200
aatgcttctt	cacggcctca	cggaattgg	gtatag			

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..411

(D) OTHER INFORMATION: / Ceres Seq. ID 2048115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

Met	Arg	Arg	Pro	Ser	Gln	Met	Met	Arg	Leu	Leu	Thr	Ser	Phe	Phe
1			5					10				15		
Gly	Val	Ile	Val	Gly	Phe	Leu	Met	Gly	Ile	Thr	Phe	Pro	Thr	Leu
			20					25				30		
Leu	Thr	Lys	Met	Asn	Leu	Pro	Ser	Thr	Leu	Phe	Pro	Ser	Ile	Asp
			35					40				45		
Ala	Tyr	Ile	Glu	Asp	Lys	Tyr	Ser	Asp	Ile	Ser	Arg	Gln	Arg	Leu
			50					55				60		
Gly	Ser	Trp	Ser	Ser	Thr	Lys	Gly	Leu	Lys	Leu	Lys	Asn	Asp	Ile
			65					70				75		80
Asp	Pro	Pro	Tyr	Asn	Tyr	Asn	Asp	Thr	Lys	Val	Asp	Asp	Arg	Thr
			85					90				95		
Glu	Leu	Leu	Gln	Ile	Trp	Val	Ser	Thr	Asn	Pro	Arg	Gly	Ala	Glu
			100					105				110		
Leu	Pro	Pro	Asp	Ile	Val	Thr	Pro	Glu	Ser	Asp	Phe	Tyr	Leu	Arg
			115					120				125		
Leu	Trp	Gly	Asp	Pro	Asn	Glu	Asp	Leu	Thr	Val	Lys	Gln	Arg	Tyr
			130					135				140		
Val	Thr	Phe	Thr	Val	Gly	Tyr	Asp	Gln	Arg	Lys	Asn	Ile	Asp	Thr

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		145				150					155					160	
		Leu	Lys	Lys	Phe	Ser	Asp	Asn	Phe	Ser	Ile	Met	Leu	Phe	His	Tyr	Asp
						165					170					175	
5		Gly	Arg	Ala	Ser	Glu	Trp	Glu	Glu	Phe	Glu	Trp	Ser	Lys	Arg	Ala	Ile
					180					185					190		
		His	Val	Ser	Ile	Arg	Lys	Gln	Thr	Lys	Trp	Trp	Tyr	Ala	Lys	Arg	Phe
				195					200					205			
		Leu	His	Pro	Asp	Ile	Val	Ala	Pro	Tyr	Glu	Tyr	Ile	Phe	Ile	Trp	Asp
		210						215					220				
10		Glu	Asp	Leu	Gly	Val	Glu	His	Phe	Asp	Ser	Glu	Lys	Tyr	Leu	Ala	Val
		225					230					235					240
		Val	Lys	Lys	His	Gly	Leu	Glu	Ile	Ser	Gln	Pro	Gly	Leu	Glu	Pro	Tyr
					245						250					255	
15		Glu	Gly	Leu	Thr	Trp	Glu	Met	Thr	Lys	Lys	Arg	Asp	Asp	Thr	Glu	Val
					260					265					270		
		His	Lys	His	Ala	Glu	Glu	Arg	Asn	Gly	Trp	Cys	Thr	Asp	Pro	Asn	Leu
				275					280					285			
		Pro	Pro	Cys	Ala	Ala	Phe	Val	Glu	Ile	Met	Ala	Pro	Val	Phe	Ser	Arg
		290					295					300					
20		Lys	Ala	Trp	Arg	Cys	Val	Trp	His	Met	Ile	Gln	Asn	Asp	Leu	Ile	His
		305					310					315					320
		Gly	Trp	Gly	Leu	Asp	Phe	Ala	Val	Arg	Lys	Cys	Val	Gln	Asn	Ala	His
					325						330				335		
25		Glu	Lys	Ile	Gly	Val	Val	Asp	Ala	Gln	Trp	Ile	Ile	His	Gln	Gly	Val
					340					345					350		
		Pro	Ser	Leu	Gly	Asn	Gln	Gly	Gln	Pro	Glu	Gln	Gly	Lys	Gln	Pro	Trp
				355					360					365			
		Glu	Gly	Val	Arg	Glu	Arg	Cys	Arg	Arg	Glu	Trp	Thr	Met	Phe	Gln	Asp
		370					375						380				
30		Arg	Leu	Asp	Asp	Ala	Glu	Lys	Ala	Tyr	Phe	Glu	Ala	Ser	Ala	His	Lys
		385					390					395					400
		Asn	Ala	Ser	Ser	Arg	Pro	His	Gly	Asn	Trp	Val					
					405						410						

(2) INFORMATION FOR SEO ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..405

(D) OTHER INFORMATION: / Ceres Seq. ID 2048116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

	Met	Met	Arg	Leu	Leu	Leu	Thr	Ser	Phe	Phe	Gly	Val	Ile	Val	Gly	Phe
	1				5					10					15	
	Leu	Met	Gly	Ile	Thr	Phe	Pro	Thr	Leu	Thr	Leu	Thr	Lys	Met	Asn	Leu
				20					25					30		
50	Pro	Ser	Thr	Leu	Phe	Pro	Ser	Ile	Asp	Leu	Ala	Tyr	Ile	Glu	Asp	Lys
			35				40						45			
	Tyr	Ser	Asp	Ile	Ser	Arg	Gln	Arg	Leu	Phe	Gly	Ser	Trp	Ser	Ser	Thr
	50					55						60				
	Lys	Gly	Leu	Lys	Leu	Lys	Asn	Asp	Ile	Pro	Asp	Pro	Pro	Tyr	Asn	Tyr
55	65					70					75					80
	Asn	Asp	Thr	Lys	Val	Asp	Asp	Arg	Thr	Phe	Glu	Leu	Leu	Gln	Ile	Trp
				85						90					95	
	Val	Ser	Thr	Asn	Pro	Arg	Gly	Ala	Glu	Arg	Leu	Pro	Pro	Asp	Ile	Val
				100				105						110		
60	Thr	Pro	Glu	Ser	Asp	Phe	Tyr	Leu	Arg	Arg	Leu	Trp	Gly	Asp	Pro	Asn
			115				120						125			
	Glu	Asp	Leu	Thr	Val	Lys	Gln	Arg	Tyr	Leu	Val	Thr	Phe	Thr	Val	Gly

560

130 135 140
 Tyr Asp Gln Arg Lys Asn Ile Asp Thr Val Leu Lys Lys Phe Ser Asp
 145 150 155 160
 5 Asn Phe Ser Ile Met Leu Phe His Tyr Asp Gly Arg Ala Ser Glu Trp
 165 170 175
 Glu Glu Phe Glu Trp Ser Lys Arg Ala Ile His Val Ser Ile Arg Lys
 180 185 190
 Gln Thr Lys Trp Trp Tyr Ala Lys Arg Phe Leu His Pro Asp Ile Val
 195 200 205
 10 Ala Pro Tyr Glu Tyr Ile Phe Ile Trp Asp Glu Asp Leu Gly Val Glu
 210 215 220
 His Phe Asp Ser Glu Lys Tyr Leu Ala Val Val Lys Lys His Gly Leu
 225 230 235 240
 15 Glu Ile Ser Gln Pro Gly Leu Glu Pro Tyr Glu Gly Leu Thr Trp Glu
 245 250 255
 Met Thr Lys Lys Arg Asp Asp Thr Glu Val His Lys His Ala Glu Glu
 260 265 270
 Arg Asn Gly Trp Cys Thr Asp Pro Asn Leu Pro Pro Cys Ala Ala Phe
 275 280 285
 20 Val Glu Ile Met Ala Pro Val Phe Ser Arg Lys Ala Trp Arg Cys Val
 290 295 300
 Trp His Met Ile Gln Asn Asp Leu Ile His Gly Trp Gly Leu Asp Phe
 305 310 315 320
 25 Ala Val Arg Lys Cys Val Gln Asn Ala His Glu Lys Ile Gly Val Val
 325 330 335
 Asp Ala Gln Trp Ile Ile His Gln Gly Val Pro Ser Leu Gly Asn Gln
 340 345 350
 Gly Gln Pro Glu Gln Gly Lys Gln Pro Trp Glu Gly Val Arg Glu Arg
 355 360 365
 30 Cys Arg Arg Glu Trp Thr Met Phe Gln Asp Arg Leu Asp Asp Ala Glu
 370 375 380
 Lys Ala Tyr Phe Glu Ala Ser Ala His Lys Asn Ala Ser Ser Arg Pro
 385 390 395 400
 35 His Gly Asn Trp Val
 405
 (2) INFORMATION FOR SEQ ID NO:454:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 404 amino acids
 (B) TYPE: amino acid
 40 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 45 (B) LOCATION: 1..404
 (D) OTHER INFORMATION: / Ceres Seq. ID 2048117
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:
 Met Arg Leu Leu Leu Thr Ser Phe Phe Gly Val Ile Val Gly Phe Leu
 1 5 10 15
 50 Met Gly Ile Thr Phe Pro Thr Leu Thr Leu Thr Lys Met Asn Leu Pro
 20 25 30
 Ser Thr Leu Phe Pro Ser Ile Asp Leu Ala Tyr Ile Glu Asp Lys Tyr
 35 40 45
 55 Ser Asp Ile Ser Arg Gln Arg Leu Phe Gly Ser Trp Ser Ser Thr Lys
 50 55 60
 Gly Leu Lys Leu Lys Asn Asp Ile Pro Asp Pro Pro Tyr Asn Tyr Asn
 65 70 75 80
 Asp Thr Lys Val Asp Asp Arg Thr Phe Glu Leu Leu Gln Ile Trp Val
 85 90 95
 60 Ser Thr Asn Pro Arg Gly Ala Glu Arg Leu Pro Pro Asp Ile Val Thr
 100 105 110
 Pro Glu Ser Asp Phe Tyr Leu Arg Arg Leu Trp Gly Asp Pro Asn Glu

561

		115				120				125						
	Asp	Leu	Thr	Val	Lys	Gln	Arg	Tyr	Leu	Val	Thr	Phe	Thr	Val	Gly	Tyr
		130					135					140				
5	Asp	Gln	Arg	Lys	Asn	Ile	Asp	Thr	Val	Leu	Lys	Lys	Phe	Ser	Asp	Asn
	145				150					155					160	
	Phe	Ser	Ile	Met	Leu	Phe	His	Tyr	Asp	Gly	Arg	Ala	Ser	Glu	Trp	Glu
				165						170					175	
	Glu	Phe	Glu	Trp	Ser	Lys	Arg	Ala	Ile	His	Val	Ser	Ile	Arg	Lys	Gln
				180						185				190		
10	Thr	Lys	Trp	Trp	Tyr	Ala	Lys	Arg	Phe	Leu	His	Pro	Asp	Ile	Val	Ala
			195					200					205			
	Pro	Tyr	Glu	Tyr	Ile	Phe	Ile	Trp	Asp	Glu	Asp	Leu	Gly	Val	Glu	His
		210					215					220				
15	Phe	Asp	Ser	Glu	Lys	Tyr	Leu	Ala	Val	Val	Lys	Lys	His	Gly	Leu	Glu
	225				230						235				240	
	Ile	Ser	Gln	Pro	Gly	Leu	Glu	Pro	Tyr	Glu	Gly	Leu	Thr	Trp	Glu	Met
				245						250					255	
	Thr	Lys	Lys	Arg	Asp	Asp	Thr	Glu	Val	His	Lys	His	Ala	Glu	Glu	Arg
				260					265					270		
20	Asn	Gly	Trp	Cys	Thr	Asp	Pro	Asn	Leu	Pro	Pro	Cys	Ala	Ala	Phe	Val
			275					280					285			
	Glu	Ile	Met	Ala	Pro	Val	Phe	Ser	Arg	Lys	Ala	Trp	Arg	Cys	Val	Trp
		290					295					300				
25	His	Met	Ile	Gln	Asn	Asp	Leu	Ile	His	Gly	Trp	Gly	Leu	Asp	Phe	Ala
	305				310					315					320	
	Val	Arg	Lys	Cys	Val	Gln	Asn	Ala	His	Glu	Lys	Ile	Gly	Val	Val	Asp
				325						330					335	
	Ala	Gln	Trp	Ile	His	Gln	Gly	Val	Pro	Ser	Leu	Gly	Asn	Gln	Gly	
			340					345					350			
30	Gln	Pro	Glu	Gln	Gly	Lys	Gln	Pro	Trp	Glu	Gly	Val	Arg	Glu	Arg	Cys
			355					360					365			
	Arg	Arg	Glu	Trp	Thr	Met	Phe	Gln	Asp	Arg	Leu	Asp	Asp	Ala	Glu	Lys
		370					375					380				
35	Ala	Tyr	Phe	Glu	Ala	Ser	Ala	His	Lys	Asn	Ala	Ser	Ser	Arg	Pro	His
	385				390						395				400	
	Gly	Asn	Trp	Val												

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 649 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

45 (ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..649
 (D) OTHER INFORMATION: / Ceres Seq. ID 2048271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

50	ggaatttctc	actctctcta	tctctcttag	ccagctctga	tcatttcgat	ttttttccgg	60
	tgaaaaggga	ggagaaacat	ggttgtagct	atcagactgt	cgagatttgg	atgcaaaaat	120
	cggccatttt	ttaggggtat	ggctgctgat	agcagatctc	caagagacgg	gaagcatctt	180
	gaggtcttag	gttacttcaa	tcctttgcc	ggccaggacg	gtggtaagag	gatgggtctc	240
	aagttcgatc	gaattaagta	ctgggtatct	gttggtgctc	agccatcaga	cccggttcaa	300
55	cgtctcctat	tcagatccgg	tttacttcct	cctcctccaa	tggtggctat	gggacgtaaa	360
	ggtggagcac	gagacacacg	cccagttgat	ccgatgactg	gtcgctatgt	ggatgcagag	420
	aataaaacag	ttaatgccaa	tgataaccag	cctaaggaag	aggatacaga	agccaagagt	480
	gcatgattca	ttagccttct	gtcatcgtag	cttttcaagt	tcactttgtt	gtcgattata	540
	ttgtgtaatg	cagcattaga	caactgactt	gtttcctttg	tttggcgata	aacggcaagg	600
60	tgtttggcac	tttttgcaga	aacggcacat	attttgcatt	gggatattt		

(2) INFORMATION FOR SEQ ID NO:456:

(i) SEQUENCE CHARACTERISTICS:

562

- (A) LENGTH: 135 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..135
 (D) OTHER INFORMATION: / Ceres Seq. ID 2048272
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:
 Met Val Val Arg Ile Arg Leu Ser Arg Phe Gly Cys Lys Asn Arg Pro
 1 5 10 15
 Phe Phe Arg Val Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly Lys
 20 25 30
 15 His Leu Glu Val Leu Gly Tyr Phe Asn Pro Leu Pro Gly Gln Asp Gly
 35 40 45
 Gly Lys Arg Met Gly Leu Lys Phe Asp Arg Ile Lys Tyr Trp Leu Ser
 50 55 60
 20 Val Gly Ala Gln Pro Ser Asp Pro Val Gln Arg Leu Leu Phe Arg Ser
 65 70 75 80
 Gly Leu Leu Pro Pro Pro Pro Met Val Ala Met Gly Arg Lys Gly Gly
 85 90 95
 Ala Arg Asp Thr Arg Pro Val Asp Pro Met Thr Gly Arg Tyr Val Asp
 100 105 110
 25 Ala Glu Asn Lys Thr Val Asn Ala Asn Asp Asn Gln Pro Lys Glu Glu
 115 120 125
 Asp Thr Glu Ala Lys Ser Ala
 130 135
- (2) INFORMATION FOR SEQ ID NO:457:
 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..115
 (D) OTHER INFORMATION: / Ceres Seq. ID 2048273
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:
 Met Ala Ala Asp Ser Arg Ser Pro Arg Asp Gly Lys His Leu Glu Val
 1 5 10 15
 Leu Gly Tyr Phe Asn Pro Leu Pro Gly Gln Asp Gly Gly Lys Arg Met
 20 25 30
 45 Gly Leu Lys Phe Asp Arg Ile Lys Tyr Trp Leu Ser Val Gly Ala Gln
 35 40 45
 Pro Ser Asp Pro Val Gln Arg Leu Leu Phe Arg Ser Gly Leu Leu Pro
 50 55 60
 50 Pro Pro Pro Met Val Ala Met Gly Arg Lys Gly Gly Ala Arg Asp Thr
 65 70 75 80
 Arg Pro Val Asp Pro Met Thr Gly Arg Tyr Val Asp Ala Glu Asn Lys
 85 90 95
 Thr Val Asn Ala Asn Asp Asn Gln Pro Lys Glu Glu Asp Thr Glu Ala
 100 105 110
 55 Lys Ser Ala
 115
- (2) INFORMATION FOR SEQ ID NO:458:
 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

563

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..84

(D) OTHER INFORMATION: / Ceres Seq. ID 2048274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

Met Gly Leu Lys Phe Asp Arg Ile Lys Tyr Trp Leu Ser Val Gly Ala
 1 5 10 15
 Gln Pro Ser Asp Pro Val Gln Arg Leu Leu Phe Arg Ser Gly Leu Leu
 10 20 25 30
 Pro Pro Pro Pro Met Val Ala Met Gly Arg Lys Gly Gly Ala Arg Asp
 35 40 45
 Thr Arg Pro Val Asp Pro Met Thr Gly Arg Tyr Val Asp Ala Glu Asn
 50 55 60
 Lys Thr Val Asn Ala Asn Asp Asn Gln Pro Lys Glu Glu Asp Thr Glu
 15 65 70 75 80
 Ala Lys Ser Ala

(2) INFORMATION FOR SEQ ID NO:459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..285

(D) OTHER INFORMATION: / Ceres Seq. ID 2048331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

atgaaactgt gtaatcacca tactggaaag tttgtttcgg agagcgtcga agatcagact 60
 gagcaggtac tcaaaaacat gggggagata ttgaaagcta gtggtgctga ttattcctcg 120
 gtggtgaaga caacaatcat gttggctgat ttggctgact tcaagacagt gaacgagata 180
 tatgccaaat acttcccagc tccttctcca gcacgatcga cgtatcaagt tgcagctttg 240
 35 cctctaaacg ccaagatcga gattgaatgt attgcaacac tctag

(2) INFORMATION FOR SEQ ID NO:460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 2048332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

Met Lys Leu Cys Asn His His Thr Gly Lys Phe Val Ser Glu Ser Val
 1 5 10 15
 Glu Asp Gln Thr Glu Gln Val Leu Lys Asn Met Gly Glu Ile Leu Lys
 50 20 25 30
 Ala Ser Gly Ala Asp Tyr Ser Ser Val Val Lys Thr Thr Ile Met Leu
 35 40 45
 Ala Asp Leu Ala Asp Phe Lys Thr Val Asn Glu Ile Tyr Ala Lys Tyr
 55 50 55 60
 Phe Pro Ala Pro Ser Pro Ala Arg Ser Thr Tyr Gln Val Ala Ala Leu
 65 70 75 80
 Pro Leu Asn Ala Lys Ile Glu Ile Glu Cys Ile Ala Thr Leu
 85 90

(2) INFORMATION FOR SEQ ID NO:461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

564

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..68
 (D) OTHER INFORMATION: / Ceres Seq. ID 2048333
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

10	Met	Gly	Glu	Ile	Leu	Lys	Ala	Ser	Gly	Ala	Asp	Tyr	Ser	Ser	Val	Val
	1				5					10					15	
	Lys	Thr	Thr	Ile	Met	Leu	Ala	Asp	Leu	Ala	Asp	Phe	Lys	Thr	Val	Asn
				20					25					30		
15	Glu	Ile	Tyr	Ala	Lys	Tyr	Phe	Pro	Ala	Pro	Ser	Pro	Ala	Arg	Ser	Thr
			35					40					45			
	Tyr	Gln	Val	Ala	Ala	Leu	Pro	Leu	Asn	Ala	Lys	Ile	Glu	Ile	Glu	Cys
		50					55					60				
	Ile	Ala	Thr	Leu												
	65															

20 (2) INFORMATION FOR SEQ ID NO:462:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..48
 (D) OTHER INFORMATION: / Ceres Seq. ID 2048334
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

30	Met	Leu	Ala	Asp	Leu	Ala	Asp	Phe	Lys	Thr	Val	Asn	Glu	Ile	Tyr	Ala
	1				5					10					15	
35	Lys	Tyr	Phe	Pro	Ala	Pro	Ser	Pro	Ala	Arg	Ser	Thr	Tyr	Gln	Val	Ala
			20					25					30			
	Ala	Leu	Pro	Leu	Asn	Ala	Lys	Ile	Glu	Ile	Glu	Cys	Ile	Ala	Thr	Leu
		35					40					45				

(2) INFORMATION FOR SEQ ID NO:463:
 (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 627 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 45 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..627
 (D) OTHER INFORMATION: / Ceres Seq. ID 2048466
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

50	atgatggaca	agaatgaaaa	ccctagtttt	ttgctctctc	gaagttccgt	gcgactctct	60
	gctcgagcaa	gatctcctac	cgatacaatg	attatctcag	aggctaaccg	caaagaaatc	120
	tgcaagtacc	tcttcaaaga	aggagtttgc	tttgcgaaga	aggatttcaa	tcttgctaag	180
	catccgttga	tcgatgtccc	caacctacaa	gtgattaagc	ttatgcagag	tttcaaattc	240
	aaggagtatg	ttagggagac	atttgccctg	atgcattact	attgggtttt	gaccaatgaa	300
55	gggatcgagt	tcttgagaac	ttatcttaat	cttccatctg	atggtgttcc	tgctactttg	360
	aagaagtcag	ctaagcctgg	tggtcgtcca	tttgggtggc	cacctggtga	tcgctcaaga	420
	ggacctcgcc	atgaaggagg	agaccgtccc	aggtttggtg	accgtgatgg	gtaccgtgca	480
	ggtcctcgag	ctggtggtga	gtttggaggt	gaaaagggtg	gagctcccgc	agattaccag	540
	ccatctttcc	aaggaagtgg	ccgtggtttt	ggccgtggtg	ctggtggcta	cagcgcagct	600
60	gcaccatctg	gttcagggtt	gccttga				

(2) INFORMATION FOR SEQ ID NO:464:
 (i) SEQUENCE CHARACTERISTICS:

565

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..208

(D) OTHER INFORMATION: / Ceres Seq. ID 2048467

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

Met	Met	Asp	Lys	Asn	Glu	Asn	Pro	Ser	Phe	Leu	Leu	Ser	Arg	Ser	Ser
1				5					10					15	
Val	Arg	Leu	Ser	Ala	Arg	Ala	Arg	Ser	Pro	Thr	Asp	Thr	Met	Ile	Ile
			20					25					30		
Ser	Glu	Ala	Asn	Arg	Lys	Glu	Ile	Cys	Lys	Tyr	Leu	Phe	Lys	Glu	Gly
		35				40					45				
Val	Cys	Phe	Ala	Lys	Lys	Asp	Phe	Asn	Leu	Ala	Lys	His	Pro	Leu	Ile
	50					55					60				
Asp	Val	Pro	Asn	Leu	Gln	Val	Ile	Lys	Leu	Met	Gln	Ser	Phe	Lys	Ser
20	65				70				75					80	
Lys	Glu	Tyr	Val	Arg	Glu	Thr	Phe	Ala	Trp	Met	His	Tyr	Tyr	Trp	Phe
			85					90						95	
Leu	Thr	Asn	Glu	Gly	Ile	Glu	Phe	Leu	Arg	Thr	Tyr	Leu	Asn	Leu	Pro
			100					105					110		
Ser	Asp	Val	Val	Pro	Ala	Thr	Leu	Lys	Lys	Ser	Ala	Lys	Pro	Gly	Gly
		115					120					125			
Arg	Pro	Phe	Gly	Gly	Pro	Pro	Gly	Asp	Arg	Ser	Arg	Gly	Pro	Arg	His
	130						135					140			
Glu	Gly	Gly	Asp	Arg	Pro	Arg	Phe	Gly	Asp	Arg	Asp	Gly	Tyr	Arg	Ala
30	145				150				155					160	
Gly	Pro	Arg	Ala	Gly	Gly	Glu	Phe	Gly	Gly	Glu	Lys	Gly	Gly	Ala	Pro
			165					170						175	
Ala	Asp	Tyr	Gln	Pro	Ser	Phe	Gln	Gly	Ser	Gly	Arg	Gly	Phe	Gly	Arg
			180					185					190		
Gly	Ala	Gly	Gly	Tyr	Ser	Ala	Ala	Pro	Ser	Gly	Ser	Gly	Leu	Pro	
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..207

(D) OTHER INFORMATION: / Ceres Seq. ID 2048468

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

Met	Asp	Lys	Asn	Glu	Asn	Pro	Ser	Phe	Leu	Leu	Ser	Arg	Ser	Ser	Val
50	1			5					10					15	
Arg	Leu	Ser	Ala	Arg	Ala	Arg	Ser	Pro	Thr	Asp	Thr	Met	Ile	Ile	Ser
			20					25					30		
Glu	Ala	Asn	Arg	Lys	Glu	Ile	Cys	Lys	Tyr	Leu	Phe	Lys	Glu	Gly	Val
		35					40					45			
Cys	Phe	Ala	Lys	Lys	Asp	Phe	Asn	Leu	Ala	Lys	His	Pro	Leu	Ile	Asp
	50					55					60				
Val	Pro	Asn	Leu	Gln	Val	Ile	Lys	Leu	Met	Gln	Ser	Phe	Lys	Ser	Lys
	65				70					75				80	
Glu	Tyr	Val	Arg	Glu	Thr	Phe	Ala	Trp	Met	His	Tyr	Tyr	Trp	Phe	Leu
			85					90						95	
Thr	Asn	Glu	Gly	Ile	Glu	Phe	Leu	Arg	Thr	Tyr	Leu	Asn	Leu	Pro	Ser
			100					105					110		

566

Asp Val Val Pro Ala Thr Leu Lys Lys Ser Ala Lys Pro Gly Gly Arg
 115 120 125
 Pro Phe Gly Gly Pro Pro Gly Asp Arg Ser Arg Gly Pro Arg His Glu
 130 135 140
 5 Gly Gly Asp Arg Pro Arg Phe Gly Asp Arg Asp Gly Tyr Arg Ala Gly
 145 150 155 160
 Pro Arg Ala Gly Gly Glu Phe Gly Gly Glu Lys Gly Gly Ala Pro Ala
 165 170 175
 10 Asp Tyr Gln Pro Ser Phe Gln Gly Ser Gly Arg Gly Phe Gly Arg Gly
 180 185 190
 Ala Gly Gly Tyr Ser Ala Ala Ala Pro Ser Gly Ser Gly Leu Pro
 195 200 205

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 179 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..179

(D) OTHER INFORMATION: / Ceres Seq. ID 2048469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

25 Met Ile Ile Ser Glu Ala Asn Arg Lys Glu Ile Cys Lys Tyr Leu Phe
 1 5 10 15
 Lys Glu Gly Val Cys Phe Ala Lys Lys Asp Phe Asn Leu Ala Lys His
 20 25 30
 30 Pro Leu Ile Asp Val Pro Asn Leu Gln Val Ile Lys Leu Met Gln Ser
 35 40 45
 Phe Lys Ser Lys Glu Tyr Val Arg Glu Thr Phe Ala Trp Met His Tyr
 50 55 60
 Tyr Trp Phe Leu Thr Asn Glu Gly Ile Glu Phe Leu Arg Thr Tyr Leu
 65 70 75 80
 35 Asn Leu Pro Ser Asp Val Val Pro Ala Thr Leu Lys Lys Ser Ala Lys
 85 90 95
 Pro Gly Gly Arg Pro Phe Gly Gly Pro Pro Gly Asp Arg Ser Arg Gly
 100 105 110
 40 Pro Arg His Glu Gly Gly Asp Arg Pro Arg Phe Gly Asp Arg Asp Gly
 115 120 125
 Tyr Arg Ala Gly Pro Arg Ala Gly Gly Glu Phe Gly Gly Glu Lys Gly
 130 135 140
 Gly Ala Pro Ala Asp Tyr Gln Pro Ser Phe Gln Gly Ser Gly Arg Gly
 145 150 155 160
 45 Phe Gly Arg Gly Ala Gly Gly Tyr Ser Ala Ala Ala Pro Ser Gly Ser
 165 170 175
 Gly Leu Pro

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..585

(D) OTHER INFORMATION: / Ceres Seq. ID 2050485

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

60 atcttcggaa agtctcat ttcgatcccc aattcgtgga ttaggggttaa aagaaccatt 60
 tttattctcg tcgcgcaaca acaaatccag atcgaaaaag gaagaagaga tcgaaatggc 120

567

gttgagaagg gtttacagtg aaatcagagg gaagaagggtg acggagcttc caggctatat 180
 caaatcgact ttttcaatgg agaccgtgaa gacctctgtg aagagaggac tcgataacta 240
 caacgaaaaa tacattcaga ccagctccgt tgatcctatc cttcatatct gtttctacgg 300
 catggctttc tcttaccttg tcgctctccc taatgagcgt cgccatcttg agcatcagca 360
 5 gcatgctaag gaggacgggtg gtcattgatc tcgtgggaat cgtttcgatc tcgagatgat 420
 tttagggggg ttgctgtgaa atctttctct gcttgatggg gacgacgact caagaattgt 480
 gtcttattgt ttcgttttct tgaattttcc tggataatgt tgacctaaag gaaaaccttt 540
 ctttcgaatt acactccatg atagtcaata attgaagcat catga

(2) INFORMATION FOR SEQ ID NO:468:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 15 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..128
 (D) OTHER INFORMATION: / Ceres Seq. ID 2050486
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

Ser Ser Glu Ser Leu Ile Ser Arg Ser Pro Ile Arg Gly Leu Gly Leu
 1 5 10 15
 Lys Glu Pro Phe Leu Phe Ser Ser Arg Asn Asn Lys Ser Arg Ser Lys
 20 25 30
 25 Lys Glu Glu Glu Ile Glu Met Ala Leu Arg Arg Val Tyr Ser Glu Ile
 35 40 45
 Arg Gly Lys Lys Val Thr Glu Leu Pro Gly Tyr Ile Lys Ser Thr Phe
 50 55 60
 Ser Met Glu Thr Val Lys Thr Ser Val Lys Arg Gly Leu Asp Asn Tyr
 30 65 70 75 80
 Asn Glu Lys Tyr Ile Gln Thr Ser Ser Val Asp Pro Ile Leu His Ile
 85 90 95
 Cys Phe Tyr Gly Met Ala Phe Ser Tyr Leu Val Ala Leu Pro Asn Glu
 100 105 110
 35 Arg Arg His Leu Glu His Gln Gln His Ala Lys Glu His Gly Gly His
 115 120 125

(2) INFORMATION FOR SEQ ID NO:469:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 45 (A) NAME/KEY: peptide
 (B) LOCATION: 1..90
 (D) OTHER INFORMATION: / Ceres Seq. ID 2050487
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

Met Ala Leu Arg Arg Val Tyr Ser Glu Ile Arg Gly Lys Lys Val Thr
 1 5 10 15
 Glu Leu Pro Gly Tyr Ile Lys Ser Thr Phe Ser Met Glu Thr Val Lys
 20 25 30
 Thr Ser Val Lys Arg Gly Leu Asp Asn Tyr Asn Glu Lys Tyr Ile Gln
 35 40 45
 55 Thr Ser Ser Val Asp Pro Ile Leu His Ile Cys Phe Tyr Gly Met Ala
 50 55 60
 Phe Ser Tyr Leu Val Ala Leu Pro Asn Glu Arg Arg His Leu Glu His
 65 70 75 80
 Gln Gln His Ala Lys Glu His Gly Gly His
 85 90

(2) INFORMATION FOR SEQ ID NO:470:

- (i) SEQUENCE CHARACTERISTICS:

568

(A) LENGTH: 516 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..516
 (D) OTHER INFORMATION: / Ceres Seq. ID 2050708

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:
 caaccaaacc aaaacataaa aaacaagtgg aagcttttaa acgagagggga gagagcaaaa 60
 atggcgacgt cgggaacgta cgtgacggaa gttccgctaa aaggatcggc cgagaaatac 120
 tacaagaggt ggaagaacga gaaccatgtc ttccctgatg ctatcggcca ccacatccaa 180
 aatgttaccg ttcacgaagg cgaacatgac tctcacgggt ctatcaggag ttggaactac 240
 15 acatgggatg gaaaggagga ggtgttcaag gagagaagag agatagacga tgagacaaaa 300
 acgttgacgt taagaggact tgagggtcac gtgatggagc agctcaaagt gtacgacgtc 360
 gtctaccaat tcattcccaa atctgaggat acctgcatcg gcaaaatcac tttaatatgg 420
 gagaagcgca acgatgattc cccagaacca agcgggtaca tgaaattcgt caagagcttg 480
 gttgctgaca tgggaaacca cgtagcaaaa acttaa

20 (2) INFORMATION FOR SEQ ID NO:471:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..151
 (D) OTHER INFORMATION: / Ceres Seq. ID 2050709

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:
 Met Ala Thr Ser Gly Thr Tyr Val Thr Glu Val Pro Leu Lys Gly Ser
 1 5 10 15
 35 Ala Glu Lys Tyr Tyr Lys Arg Trp Lys Asn Glu Asn His Val Phe Pro
 20 25 30
 Asp Ala Ile Gly His His Ile Gln Asn Val Thr Val His Glu Gly Glu
 35 40 45
 His Asp Ser His Gly Ser Ile Arg Ser Trp Asn Tyr Thr Trp Asp Gly
 50 55 60
 40 Lys Glu Glu Val Phe Lys Glu Arg Arg Glu Ile Asp Asp Glu Thr Lys
 65 70 75 80
 Thr Leu Thr Leu Arg Gly Leu Glu Gly His Val Met Glu Gln Leu Lys
 85 90 95
 Val Tyr Asp Val Val Tyr Gln Phe Ile Pro Lys Ser Glu Asp Thr Cys
 45 100 105 110
 Ile Gly Lys Ile Thr Leu Ile Trp Glu Lys Arg Asn Asp Asp Ser Pro
 115 120 125
 Glu Pro Ser Gly Tyr Met Lys Phe Val Lys Ser Leu Val Ala Asp Met
 130 135 140
 50 Gly Asn His Val Ser Lys Thr
 145 150

(2) INFORMATION FOR SEQ ID NO:472:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1730 base pairs
 55 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 60 (A) NAME/KEY: -
 (B) LOCATION: 1..1730
 (D) OTHER INFORMATION: / Ceres Seq. ID 2050901

569

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

	atcgcgtggtt	actcctttct	aaaggaacca	ttgtatatca	tggaaggctt	gacttacttg	60
	aagcattctt	gctctccaag	ggattcacgg	ttccttctca	gctgaattct	cttgagtacg	120
	ctatggagat	acttcagaac	atccgtgata	cctacgaaaa	cgccaacatt	gctcttccag	180
5	accactgccc	tgaagtaaaa	aaacagaacc	aaaaacagag	cattgttcga	tataaaagct	240
	cgagaatcac	cgaaataagc	cttctctcta	gcagggtttg	gaagatcata	taccgtacaa	300
	ggcagttgct	tctaacaaac	atcttagaat	ctctttagt	cggtcttgct	ttaggcacta	360
	tctaccttaa	tatcggaact	ggcaaagaag	gaatcaggaa	acgatttggc	cttttcgcat	420
	tcaccctcac	attcctcctc	tcttccacta	cccaaaccct	tccaatattc	attgatgaac	480
10	gacctattct	tctccgagaa	acctcaagcg	gactctacag	actctcctct	cacattcttg	540
	caaacacttt	ggttttcttg	ccatacttgc	tactcatcgc	aatcatctac	tctgtctcac	600
	tctatttctt	tgtaggactc	tgcttttcat	ggcaagctct	cgcctacttt	gtgctcgtaa	660
	tctggatcat	tgtcctaata	gctaactctt	ttgtactttt	cttgagctct	ctcgcaccta	720
	actacattgc	tggaacatct	tcagtgaacca	ttcttcttgc	ggctttcttc	ttgttctctg	780
15	gttacttcat	ctctaaagag	agtcttccca	agtactggct	cttcatgtac	ttcttctcaa	840
	tgtacaagta	tgcgttggac	gcacttctga	taaataagta	ctcgtgtctg	cacaacaagt	900
	gcctgggtctg	gtttgaggaa	gcttctgtga	atagtctgct	agttactgga	ggtgacgtgt	960
	tagacaagaa	tgggcttcat	gagagacaga	ggatatatgt	gttgggacgt	ccgtcattgg	1020
	tatccgggtt	caaacttgag	aaacaaggaa	tacgtttctt	gagaagcaag	aaaaccctat	1080
20	tgctcccctt	tgtctcaagct	cagtgcctct	ttgcagcgaa	agctcaacca	acaagacgat	1140
	ggaattatcc	gagatattaat	tgtgatcttg	ttcgtccttt	tatcagatta	tctcagagaa	1200
	caatcgcala	gagatctgca	aatacctttt	caaagctagt	ggaaccagag	gtagtatgct	1260
	ttgctaagaa	ggatttcaat	ctcccaaagc	atccgttgat	tgatgtacca	aacctgcaag	1320
	tgattaagct	catgcagagt	ttcaagtcca	aggagtacgt	tagggagaca	tttgcgtgga	1380
25	tgcattatta	ttggtttctg	actaatgaag	gaattgagtt	cttgagaact	tatcttaacc	1440
	ttccttccga	tgttgccct	gctactttga	agaagtctgc	taagcccggg	ggtcgtccct	1500
	ttggtggccc	acctgggtgat	cgccaaagag	gaccacctcg	ctctgatgga	gaccgtccca	1560
	gatttggtga	ccgtgatgga	taccgtggag	gcccacgtgg	tggtgatgag	aagggtggag	1620
	ctccagctga	tttccagccg	tctttccaag	gaggtggtgg	taggcctggt	tttggccgtg	1680
30	gtgcaggcgg	ttacagtgca	gcagcaccat	ctggttcagg	gttcccttga		

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 575 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..575

(D) OTHER INFORMATION: / Ceres Seq. ID 2050902

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

	Arg	Val	Leu	Leu	Leu	Ser	Lys	Gly	Thr	Ile	Val	Tyr	His	Gly	Arg	Leu
	1				5					10					15	
45	Asp	Leu	Leu	Glu	Ala	Phe	Leu	Leu	Ser	Lys	Gly	Phe	Thr	Val	Pro	Ser
				20					25					30		
	Gln	Leu	Asn	Ser	Leu	Glu	Tyr	Ala	Met	Glu	Ile	Leu	Gln	Asn	Ile	Arg
			35					40					45			
50	Asp	Pro	Tyr	Glu	Asn	Ala	Asn	Ile	Ala	Leu	Pro	Asp	His	Cys	Pro	Glu
		50					55					60				
	Ser	Lys	Lys	Gln	Asn	Gln	Lys	Gln	Ser	Ile	Val	Arg	Tyr	Lys	Ser	Ser
		65				70					75				80	
	Arg	Ile	Thr	Glu	Ile	Ser	Leu	Leu	Ser	Ser	Arg	Phe	Trp	Lys	Ile	Ile
				85					90					95		
55	Tyr	Arg	Thr	Arg	Gln	Leu	Leu	Leu	Thr	Asn	Ile	Leu	Glu	Ser	Leu	Val
				100					105					110		
	Val	Gly	Leu	Val	Leu	Gly	Thr	Ile	Tyr	Leu	Asn	Ile	Gly	Thr	Gly	Lys
			115					120					125			
	Glu	Gly	Ile	Arg	Lys	Arg	Phe	Gly	Leu	Phe	Ala	Phe	Thr	Leu	Thr	Phe
60		130					135					140				
	Leu	Leu	Ser	Ser	Thr	Thr	Gln	Thr	Leu	Pro	Ile	Phe	Ile	Asp	Glu	Arg
		145				150				155					160	

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	Pro	Ile	Leu	Leu	Arg	Glu	Thr	Ser	Ser	Gly	Leu	Tyr	Arg	Leu	Ser	Ser
					165					170					175	
	His	Ile	Leu	Ala	Asn	Thr	Leu	Val	Phe	Leu	Pro	Tyr	Leu	Leu	Leu	Ile
				180					185					190		
5	Ala	Ile	Ile	Tyr	Ser	Val	Ser	Leu	Tyr	Phe	Leu	Val	Gly	Leu	Cys	Phe
			195				200						205			
	Ser	Trp	Gln	Ala	Leu	Ala	Tyr	Phe	Val	Leu	Val	Ile	Trp	Ile	Ile	Val
		210					215					220				
10	Leu	Met	Ala	Asn	Ser	Phe	Val	Leu	Phe	Leu	Ser	Ser	Leu	Ala	Pro	Asn
	225					230					235					240
	Tyr	Ile	Ala	Gly	Thr	Ser	Ser	Val	Thr	Ile	Leu	Leu	Ala	Ala	Phe	Phe
					245					250					255	
	Leu	Phe	Ser	Gly	Tyr	Phe	Ile	Ser	Lys	Glu	Ser	Leu	Pro	Lys	Tyr	Trp
				260					265					270		
15	Leu	Phe	Met	Tyr	Phe	Phe	Ser	Met	Tyr	Lys	Tyr	Ala	Leu	Asp	Ala	Leu
			275					280					285			
	Leu	Ile	Asn	Glu	Tyr	Ser	Cys	Leu	His	Asn	Lys	Cys	Leu	Val	Trp	Phe
		290					295					300				
20	Glu	Glu	Ala	Ser	Val	Asn	Ser	Cys	Leu	Val	Thr	Gly	Gly	Asp	Val	Leu
	305					310					315					320
	Asp	Lys	Asn	Gly	Leu	His	Glu	Arg	Gln	Arg	Ile	Tyr	Val	Leu	Gly	Arg
					325					330					335	
	Pro	Ser	Leu	Val	Ser	Gly	Phe	Lys	Leu	Glu	Lys	Gln	Gly	Ile	Arg	Phe
				340					345					350		
25	Leu	Arg	Ser	Lys	Lys	Thr	Leu	Leu	Leu	Pro	Phe	Ala	Gln	Ala	Gln	Cys
			355					360					365			
	Leu	Phe	Ala	Ala	Lys	Ala	Gln	Pro	Thr	Arg	Arg	Trp	Asn	Tyr	Pro	Ser
		370					375					380				
30	Ile	Asn	Cys	Asp	Leu	Val	Arg	Pro	Phe	Ile	Arg	Leu	Ser	Gln	Arg	Thr
	385					390					395					400
	Ile	Ala	Glu	Arg	Ser	Ala	Asn	Thr	Phe	Ser	Lys	Leu	Val	Glu	Pro	Glu
					405					410					415	
	Gly	Val	Cys	Phe	Ala	Lys	Lys	Asp	Phe	Asn	Leu	Pro	Lys	His	Pro	Leu
				420					425					430		
35	Ile	Asp	Val	Pro	Asn	Leu	Gln	Val	Ile	Lys	Leu	Met	Gln	Ser	Phe	Lys
		435						440					445			
	Ser	Lys	Glu	Tyr	Val	Arg	Glu	Thr	Phe	Ala	Trp	Met	His	Tyr	Tyr	Trp
		450					455					460				
40	Phe	Leu	Thr	Asn	Glu	Gly	Ile	Glu	Phe	Leu	Arg	Thr	Tyr	Leu	Asn	Leu
	465					470					475					480
	Pro	Ser	Asp	Val	Val	Pro	Ala	Thr	Leu	Lys	Lys	Ser	Ala	Lys	Pro	Gly
					485					490					495	
	Gly	Arg	Pro	Phe	Gly	Gly	Pro	Pro	Gly	Asp	Arg	Gln	Arg	Gly	Pro	Pro
				500					505					510		
45	Arg	Ser	Asp	Gly	Asp	Arg	Pro	Arg	Phe	Gly	Asp	Arg	Asp	Gly	Tyr	Arg
		515					520						525			
	Gly	Gly	Pro	Arg	Gly	Gly	Asp	Glu	Lys	Gly	Gly	Ala	Pro	Ala	Asp	Phe
		530					535					540				
50	Gln	Pro	Ser	Phe	Gln	Gly	Gly	Gly	Arg	Pro	Gly	Phe	Gly	Arg	Gly	
	545					550				555						560
	Ala	Gly	Gly	Tyr	Ser	Ala	Ala	Ala	Pro	Ser	Gly	Ser	Gly	Phe	Pro	
					565					570					575	

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 535 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

60 (ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..535

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(D) OTHER INFORMATION: / Ceres Seq. ID 2050903

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

	Met	Glu	Ile	Leu	Gln	Asn	Ile	Arg	Asp	Pro	Tyr	Glu	Asn	Ala	Asn	Ile	
	1				5					10					15		
5	Ala	Leu	Pro	Asp	His	Cys	Pro	Glu	Ser	Lys	Lys	Gln	Asn	Gln	Lys	Gln	
				20					25					30			
	Ser	Ile	Val	Arg	Tyr	Lys	Ser	Ser	Arg	Ile	Thr	Glu	Ile	Ser	Leu	Leu	
			35					40					45				
	Ser	Ser	Arg	Phe	Trp	Lys	Ile	Ile	Tyr	Arg	Thr	Arg	Gln	Leu	Leu	Leu	
10			50				55					60					
	Thr	Asn	Ile	Leu	Glu	Ser	Leu	Val	Val	Gly	Leu	Val	Leu	Gly	Thr	Ile	
	65					70					75					80	
	Tyr	Leu	Asn	Ile	Gly	Thr	Gly	Lys	Glu	Gly	Ile	Arg	Lys	Arg	Phe	Gly	
				85						90					95		
15	Leu	Phe	Ala	Phe	Thr	Leu	Thr	Phe	Leu	Leu	Ser	Ser	Thr	Thr	Gln	Thr	
				100					105					110			
	Leu	Pro	Ile	Phe	Ile	Asp	Glu	Arg	Pro	Ile	Leu	Leu	Arg	Glu	Thr	Ser	
			115					120					125				
	Ser	Gly	Leu	Tyr	Arg	Leu	Ser	Ser	His	Ile	Leu	Ala	Asn	Thr	Leu	Val	
20		130					135					140					
	Phe	Leu	Pro	Tyr	Leu	Leu	Ile	Ala	Ile	Ile	Tyr	Ser	Val	Ser	Leu		
	145					150					155					160	
	Tyr	Phe	Leu	Val	Gly	Leu	Cys	Phe	Ser	Trp	Gln	Ala	Leu	Ala	Tyr	Phe	
				165						170					175		
25	Val	Leu	Val	Ile	Trp	Ile	Ile	Val	Leu	Met	Ala	Asn	Ser	Phe	Val	Leu	
				180					185					190			
	Phe	Leu	Ser	Ser	Leu	Ala	Pro	Asn	Tyr	Ile	Ala	Gly	Thr	Ser	Ser	Val	
			195					200					205				
	Thr	Ile	Leu	Leu	Ala	Ala	Phe	Phe	Leu	Phe	Ser	Gly	Tyr	Phe	Ile	Ser	
30		210					215					220					
	Lys	Glu	Ser	Leu	Pro	Lys	Tyr	Trp	Leu	Phe	Met	Tyr	Phe	Phe	Ser	Met	
	225					230					235					240	
	Tyr	Lys	Tyr	Ala	Leu	Asp	Ala	Leu	Leu	Ile	Asn	Glu	Tyr	Ser	Cys	Leu	
				245						250					255		
35	His	Asn	Lys	Cys	Leu	Val	Trp	Phe	Glu	Glu	Ala	Ser	Val	Asn	Ser	Cys	
				260					265					270			
	Leu	Val	Thr	Gly	Gly	Asp	Val	Leu	Asp	Lys	Asn	Gly	Leu	His	Glu	Arg	
			275					280					285				
	Gln	Arg	Ile	Tyr	Val	Leu	Gly	Arg	Pro	Ser	Leu	Val	Ser	Gly	Phe	Lys	
40		290					295					300					
	Leu	Glu	Lys	Gln	Gly	Ile	Arg	Phe	Leu	Arg	Ser	Lys	Lys	Thr	Leu	Leu	
	305					310					315					320	
	Leu	Pro	Phe	Ala	Gln	Ala	Gln	Cys	Leu	Phe	Ala	Ala	Lys	Ala	Gln	Pro	
				325						330					335		
45	Thr	Arg	Arg	Trp	Asn	Tyr	Pro	Ser	Ile	Asn	Cys	Asp	Leu	Val	Arg	Pro	
				340					345					350			
	Phe	Ile	Arg	Leu	Ser	Gln	Arg	Thr	Ile	Ala	Glu	Arg	Ser	Ala	Asn	Thr	
			355					360					365				
	Phe	Ser	Lys	Leu	Val	Glu	Pro	Glu	Gly	Val	Cys	Phe	Ala	Lys	Lys	Asp	
50		370					375					380					
	Phe	Asn	Leu	Pro	Lys	His	Pro	Leu	Ile	Asp	Val	Pro	Asn	Leu	Gln	Val	
	385					390					395					400	
	Ile	Lys	Leu	Met	Gln	Ser	Phe	Lys	Ser	Lys	Glu	Tyr	Val	Arg	Glu	Thr	
				405						410					415		
55	Phe	Ala	Trp	Met	His	Tyr	Tyr	Trp	Phe	Leu	Thr	Asn	Glu	Gly	Ile	Glu	
				420					425					430			
	Phe	Leu	Arg	Thr	Tyr	Leu	Asn	Leu	Pro	Ser	Asp	Val	Val	Pro	Ala	Thr	
			435					440					445				
	Leu	Lys	Lys	Ser	Ala	Lys	Pro	Gly	Gly	Arg	Pro	Phe	Gly	Gly	Pro	Pro	
60		450					455					460					
	Gly	Asp	Arg	Gln	Arg	Gly	Pro	Pro	Arg	Ser	Asp	Gly	Asp	Arg	Pro	Arg	
	465					470					475					480	

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Phe	Gly	Asp	Arg	Asp	Gly	Tyr	Arg	Gly	Gly	Pro	Arg	Gly	Gly	Asp	Glu
				485					490					495	
Lys	Gly	Gly	Ala	Pro	Ala	Asp	Phe	Gln	Pro	Ser	Phe	Gln	Gly	Gly	Gly
			500					505					510		
Gly	Arg	Pro	Gly	Phe	Gly	Arg	Gly	Ala	Gly	Gly	Tyr	Ser	Ala	Ala	Ala
		515					520					525			
Pro	Ser	Gly	Ser	Gly	Phe	Pro									
	530					535									

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..350

(D) OTHER INFORMATION: / Ceres Seq. ID 2050904

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

Met 1	Ala	Asn	Ser	Phe 5	Val	Leu	Phe	Leu	Ser 10	Ser	Leu	Ala	Pro	Asn 15	Tyr
Ile	Ala	Gly	Thr	Ser	Ser	Val	Thr	Ile	Leu	Leu	Ala	Ala	Phe	Phe	Leu
			20					25					30		
Phe	Ser	Gly	Tyr	Phe	Ile	Ser	Lys	Glu	Ser	Leu	Pro	Lys	Tyr	Trp	Leu
		35					40					45			
Phe	Met	Tyr	Phe	Phe	Ser	Met	Tyr	Lys	Tyr	Ala	Leu	Asp	Ala	Leu	Leu
	50					55					60				
Ile	Asn	Glu	Tyr	Ser	Cys	Leu	His	Asn	Lys	Cys	Leu	Val	Trp	Phe	Glu
65					70					75					80
Glu	Ala	Ser	Val	Asn	Ser	Cys	Leu	Val	Thr	Gly	Gly	Asp	Val	Leu	Asp
				85					90					95	
Lys	Asn	Gly	Leu	His	Glu	Arg	Gln	Arg	Ile	Tyr	Val	Leu	Gly	Arg	Pro
			100					105					110		
Ser	Leu	Val	Ser	Gly	Phe	Lys	Leu	Glu	Lys	Gln	Gly	Ile	Arg	Phe	Leu
		115					120					125			
Arg	Ser	Lys	Lys	Thr	Leu	Leu	Leu	Pro	Phe	Ala	Gln	Ala	Gln	Cys	Leu
	130					135					140				
Phe	Ala	Ala	Lys	Ala	Gln	Pro	Thr	Arg	Arg	Trp	Asn	Tyr	Pro	Ser	Ile
145					150					155					160
Asn	Cys	Asp	Leu	Val	Arg	Pro	Phe	Ile	Arg	Leu	Ser	Gln	Arg	Thr	Ile
				165					170					175	
Ala	Glu	Arg	Ser	Ala	Asn	Thr	Phe	Ser	Lys	Leu	Val	Glu	Pro	Glu	Gly
			180					185					190		
Val	Cys	Phe	Ala	Lys	Lys	Asp	Phe	Asn	Leu	Pro	Lys	His	Pro	Leu	Ile
		195					200					205			
Asp	Val	Pro	Asn	Leu	Gln	Val	Ile	Lys	Leu	Met	Gln	Ser	Phe	Lys	Ser
	210					215					220				
Lys	Glu	Tyr	Val	Arg	Glu	Thr	Phe	Ala	Trp	Met	His	Tyr	Tyr	Trp	Phe
225					230					235					240
Leu	Thr	Asn	Glu	Gly	Ile	Glu	Phe	Leu	Arg	Thr	Tyr	Leu	Asn	Leu	Pro
				245					250					255	
Ser	Asp	Val	Val	Pro	Ala	Thr	Leu	Lys	Lys	Ser	Ala	Lys	Pro	Gly	Gly
			260					265					270		
Arg	Pro	Phe	Gly	Gly	Pro	Pro	Gly	Asp	Arg	Gln	Arg	Gly	Pro	Pro	Arg
		275					280					285			
Ser	Asp	Gly	Asp	Arg	Pro	Arg	Phe	Gly	Asp	Arg	Asp	Gly	Tyr	Arg	Gly
	290					295					300				
Gly	Pro	Arg	Gly	Gly	Asp	Glu	Lys	Gly	Gly	Ala	Pro	Ala	Asp	Phe	Gln
305					310					315					320
Pro	Ser	Phe	Gln	Gly	Gly	Gly	Gly	Arg	Pro	Gly	Phe	Gly	Arg	Gly	Ala
				325					330					335	

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Gly Gly Tyr Ser Ala Ala Ala Pro Ser Gly Ser Gly Phe Pro
 340 345 350

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..535
 (D) OTHER INFORMATION: / Ceres Seq. ID 2051325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

```

15 gctacataac tcaaagtaac aaacatacac atataacata tagaaagatc gaaaacaaaa 60
   gatcgggatg agtatggctc caaagacctc aactacactt gctttattcc ttgtgaccaa 120
   tattctcttc ctcaacctca ttaccctgag ttgcgcagac aatacttgcc caagagacgt 180
   tctcaaactt tgcacatgct cgaatgttct caacctcatc aacttgaagc tcggggcacc 240
   agctatgagg ccttggttgc ctattctctt tgggtctaatt gatctcgatg ttgctggttg 300
20 cctttgcacc gcgctcaagc tcagccttct tggcatcacc atcgacactc ctattcacct 360
   taacttggtc cttaacgcct gtggaggtac ccttccctgat ggattccggt gcccaacata 420
   gctacaatat attcatattt tctatctatg ttcttgaatt ggttttgtct aacatccaaa 480
   tttaaaccct aaattcatgt ataagcaaat aacaagtaaa attaagactt ttatg

```

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..117
 (D) OTHER INFORMATION: / Ceres Seq. ID 2051326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

```

35 Met Ser Met Ala Pro Lys Thr Ser Thr Thr Leu Ala Leu Phe Leu Val
   1 5 10 15
   Thr Asn Ile Leu Phe Leu Asn Leu Ile Thr Leu Ser Cys Ala Asp Asn
   20 25 30
40 Thr Cys Pro Arg Asp Val Leu Lys Leu Ser Thr Cys Ser Asn Val Leu
   35 40 45
   Asn Leu Ile Asn Leu Lys Leu Gly Ala Pro Ala Met Arg Pro Cys Cys
   50 55 60
   Ser Ile Leu Phe Gly Leu Ile Asp Leu Asp Val Ala Val Cys Leu Cys
45 65 70 75 80
   Thr Ala Leu Lys Leu Ser Leu Leu Gly Ile Thr Ile Asp Thr Pro Ile
   85 90 95
   His Leu Asn Leu Ala Leu Asn Ala Cys Gly Gly Thr Leu Pro Asp Gly
   100 105 110
50 Phe Arg Cys Pro Thr
   115

```

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..115
 (D) OTHER INFORMATION: / Ceres Seq. ID 2051327

574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

Met Ala Pro Lys Thr Ser Thr Thr Leu Ala Leu Phe Leu Val Thr Asn
 1 5 10 15
 Ile Leu Phe Leu Asn Leu Ile Thr Leu Ser Cys Ala Asp Asn Thr Cys
 5 20 25 30
 Pro Arg Asp Val Leu Lys Leu Ser Thr Cys Ser Asn Val Leu Asn Leu
 35 40 45
 Ile Asn Leu Lys Leu Gly Ala Pro Ala Met Arg Pro Cys Cys Ser Ile
 50 55 60
 10 Leu Phe Gly Leu Ile Asp Leu Asp Val Ala Val Cys Leu Cys Thr Ala
 65 70 75 80
 Leu Lys Leu Ser Leu Leu Gly Ile Thr Ile Asp Thr Pro Ile His Leu
 85 90 95
 Asn Leu Ala Leu Asn Ala Cys Gly Gly Thr Leu Pro Asp Gly Phe Arg
 15 100 105 110
 Cys Pro Thr
 115

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 2051328

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

30 Met Leu Leu Phe Ala Phe Ala Pro Arg Ser Ser Ala Phe Leu Ala
 1 5 10 15
 Ser Pro Ser Thr Leu Leu Phe Thr Leu Thr Trp Leu Leu Thr Pro Val
 20 25 30
 Glu Val Pro Phe Leu Met Asp Ser Val Ala Gln His Ser Tyr Asn Ile
 35 35 40 45
 Phe Ile Phe Ser Ile Tyr Val Leu Glu Leu Val Leu Ser Asn Ile Gln
 50 55 60
 Ile Ser Asn Leu Asn Ser Cys Ile Ser Lys
 65 70

40 (2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 517 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..517

(D) OTHER INFORMATION: / Ceres Seq. ID 2051633

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

cataaccctc ttggaaagag tctcaacact tgcagagaaa aagaacaagg aagatcccgg 60
 aaaatggcaa cggcgattgt acgttcagct ctttcccagag cagtgactcg cgcagctccg 120
 aagacatccg tgcgtcctaa gcgaaacttt tcctcttccg ccggccatga cgatgcttat 180
 55 gaagctgcca agtgggagaa gataacttat ctgggtattg ctagttgcac tgctctagct 240
 gtctatgttt tatccaaggg ccatcatcac ggcgaagacc ctctgccta tccgcatacg 300
 cacatccgca acaaggagtt tccttggggt ccgcatggtc tgtttgaggt gaagcacaac 360
 aaagagcact gactcttgcg tggtcataat aacgtcttct tggtttattt gaaaggctaa 420
 aatgtttttac cgtatttgtt ctaccggttt gtcaacgatt tgctactcca atctcttttc 480
 60 ttttggtggg aaataaaaagt taatactttg cttggtc

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

575

(A) LENGTH: 123 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..123
 (D) OTHER INFORMATION: / Ceres Seq. ID 2051634

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:
 His Asn Pro Leu Gly Lys Ser Leu Asn Thr Cys Arg Glu Lys Glu Gln
 1 5 10 15
 Gly Arg Ser Arg Lys Met Ala Thr Ala Ile Val Arg Ser Ala Leu Ser
 20 25 30
 15 Arg Ala Val Thr Arg Ala Ala Pro Lys Thr Ser Val Ala Pro Lys Arg
 35 40 45
 Asn Phe Ser Ser Ser Ala Gly His Asp Asp Ala Tyr Glu Ala Ala Lys
 50 55 60
 Trp Glu Lys Ile Thr Tyr Leu Gly Ile Ala Ser Cys Thr Ala Leu Ala
 65 70 75 80
 20 Val Tyr Val Leu Ser Lys Gly His His His Gly Glu Asp Pro Pro Ala
 85 90 95
 Tyr Pro His Met His Ile Arg Asn Lys Glu Phe Pro Trp Gly Pro Asp
 100 105 110
 25 Gly Leu Phe Glu Val Lys His Asn Lys Glu His
 115 120

(2) INFORMATION FOR SEQ ID NO:482:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..102
 (D) OTHER INFORMATION: / Ceres Seq. ID 2051635

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:
 Met Ala Thr Ala Ile Val Arg Ser Ala Leu Ser Arg Ala Val Thr Arg
 40 1 5 10 15
 Ala Ala Pro Lys Thr Ser Val Ala Pro Lys Arg Asn Phe Ser Ser Ser
 20 25 30
 Ala Gly His Asp Asp Ala Tyr Glu Ala Ala Lys Trp Glu Lys Ile Thr
 35 40 45
 45 Tyr Leu Gly Ile Ala Ser Cys Thr Ala Leu Ala Val Tyr Val Leu Ser
 50 55 60
 Lys Gly His His His Gly Glu Asp Pro Pro Ala Tyr Pro His Met His
 65 70 75 80
 Ile Arg Asn Lys Glu Phe Pro Trp Gly Pro Asp Gly Leu Phe Glu Val
 85 90 95
 50 Lys His Asn Lys Glu His
 100

(2) INFORMATION FOR SEQ ID NO:483:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..410

60

576

(D) OTHER INFORMATION: / Ceres Seq. ID 2051906

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

```

ttccttcttt ttcacatcta cccaaaattc caaaacacca tcgatttttt gctctcttga      60
aatgtgtctt tttatgtcca attcttctct tccaactaaa ccgaaccgga aaaccagggt      120
5  cggagatcgg tgtttactga tggccaaaca gcaacgaacc cgactttaca tacttcgacg      180
atgtgtctcc atgtctgttt gctggcacga ccaactctatt tctgattagt ttgattcatg      240
aaccggacgg accaagaagt agaaatcaga agaatgtgat gtcatttaga gtttttcttg      300
ttttctttta gaactcttca aggaatcttt tgtaattgaa gaagactcta aggattgggc      360
cttttggggc tttgtacata ttgtgtaa ataatatgaa ctttttttac

```

(2) INFORMATION FOR SEQ ID NO:484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 2051907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

```

Ser Phe Phe Phe Thr Ser Thr Gln Asn Ser Lys Thr Pro Ser Ile Phe
1      5      10      15
Cys Ser Leu Glu Met Cys Leu Phe Met Ser Asn Ser Ser Leu Pro Thr
25      20      25      30
Lys Pro Asn Arg Lys Thr Arg Phe Gly Asp Arg Cys Leu Leu Met Ala
35      40      45
Lys Gln Gln Arg Thr Arg Leu Tyr Ile Leu Arg Arg Cys Val Ser Met
50      55      60
30 Leu Leu Cys Trp His Asp His Ser Ile Ser Asp
65      70      75

```

(2) INFORMATION FOR SEQ ID NO:485:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 2051908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

```

Met Cys Leu Phe Met Ser Asn Ser Ser Leu Pro Thr Lys Pro Asn Arg
45 1      5      10      15
Lys Thr Arg Phe Gly Asp Arg Cys Leu Leu Met Ala Lys Gln Gln Arg
20      25      30
Thr Arg Leu Tyr Ile Leu Arg Arg Cys Val Ser Met Leu Leu Cys Trp
35      40      45
50 His Asp His Ser Ile Ser Asp
50      55

```

(2) INFORMATION FOR SEQ ID NO:486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..51

(D) OTHER INFORMATION: / Ceres Seq. ID 2051909

577

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:

Met Ser Asn Ser Ser Leu Pro Thr Lys Pro Asn Arg Lys Thr Arg Phe
 1 5 10 15
 Gly Asp Arg Cys Leu Leu Met Ala Lys Gln Gln Arg Thr Arg Leu Tyr
 5 20 25 30
 Ile Leu Arg Arg Cys Val Ser Met Leu Leu Cys Trp His Asp His Ser
 35 40 45
 Ile Ser Asp
 50

(2) INFORMATION FOR SEQ ID NO:487:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..719

(D) OTHER INFORMATION: / Ceres Seq. ID 2052403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:

acaaatcatt caaagacata caaaataatt gagttttttt ttaattaga aacaaatggg 60
 gttgagtggt gttcttcacg tggaggttga ggtaagtct ccggtgaaa agttctgggt 120
 agcccttggc gacggcatca atctcttccc caaagctttc cctaacgact acaaaacat 180
 25 ccaagttcta gccggcgatg gcaacgctcc tggctccatt cgctcatta cttatggaga 240
 aggatctcca ctggtgaaga tatcggcgga gaggatcgaa gcagtggatt tggagaacaa 300
 aagcatgtcg tacagcatca ttggcggaga aatgttgagg tactacaaaa ctttcaaagg 360
 aaccatcacc gttatcccta aggatggtgg tagccttctg aaatggtctg gtgagtttga 420
 gaagaccgcc catgagatcg atgatccaca tgcacaaag gactttgctg tcaagaactt 480
 30 caaagagata gatgagtatc ttcttaagca aactagtgcc taacactaga acctttaa 540
 tatataagag gggtcgaccg tctctataag atttttctaa ttaagaagtg gaataaagtg 600
 gaaccctttt atgaatatcc acgttttatg atttcggagt ttatgcagcc tagtaggcca 660
 taagcttttt acaaaagcca atttagtcga acattttgaa aaaatcgaac cttgtggtg

(2) INFORMATION FOR SEQ ID NO:488:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 2052404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:

Met Gly Leu Ser Gly Val Leu His Val Glu Val Glu Val Lys Ser Pro
 1 5 10 15
 Ala Glu Lys Phe Trp Val Ala Leu Gly Asp Gly Ile Asn Leu Phe Pro
 20 25 30
 50 Lys Ala Phe Pro Asn Asp Tyr Lys Thr Ile Gln Val Leu Ala Gly Asp
 35 40 45
 Gly Asn Ala Pro Gly Ser Ile Arg Leu Ile Thr Tyr Gly Glu Gly Ser
 50 55 60
 55 Pro Leu Val Lys Ile Ser Ala Glu Arg Ile Glu Ala Val Asp Leu Glu
 65 70 75 80
 Asn Lys Ser Met Ser Tyr Ser Ile Ile Gly Gly Glu Met Leu Glu Tyr
 85 90 95
 Tyr Lys Thr Phe Lys Gly Thr Ile Thr Val Ile Pro Lys Asp Gly Gly
 100 105 110
 60 Ser Leu Leu Lys Trp Ser Gly Glu Phe Glu Lys Thr Ala His Glu Ile
 115 120 125
 Asp Asp Pro His Val Ile Lys Asp Phe Ala Val Lys Asn Phe Lys Glu

578

130 135 140
 Ile Asp Glu Tyr Leu Leu Lys Gln Thr Ser Ala
 145 150 155

(2) INFORMATION FOR SEQ ID NO:489:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..739
- (D) OTHER INFORMATION: / Ceres Seq. ID 2053545

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:

atatttagtac	attgttgacc	atcttttttcg	tatagactac	tatctctgat	ctcttgcgag	60
ttaagtcagt	aactaggaaa	attcagaagc	gctctcaatc	tcaaaaatat	ccatggcggc	120
gattacagaa	tttctaccaa	aagagtacgg	atatgtcgtt	ctcgtcctcg	tcttctactg	180
tttccccaac	ctctgggatg	gtgctcaagt	cggcagagct	cgcaaaaggt	acaacgtccc	240
gtatccaaact	ctatatgcaa	tagaatcaga	aaacaaaagat	gctaagctct	tcaactgtgt	300
tcagagagga	catcaaaact	cttttagagat	gatgccaatg	tatttcatac	tgatgatcct	360
cgggtgggatg	aagcaccctt	gtatctgtac	tggccttggg	ttgctttaca	acgttagccg	420
attcttctac	tttaaagggt	atgctactgg	agatcccatg	aagcgtctta	cgatcgggaa	480
atacgggtttc	ttgggggttg	taggtctgat	gatatgtacc	atctcgtttg	gtgtcactct	540
gaccccttgc	tgagctactc	gtttctgggg	ttaatgattc	tctgggtttg	tcgaagaata	600
tagaaccaat	gcttgtaagc	tgccacaaa	acttgtgtaa	tacttttagag	tttgtcactt	660
ttaaaagttt	gtaataaatc	atggcttcac	agaacagttg	aaatttcaca	tcgtagacg	720
tttaataaaga	tttgaatta					

(2) INFORMATION FOR SEQ ID NO:490:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..146
- (D) OTHER INFORMATION: / Ceres Seq. ID 2053546

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:

Met	Ala	Ala	Ile	Thr	Glu	Phe	Leu	Pro	Lys	Glu	Tyr	Gly	Tyr	Val	Val
1			5					10					15		
Leu	Val	Leu	Val	Phe	Tyr	Cys	Phe	Leu	Asn	Leu	Trp	Met	Gly	Ala	Gln
			20					25					30		
Val	Gly	Arg	Ala	Arg	Lys	Arg	Tyr	Asn	Val	Pro	Tyr	Pro	Thr	Leu	Tyr
			35					40					45		
Ala	Ile	Glu	Ser	Glu	Asn	Lys	Asp	Ala	Lys	Leu	Phe	Asn	Cys	Val	Gln
			50					55				60			
Arg	Gly	His	Gln	Asn	Ser	Leu	Glu	Met	Met	Pro	Met	Tyr	Phe	Ile	Leu
			65					70				75			80
Met	Ile	Leu	Gly	Gly	Met	Lys	His	Pro	Cys	Ile	Cys	Thr	Gly	Leu	Gly
			85					90					95		
Leu	Leu	Tyr	Asn	Val	Ser	Arg	Phe	Phe	Tyr	Phe	Lys	Gly	Tyr	Ala	Thr
			100					105					110		
Gly	Asp	Pro	Met	Lys	Arg	Leu	Thr	Ile	Gly	Lys	Tyr	Gly	Phe	Leu	Gly
			115					120					125		
Leu	Leu	Gly	Leu	Met	Ile	Cys	Thr	Ile	Ser	Phe	Gly	Val	Thr	Leu	Ile
			130					135					140		
Leu	Ala														

60

(2) INFORMATION FOR SEQ ID NO:491:

(i) SEQUENCE CHARACTERISTICS:

579

(A) LENGTH: 118 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..118
 (D) OTHER INFORMATION: / Ceres Seq. ID 2053547

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:
 Met Gly Ala Gln Val Gly Arg Ala Arg Lys Arg Tyr Asn Val Pro Tyr
 1 5 10 15
 Pro Thr Leu Tyr Ala Ile Glu Ser Glu Asn Lys Asp Ala Lys Leu Phe
 20 25 30
 15 Asn Cys Val Gln Arg Gly His Gln Asn Ser Leu Glu Met Met Pro Met
 35 40 45
 Tyr Phe Ile Leu Met Ile Leu Gly Gly Met Lys His Pro Cys Ile Cys
 50 55 60
 Thr Gly Leu Gly Leu Leu Tyr Asn Val Ser Arg Phe Phe Tyr Phe Lys
 20 65 70 75 80
 Gly Tyr Ala Thr Gly Asp Pro Met Lys Arg Leu Thr Ile Gly Lys Tyr
 85 90 95
 Gly Phe Leu Gly Leu Leu Gly Leu Met Ile Cys Thr Ile Ser Phe Gly
 100 105 110
 25 Val Thr Leu Ile Leu Ala
 115

(2) INFORMATION FOR SEQ ID NO:492:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..74
 (D) OTHER INFORMATION: / Ceres Seq. ID 2053548

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:
 Met Met Pro Met Tyr Phe Ile Leu Met Ile Leu Gly Gly Met Lys His
 40 1 5 10 15
 Pro Cys Ile Cys Thr Gly Leu Gly Leu Leu Tyr Asn Val Ser Arg Phe
 20 25 30
 Phe Tyr Phe Lys Gly Tyr Ala Thr Gly Asp Pro Met Lys Arg Leu Thr
 35 40 45
 45 Ile Gly Lys Tyr Gly Phe Leu Gly Leu Leu Gly Leu Met Ile Cys Thr
 50 55 60
 Ile Ser Phe Gly Val Thr Leu Ile Leu Ala
 65 70

(2) INFORMATION FOR SEQ ID NO:493:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 681 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..681
 (D) OTHER INFORMATION: / Ceres Seq. ID 2053884

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:
 ccattccaaaa aaaacaaaac aaaaaattat attcaagaga aaaaggaaaa aatgaatttc 60
 atctccgatc aggtaaagaa actctcaagc tcaacaccag aggagccaga ccacaacaag 120

580

ccagtcgaag gaaccgaaac agctacaaga ccagctacca acgccgagct catggcaagt 180
 gccaaggttg tagctgaagc tgctcaagcc gcagctcgta acgaatcaga caaactcgac 240
 aagggtaaaag tcgccggagc ctctgctgat atcttagacg ctgccgagaa atacggtaag 300
 ttcgatgaaa agagtagcac tggtcagtac ctcgacaagg ctgagaagta tctcaacgac 360
 5 tacgagtcgt cacactccac cgggtgctggt ggctcctctc ctccgacgag tcaggctgag 420
 ccagcaagtc agcctgagcc ggcggtctaag aaagacgatg aagagtctgg tgggtgggctt 480
 ggaggttatg ccaagatggc tcaagggtttc ttgaagtgat ttgatcttta attgttggtc 540
 atcatttttcg taataataaaa ttaaataact agtatcggtt gtgactagtt tatgttgctt 600
 cgtttatggt tatggggagt gacgagttag tgtaataact tctgggtgatc atgaatctaa 660
 10 tccatctttg ttgtgattat g

(2) INFORMATION FOR SEQ ID NO:494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..172

(D) OTHER INFORMATION: / Ceres Seq. ID 2053885

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:494:

Pro Ser Lys Lys Lys Thr Lys Asn Tyr Ile Gln Glu Lys Lys Glu
 1 5 10 15
 25 Lys Met Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr
 20 25 30
 Pro Glu Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala
 35 40 45
 Thr Arg Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val
 50 55 60
 30 Ala Glu Ala Ala Gln Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp
 65 70 75 80
 Lys Gly Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ala Glu
 85 90 95
 35 Lys Tyr Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly Gln Tyr Leu Asp
 100 105 110
 Lys Ala Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly
 115 120 125
 40 Ala Gly Gly Pro Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln
 130 135 140
 Pro Glu Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Gly Leu
 145 150 155 160
 Gly Gly Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..155

(D) OTHER INFORMATION: / Ceres Seq. ID 2053886

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:495:

Met Asn Phe Ile Ser Asp Gln Val Lys Lys Leu Ser Ser Ser Thr Pro
 1 5 10 15
 60 Glu Glu Pro Asp His Asn Lys Pro Val Glu Gly Thr Glu Thr Ala Thr
 20 25 30
 Arg Pro Ala Thr Asn Ala Glu Leu Met Ala Ser Ala Lys Val Val Ala
 35 40 45

581

Glu Ala Ala Gln Ala Ala Ala Arg Asn Glu Ser Asp Lys Leu Asp Lys
 50 55 60
 Gly Lys Val Ala Gly Ala Ser Ala Asp Ile Leu Asp Ala Ala Glu Lys
 65 70 75 80
 5 Tyr Gly Lys Phe Asp Glu Lys Ser Ser Thr Gly Gln Tyr Leu Asp Lys
 85 90 95
 Ala Glu Lys Tyr Leu Asn Asp Tyr Glu Ser Ser His Ser Thr Gly Ala
 100 105 110
 Gly Gly Pro Pro Pro Pro Thr Ser Gln Ala Glu Pro Ala Ser Gln Pro
 115 120 125
 10 Glu Pro Ala Ala Lys Lys Asp Asp Glu Glu Ser Gly Gly Gly Leu Gly
 130 135 140
 Gly Tyr Ala Lys Met Ala Gln Gly Phe Leu Lys
 145 150 155

15 (2) INFORMATION FOR SEQ ID NO:496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

25 (D) OTHER INFORMATION: / Ceres Seq. ID 2053887

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:

Met Ala Ser Ala Lys Val Val Ala Glu Ala Ala Gln Ala Ala Ala Arg
 1 5 10 15
 Asn Glu Ser Asp Lys Leu Asp Lys Gly Lys Val Ala Gly Ala Ser Ala
 20 25 30
 Asp Ile Leu Asp Ala Ala Glu Lys Tyr Gly Lys Phe Asp Glu Lys Ser
 35 40 45
 Ser Thr Gly Gln Tyr Leu Asp Lys Ala Glu Lys Tyr Leu Asn Asp Tyr
 50 55 60
 35 Glu Ser Ser His Ser Thr Gly Ala Gly Gly Pro Pro Pro Pro Thr Ser
 65 70 75 80
 Gln Ala Glu Pro Ala Ser Gln Pro Glu Pro Ala Ala Lys Lys Asp Asp
 85 90 95
 Glu Glu Ser Gly Gly Gly Leu Gly Gly Tyr Ala Lys Met Ala Gln Gly
 100 105 110
 Phe Leu Lys
 115

(2) INFORMATION FOR SEQ ID NO:497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 797 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

50 (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..797

(D) OTHER INFORMATION: / Ceres Seq. ID 2053908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:

55 ttctctcaaa atccataaaa agagagagag ataaataaag agaaaactaa agaagctaga 60
 agatggagaa aagtaatgat catgacaagg ctagccacgg cggctccggt ggtggtgcca 120
 cggagaagtg ggaggagact agcctcggaa tccgaactgc cgagacaatg ctccggttag 180
 ctccggtggg cctttgtggt gcagcacttg ttgtcatgct taaggactct gagactaatg 240
 agttcggttc aatttcttac tccaatctca cagcctttag gtacttggtg cagcgaatg 300
 60 gaatatgtgc aggtactct cttctatcag cagccattgc agcgatgcct cgttcttctt 360
 cgacaatgcc tcgtgttttg accttctttt gtctcgacca gcttctgacc tacctggttc 420
 ttgctgctgg agctgtatca gctgaggttc tatacttggc ttacaatgga gactcagcca 480

582

ttacttggag cgatgcatgt agctcctatg gcggtttctg tcatagagcc actgcttctg 540
 ttataatcac attctttgtg gtttgtttct acatcgttct ctctctaatac tcctcttata 600
 agctctttac tcgctttgat cctccttcca ttgttgactc cgccaagaat ctcgaagtcg 660
 ctgtcttcgg aagtttagatc ctccatttgc tcttcaagta catctagttt gtcatgtttc 720
 5 aaatgttggtg tgtttttaac tttggtcaag agaaagaatg cttatgtgtt tgctcttctt 780
 tcattgcttt tcttctt

(2) INFORMATION FOR SEQ ID NO:498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..204

(D) OTHER INFORMATION: / Ceres Seq. ID 2053909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:

Met Glu Lys Ser Asn Asp His Asp Lys Ala Ser His Gly Gly Ser Gly
 1 5 10 15
 Gly Gly Ala Thr Glu Lys Trp Glu Glu Thr Ser Leu Gly Ile Arg Thr
 20 25 30
 Ala Glu Thr Met Leu Arg Leu Ala Pro Val Gly Leu Cys Val Ala Ala
 35 40 45
 25 Leu Val Val Met Leu Lys Asp Ser Glu Thr Asn Glu Phe Gly Ser Ile
 50 55 60
 Ser Tyr Ser Asn Leu Thr Ala Phe Arg Tyr Leu Val His Ala Asn Gly
 65 70 75 80
 Ile Cys Ala Gly Tyr Ser Leu Leu Ser Ala Ala Ile Ala Ala Met Pro
 85 90 95
 30 Arg Ser Ser Ser Thr Met Pro Arg Val Trp Thr Phe Phe Cys Leu Asp
 100 105 110
 Gln Leu Leu Thr Tyr Leu Val Leu Ala Ala Gly Ala Val Ser Ala Glu
 115 120 125
 35 Val Leu Tyr Leu Ala Tyr Asn Gly Asp Ser Ala Ile Thr Trp Ser Asp
 130 135 140
 Ala Cys Ser Ser Tyr Gly Gly Phe Cys His Arg Ala Thr Ala Ser Val
 145 150 155 160
 Ile Ile Thr Phe Phe Val Val Cys Phe Tyr Ile Val Leu Ser Leu Ile
 165 170 175
 40 Ser Ser Tyr Lys Leu Phe Thr Arg Phe Asp Pro Pro Ser Ile Val Asp
 180 185 190
 Ser Ala Lys Asn Leu Glu Val Ala Val Phe Gly Ser
 195 200

(2) INFORMATION FOR SEQ ID NO:499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..169

(D) OTHER INFORMATION: / Ceres Seq. ID 2053910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:

Met Leu Arg Leu Ala Pro Val Gly Leu Cys Val Ala Ala Leu Val Val
 1 5 10 15
 Met Leu Lys Asp Ser Glu Thr Asn Glu Phe Gly Ser Ile Ser Tyr Ser
 20 25 30
 60 Asn Leu Thr Ala Phe Arg Tyr Leu Val His Ala Asn Gly Ile Cys Ala
 35 40 45

583

Gly Tyr Ser Leu Leu Ser Ala Ala Ile Ala Ala Met Pro Arg Ser Ser
 50 55 60
 Ser Thr Met Pro Arg Val Trp Thr Phe Phe Cys Leu Asp Gln Leu Leu
 65 70 75 80
 5 Thr Tyr Leu Val Leu Ala Ala Gly Ala Val Ser Ala Glu Val Leu Tyr
 85 90 95
 Leu Ala Tyr Asn Gly Asp Ser Ala Ile Thr Trp Ser Asp Ala Cys Ser
 100 105 110
 10 Ser Tyr Gly Gly Phe Cys His Arg Ala Thr Ala Ser Val Ile Ile Thr
 115 120 125
 Phe Phe Val Val Cys Phe Tyr Ile Val Leu Ser Leu Ile Ser Ser Tyr
 130 135 140
 Lys Leu Phe Thr Arg Phe Asp Pro Pro Ser Ile Val Asp Ser Ala Lys
 145 150 155 160
 15 Asn Leu Glu Val Ala Val Phe Gly Ser
 165

(2) INFORMATION FOR SEQ ID NO:500:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 153 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25 (A) NAME/KEY: peptide
 (B) LOCATION: 1..153
 (D) OTHER INFORMATION: / Ceres Seq. ID 2053911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:

30 Met Leu Lys Asp Ser Glu Thr Asn Glu Phe Gly Ser Ile Ser Tyr Ser
 1 5 10 15
 Asn Leu Thr Ala Phe Arg Tyr Leu Val His Ala Asn Gly Ile Cys Ala
 20 25 30
 Gly Tyr Ser Leu Leu Ser Ala Ala Ile Ala Ala Met Pro Arg Ser Ser
 35 35 40 45
 Ser Thr Met Pro Arg Val Trp Thr Phe Phe Cys Leu Asp Gln Leu Leu
 50 55 60
 Thr Tyr Leu Val Leu Ala Ala Gly Ala Val Ser Ala Glu Val Leu Tyr
 65 70 75 80
 Leu Ala Tyr Asn Gly Asp Ser Ala Ile Thr Trp Ser Asp Ala Cys Ser
 40 85 90 95
 Ser Tyr Gly Gly Phe Cys His Arg Ala Thr Ala Ser Val Ile Ile Thr
 100 105 110
 Phe Phe Val Val Cys Phe Tyr Ile Val Leu Ser Leu Ile Ser Ser Tyr
 115 120 125
 45 Lys Leu Phe Thr Arg Phe Asp Pro Pro Ser Ile Val Asp Ser Ala Lys
 130 135 140
 Asn Leu Glu Val Ala Val Phe Gly Ser
 145 150

(2) INFORMATION FOR SEQ ID NO:501:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 652 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

55 (A) NAME/KEY: -
 (B) LOCATION: 1..652
 (D) OTHER INFORMATION: / Ceres Seq. ID 2056123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:

60 attttttctt tctctctctc ctccctaagc aaaactaaaa caagctatgg ctgggtatgct
 tcccggagtt gagtgtgcaa ggaggcggcg cttccacggt ggtgctcctc cgattgaatc

60
 120

584

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ctcgaacaca gcttctgtgg cggctgctggc gggacacgtc tggacacggc gaccatcggt 180
ctctcttttac actaccaatc atgagagcca ccaggcccat gtctccttct cggagagaag 240
tgtaggaat aaatcttatg gagaagacaa cgatgagaaa cttgacggag cagccaaaga 300
ggcaaagcag aggcttaaca agcggctgag aatcccacca cgtacaaggc aaaatggtaa 360
5 agacaaaggg aataaattgg agcaaggaaa gggtaaacct ctcggggact taccgaccga 420
ggtggtcggg ttaaagaaga gccgaggaag gttgatggaa tggttcaagc ggcgagttag 480
ggaacaacaa gattgtgcta tatgtctaga ccggttcaag aagggtgaga ccttggtaca 540
cctaccatgt gcccataagt ttcactccat atgcttattg ccttggctag acaccaatgt 600
ttattgcccc tattgtagaa ctgatatttg gaattaaatg ttatattttt ga

```

(2) INFORMATION FOR SEQ ID NO:502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 196 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..196

(D) OTHER INFORMATION: / Ceres Seq. ID 2056124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:

```

Met Ala Gly Met Leu Pro Gly Val Glu Cys Ala Arg Arg Arg Arg Phe
1      5      10      15
His Gly Gly Ala Pro Pro Ile Glu Ser Ser Asn Thr Ala Ser Val Ala
25      20      25      30
Ala Ala Ala Gly His Val Trp Thr Arg Arg Pro Ser Phe Ser Leu Tyr
35      40      45
Thr Thr Asn His Glu Ser His Gln Ala His Val Ser Phe Ser Glu Arg
50      55      60
30 Ser Val Arg Asn Lys Ser Tyr Gly Glu Asp Asn Asp Glu Lys Leu Asp
65      70      75      80
Gly Ala Ala Lys Glu Ala Lys Gln Arg Leu Asn Lys Arg Leu Arg Ile
85      90      95
Pro Pro Arg Thr Arg Gln Asn Gly Lys Asp Lys Gly Asn Lys Leu Glu
35      100      105      110
Gln Gly Lys Gly Lys Pro Leu Gly Asp Leu Pro Thr Glu Val Val Gly
115      120      125
Leu Lys Lys Ser Arg Gly Arg Leu Met Glu Trp Phe Lys Arg Arg Val
130      135      140
40 Arg Glu Gln Gln Asp Cys Ala Ile Cys Leu Asp Arg Phe Lys Lys Gly
145      150      155      160
Glu Thr Leu Val His Leu Pro Cys Ala His Lys Phe His Ser Ile Cys
165      170      175
Leu Leu Pro Trp Leu Asp Thr Asn Val Tyr Cys Pro Tyr Cys Arg Thr
45      180      185      190
Asp Ile Trp Asn
195

```

(2) INFORMATION FOR SEQ ID NO:503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..193

(D) OTHER INFORMATION: / Ceres Seq. ID 2056125

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:

```

Met Leu Pro Gly Val Glu Cys Ala Arg Arg Arg Phe His Gly Gly
1      5      10      15
Ala Pro Pro Ile Glu Ser Ser Asn Thr Ala Ser Val Ala Ala Ala Ala

```


[illegible]

586

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accgaacagc aagttatgaa ccgaaaacgg tttttggaag aagaggcgga agcggaggag 1680
gagaaagggt tagtggctcg tgggttaaca tggaattata gtttgcaagg acttgagacg 1740
ggtcattgta aagttttcat ggaatctgag gatgttggaac gcacactcga tctctcggtt 1800
attggctcgt accaagaatt gtaccggaaa ttggctgaga tgtttcatat agaagagagg 1860
5 tccgatttgt tgactcatgt tgtgtaccgg gatgcaaagtg gtgttatcaa acgtattgga 1920
gacgaacctt tcagtgattt catgaaagca actaaacggc taacaatcaa gatggatatt 1980
ggtggcgaca acgtgagaaa catttttagt ttccttcaaa taatattttt tttctttttt 2040
ttcaaaaaat taattttttt tttgttcttt tccgatgggtg gatactatac tcatatacat 2100
10 atatattcat cagattatat atatatatat atatatatat atataagtaa tataaaaaaa 2160
aaacttattt tgttcattct ttttaagtta aaaacagtca attcatttat atcatctatg 2220
atgaagaaac tcattcaact ctcgttcact gttatgatta tcttcaccat tcttgtgcta 2280
ggagtgggtg caaatgaggg gctaggaaaa ccaaaaaaac aatgtaatga gattctaaag 2340
caatccaact gtgttgctgc agagtgtgac tctatgtgtg tgaagaagag ggggaaagga 2400
gccggttact gctctccttc taaaaagtgt tactgtctatt atcattgccc ttaacgattt 2460
15 tattatttac aataataaga gatttatgat aaagtagtaa aataatgaat cgggtgttta 2520
tagcctaacg attgatatag ttgtctctat caaataaact atatagacta aaagtaataa 2580
taataatgac aatcataact cagaagtttt tgtttagtc

```

(2) INFORMATION FOR SEQ ID NO:505:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 817 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (ix) FEATURE:

(A) NAME/KEY: peptide
 (B) LOCATION: 1..817

(D) OTHER INFORMATION: / Ceres Seq. ID 2056246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:

```

30 Met Glu Gln Glu Lys Ser Leu Asp Pro Gln Leu Trp His Ala Cys Ala
1 5 10 15
Gly Ser Met Val Gln Ile Pro Ser Leu Asn Ser Thr Val Phe Tyr Phe
20 25 30
Ala Gln Gly His Thr Glu His Ala His Ala Pro Pro Asp Phe His Ala
35 35 40 45
Pro Arg Val Pro Pro Leu Ile Leu Cys Arg Val Val Ser Val Lys Phe
50 55 60
Leu Ala Asp Ala Glu Thr Asp Glu Val Phe Ala Lys Ile Thr Leu Leu
65 70 75 80
40 Pro Leu Pro Gly Asn Asp Leu Asp Leu Glu Asn Asp Ala Val Leu Gly
85 90 95
Leu Thr Pro Pro Ser Ser Asp Gly Asn Gly Asn Gly Lys Glu Lys Pro
100 105 110
Ala Ser Phe Ala Lys Thr Leu Thr Gln Ser Asp Ala Asn Asn Gly Gly
45 115 120 125
Gly Phe Ser Val Pro Arg Tyr Cys Ala Glu Thr Ile Phe Pro Arg Leu
130 135 140
Asp Tyr Ser Ala Glu Pro Pro Val Gln Thr Val Ile Ala Lys Asp Ile
145 150 155 160
50 His Gly Glu Thr Trp Lys Phe Arg His Ile Tyr Arg Gly Thr Pro Arg
165 170 175
Arg His Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Asn Gln Lys Lys
180 185 190
Leu Ile Ala Gly Asp Ser Ile Val Phe Leu Arg Ser Glu Ser Gly Asp
55 195 200 205
Leu Cys Val Gly Ile Arg Arg Ala Lys Arg Gly Gly Leu Gly Ser Asn
210 215 220
Ala Gly Ser Asp Asn Pro Tyr Pro Gly Phe Ser Gly Phe Leu Arg Asp
225 230 235 240
60 Asp Glu Ser Thr Thr Thr Thr Ser Lys Leu Met Met Met Lys Arg Asn
245 250 255
Gly Asn Asn Asp Gly Asn Ala Ala Ala Thr Gly Arg Val Arg Val Glu

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587

					260					265				270					
		Ala	Val	Ala	Glu	Ala	Val	Ala	Arg	Ala	Ala	Cys	Gly	Gln	Ala	Phe	Glu		
				275					280					285					
5		Val	Val	Tyr	Tyr	Pro	Arg	Ala	Ser	Thr	Pro	Glu	Phe	Cys	Val	Lys	Ala		
			290					295					300						
		Ala	Asp	Val	Arg	Ser	Ala	Met	Arg	Ile	Arg	Trp	Cys	Ser	Gly	Met	Arg		
		305				310						315					320		
		Phe	Lys	Met	Ala	Phe	Glu	Thr	Glu	Asp	Ser	Ser	Arg	Ile	Ser	Trp	Phe		
					325						330					335			
10		Met	Gly	Thr	Val	Ser	Ala	Val	Gln	Val	Ala	Asp	Pro	Ile	Arg	Trp	Pro		
					340					345					350				
		Asn	Ser	Pro	Trp	Arg	Leu	Leu	Gln	Val	Ala	Trp	Asp	Glu	Pro	Asp	Leu		
				355					360					365					
15		Leu	Gln	Asn	Val	Lys	Arg	Val	Ser	Pro	Trp	Leu	Val	Glu	Leu	Val	Ser		
			370					375					380						
		Asn	Met	Pro	Thr	Ile	His	Leu	Ser	Pro	Phe	Ser	Pro	Arg	Lys	Lys	Ile		
		385					390					395					400		
		Arg	Ile	Pro	Gln	Pro	Phe	Glu	Phe	Pro	Phe	His	Gly	Thr	Lys	Phe	Pro		
					405						410					415			
20		Ile	Phe	Ser	Pro	Gly	Phe	Ala	Asn	Asn	Gly	Gly	Gly	Glu	Ser	Met	Cys		
					420					425					430				
		Tyr	Leu	Ser	Asn	Asp	Asn	Asn	Asn	Ala	Pro	Ala	Gly	Ile	Gln	Gly	Ala		
				435					440					445					
25		Arg	Gln	Ala	Gln	Gln	Leu	Phe	Gly	Ser	Pro	Ser	Pro	Ser	Leu	Leu	Ser		
			450					455					460						
		Asp	Leu	Asn	Leu	Ser	Ser	Tyr	Thr	Gly	Asn	Asn	Lys	Leu	His	Ser	Pro		
		465					470				475					480			
		Ala	Met	Phe	Leu	Ser	Ser	Phe	Asn	Pro	Arg	His	His	His	Tyr	Gln	Ala		
					485						490					495			
30		Arg	Asp	Ser	Glu	Asn	Ser	Asn	Asn	Ile	Ser	Cys	Ser	Leu	Thr	Met	Gly		
					500					505					510				
		Asn	Pro	Ala	Met	Val	Gln	Asp	Lys	Lys	Lys	Ser	Val	Gly	Ser	Val	Lys		
				515					520					525					
35		Thr	His	Gln	Phe	Val	Leu	Phe	Gly	Gln	Pro	Ile	Leu	Thr	Glu	Gln	Gln		
								535					540						
		Val	Met	Asn	Arg	Lys	Arg	Phe	Leu	Glu	Glu	Glu	Ala	Glu	Ala	Glu	Glu		
		545																	

588

755 760 765
 Gly Lys Pro Lys Lys Gln Cys Asn Glu Ile Leu Lys Gln Ser Asn Cys
 770 775 780
 Val Ala Ala Glu Cys Asp Ser Met Cys Val Lys Lys Arg Gly Lys Gly
 5 785 790 795 800
 Ala Gly Tyr Cys Ser Pro Ser Lys Lys Cys Tyr Cys Tyr Tyr His Cys
 805 810 815
 Pro

10 (2) INFORMATION FOR SEQ ID NO:506:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 799 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 15 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..799
 20 (D) OTHER INFORMATION: / Ceres Seq. ID 2056247
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:

Met Val Gln Ile Pro Ser Leu Asn Ser Thr Val Phe Tyr Phe Ala Gln
 1 5 10 15
 Gly His Thr Glu His Ala His Ala Pro Pro Asp Phe His Ala Pro Arg
 25 20 25 30
 Val Pro Pro Leu Ile Leu Cys Arg Val Val Ser Val Lys Phe Leu Ala
 35 40 45
 Asp Ala Glu Thr Asp Glu Val Phe Ala Lys Ile Thr Leu Leu Pro Leu
 50 55 60
 30 Pro Gly Asn Asp Leu Asp Leu Glu Asn Asp Ala Val Leu Gly Leu Thr
 65 70 75 80
 Pro Pro Ser Ser Asp Gly Asn Gly Asn Gly Lys Glu Lys Pro Ala Ser
 85 90 95
 Phe Ala Lys Thr Leu Thr Gln Ser Asp Ala Asn Asn Gly Gly Gly Phe
 35 100 105 110
 Ser Val Pro Arg Tyr Cys Ala Glu Thr Ile Phe Pro Arg Leu Asp Tyr
 115 120 125
 Ser Ala Glu Pro Pro Val Gln Thr Val Ile Ala Lys Asp Ile His Gly
 130 135 140
 40 Glu Thr Trp Lys Phe Arg His Ile Tyr Arg Gly Thr Pro Arg Arg His
 145 150 155 160
 Leu Leu Thr Thr Gly Trp Ser Thr Phe Val Asn Gln Lys Lys Leu Ile
 165 170 175
 Ala Gly Asp Ser Ile Val Phe Leu Arg Ser Glu Ser Gly Asp Leu Cys
 45 180 185 190
 Val Gly Ile Arg Arg Ala Lys Arg Gly Gly Leu Gly Ser Asn Ala Gly
 195 200 205
 Ser Asp Asn Pro Tyr Pro Gly Phe Ser Gly Phe Leu Arg Asp Asp Glu
 210 215 220
 50 Ser Thr Thr Thr Thr Ser Lys Leu Met Met Met Lys Arg Asn Gly Asn
 225 230 235 240
 Asn Asp Gly Asn Ala Ala Ala Thr Gly Arg Val Arg Val Glu Ala Val
 245 250 255
 Ala Glu Ala Val Ala Arg Ala Ala Cys Gly Gln Ala Phe Glu Val Val
 55 260 265 270
 Tyr Tyr Pro Arg Ala Ser Thr Pro Glu Phe Cys Val Lys Ala Ala Asp
 275 280 285
 Val Arg Ser Ala Met Arg Ile Arg Trp Cys Ser Gly Met Arg Phe Lys
 290 295 300
 60 Met Ala Phe Glu Thr Glu Asp Ser Ser Arg Ile Ser Trp Phe Met Gly
 305 310 315 320
 Thr Val Ser Ala Val Gln Val Ala Asp Pro Ile Arg Trp Pro Asn Ser

589
 325 330 335
 Pro Trp Arg Leu Leu Gln Val Ala Trp Asp Glu Pro Asp Leu Leu Gln
 340 345 350
 5 Asn Val Lys Arg Val Ser Pro Trp Leu Val Glu Leu Val Ser Asn Met
 355 360 365
 Pro Thr Ile His Leu Ser Pro Phe Ser Pro Arg Lys Lys Ile Arg Ile
 370 375 380
 Pro Gln Pro Phe Glu Phe Pro Phe His Gly Thr Lys Phe Pro Ile Phe
 385 390 395 400
 10 Ser Pro Gly Phe Ala Asn Asn Gly Gly Gly Glu Ser Met Cys Tyr Leu
 405 410 415
 Ser Asn Asp Asn Asn Asn Ala Pro Ala Gly Ile Gln Gly Ala Arg Gln
 420 425 430
 15 Ala Gln Gln Leu Phe Gly Ser Pro Ser Pro Ser Leu Leu Ser Asp Leu
 435 440 445
 Asn Leu Ser Ser Tyr Thr Gly Asn Asn Lys Leu His Ser Pro Ala Met
 450 455 460
 Phe Leu Ser Ser Phe Asn Pro Arg His His His Tyr Gln Ala Arg Asp
 465 470 475 480
 20 Ser Glu Asn Ser Asn Asn Ile Ser Cys Ser Leu Thr Met Gly Asn Pro
 485 490 495
 Ala Met Val Gln Asp Lys Lys Lys Ser Val Gly Ser Val Lys Thr His
 500 505 510
 25 Gln Phe Val Leu Phe Gly Gln Pro Ile Leu Thr Glu Gln Gln Val Met
 515 520 525
 Asn Arg Lys Arg Phe Leu Glu Glu Glu Ala Glu Ala Glu Glu Glu Lys
 530 535 540
 Gly Leu Val Ala Arg Gly Leu Thr Trp Asn Tyr Ser Leu Gln Gly Leu
 545 550 555 560
 30 Glu Thr Gly His Cys Lys Val Phe Met Glu Ser Glu Asp Val Gly Arg
 565 570 575
 Thr Leu Asp Leu Ser Val Ile Gly Ser Tyr Gln Glu Leu Tyr Arg Lys
 580 585 590
 35 Leu Ala Glu Met Phe His Ile Glu Arg Ser Asp Leu Leu Thr His
 595 600 605
 Val Val Tyr Arg Asp Ala Asn Gly Val Ile Lys Arg Ile Gly Asp Glu
 610 615 620
 Pro Phe Ser Asp Phe Met Lys Ala Thr Lys Arg Leu Thr Ile Lys Met
 625 630 635 640
 40 Asp Ile Gly Gly Asp Asn Val Arg Asn Ile Phe Ser Phe Leu Gln Ile
 645 650 655
 Ile Phe Phe Phe Phe Phe Phe Lys Lys Leu Ile Phe Phe Leu Phe Phe
 660 665 670
 45 Ser Asp Gly Gly Tyr Tyr Thr His Ile His Ile Tyr Ser Ser Asp Tyr
 675 680 685
 Ile Tyr Ile Tyr Ile Tyr Ile Tyr Ile Ser Asn Ile Lys Lys Lys Leu
 690 695 700
 Ile Leu Phe Ile Leu Leu Ser Leu Lys Thr Val Asn Ser Phe Ile Ser
 705 710 715 720
 50 Ser Met Met Lys Lys Leu Ile Gln Leu Ser Phe Thr Val Met Ile Ile
 725 730 735
 Phe Thr Ile Leu Val Leu Gly Val Val Ala Asn Glu Gly Leu Gly Lys
 740 745 750
 55 Pro Lys Lys Gln Cys Asn Glu Ile Leu Lys Gln Ser Asn Cys Val Ala
 755 760 765
 Ala Glu Cys Asp Ser Met Cys Val Lys Lys Arg Gly Lys Gly Ala Gly
 770 775 780
 Tyr Cys Ser Pro Ser Lys Lys Cys Tyr Cys Tyr Tyr His Cys Pro
 785 790 795
 60 (2) INFORMATION FOR SEQ ID NO:507:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 567 amino acids

590

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..567
 (D) OTHER INFORMATION: / Ceres Seq. ID 2056248
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:

10	Met	Met	Met	Lys	Arg	Asn	Gly	Asn	Asn	Asp	Gly	Asn	Ala	Ala	Ala	Thr
	1			5						10					15	
	Gly	Arg	Val	Arg	Val	Glu	Ala	Val	Ala	Glu	Ala	Val	Ala	Arg	Ala	Ala
				20					25					30		
15	Cys	Gly	Gln	Ala	Phe	Glu	Val	Val	Tyr	Tyr	Pro	Arg	Ala	Ser	Thr	Pro
			35					40					45			
	Glu	Phe	Cys	Val	Lys	Ala	Ala	Asp	Val	Arg	Ser	Ala	Met	Arg	Ile	Arg
		50					55					60				
	Trp	Cys	Ser	Gly	Met	Arg	Phe	Lys	Met	Ala	Phe	Glu	Thr	Glu	Asp	Ser
	65				70						75				80	
20	Ser	Arg	Ile	Ser	Trp	Phe	Met	Gly	Thr	Val	Ser	Ala	Val	Gln	Val	Ala
				85					90					95		
	Asp	Pro	Ile	Arg	Trp	Pro	Asn	Ser	Pro	Trp	Arg	Leu	Leu	Gln	Val	Ala
				100					105					110		
25	Trp	Asp	Glu	Pro	Asp	Leu	Leu	Gln	Asn	Val	Lys	Arg	Val	Ser	Pro	Trp
			115					120					125			
	Leu	Val	Glu	Leu	Val	Ser	Asn	Met	Pro	Thr	Ile	His	Leu	Ser	Pro	Phe
			130				135					140				
	Ser	Pro	Arg	Lys	Lys	Ile	Arg	Ile	Pro	Gln	Pro	Phe	Glu	Phe	Pro	Phe
	145					150					155				160	
30	His	Gly	Thr	Lys	Phe	Pro	Ile	Phe	Ser	Pro	Gly	Phe	Ala	Asn	Asn	Gly
				165						170					175	
	Gly	Gly	Glu	Ser	Met	Cys	Tyr	Leu	Ser	Asn	Asp	Asn	Asn	Asn	Ala	Pro
				180					185					190		
35	Ala	Gly	Ile	Gln	Gly	Ala	Arg	Gln	Ala	Gln	Gln	Leu	Phe	Gly	Ser	Pro
			195					200					205			
	Ser	Pro	Ser	Leu	Leu	Ser	Asp	Leu	Asn	Leu	Ser	Ser	Tyr	Thr	Gly	Asn
			210				215					220				
	Asn	Lys	Leu	His	Ser	Pro	Ala	Met	Phe	Leu	Ser	Ser	Phe	Asn	Pro	Arg
	225					230					235				240	
40	His	His	His	Tyr	Gln	Ala	Arg	Asp	Ser	Glu	Asn	Ser	Asn	Asn	Ile	Ser
				245						250					255	
	Cys	Ser	Leu	Thr	Met	Gly	Asn	Pro	Ala	Met	Val	Gln	Asp	Lys	Lys	Lys
			260						265					270		
45	Ser	Val	Gly	Ser	Val	Lys	Thr	His	Gln	Phe	Val	Leu	Phe	Gly	Gln	Pro
			275				280						285			
	Ile	Leu	Thr	Glu	Gln	Gln	Val	Met	Asn	Arg	Lys	Arg	Phe	Leu	Glu	Glu
			290				295					300				
	Glu	Ala	Glu	Ala	Glu	Glu	Glu	Lys	Gly	Leu	Val	Ala	Arg	Gly	Leu	Thr
	305					310					315				320	
50	Trp	Asn	Tyr	Ser	Leu	Gln	Gly	Leu	Glu	Thr	Gly	His	Cys	Lys	Val	Phe
				325						330					335	
	Met	Glu	Ser	Glu	Asp	Val	Gly	Arg	Thr	Leu	Asp	Leu	Ser	Val	Ile	Gly
			340						345					350		
55	Ser	Tyr	Gln	Glu	Leu	Tyr	Arg	Lys	Leu	Ala	Glu	Met	Phe	His	Ile	Glu
			355					360					365			
	Glu	Arg	Ser	Asp	Leu	Leu	Thr	His	Val	Val	Tyr	Arg	Asp	Ala	Asn	Gly
			370				375					380				
	Val	Ile	Lys	Arg	Ile	Gly	Asp	Glu	Pro	Phe	Ser	Asp	Phe	Met	Lys	Ala
	385					390					395				400	
60	Thr	Lys	Arg	Leu	Thr	Ile	Lys	Met	Asp	Ile	Gly	Gly	Asp	Asn	Val	Arg
				405							410				415	
	Asn	Ile	Phe	Ser	Phe	Leu	Gln	Ile	Ile	Phe	Phe	Phe	Phe	Phe	Phe	Lys

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420 425 430
 Lys Leu Ile Phe Phe Leu Phe Phe Ser Asp Gly Gly Tyr Tyr Thr His
 435 440 445
 5 Ile His Ile Tyr Ser Ser Asp Tyr Ile Tyr Ile Tyr Ile Tyr
 450 455 460
 Ile Ser Asn Ile Lys Lys Lys Leu Ile Leu Phe Ile Leu Leu Ser Leu
 465 470 475 480
 Lys Thr Val Asn Ser Phe Ile Ser Ser Met Met Lys Lys Leu Ile Gln
 485 490 495
 10 Leu Ser Phe Thr Val Met Ile Ile Phe Thr Ile Leu Val Leu Gly Val
 500 505 510
 Val Ala Asn Glu Gly Leu Gly Lys Pro Lys Lys Gln Cys Asn Glu Ile
 515 520 525
 15 Leu Lys Gln Ser Asn Cys Val Ala Ala Glu Cys Asp Ser Met Cys Val
 530 535 540
 Lys Lys Arg Gly Lys Gly Ala Gly Tyr Cys Ser Pro Ser Lys Lys Cys
 545 550 555 560
 Tyr Cys Tyr Tyr His Cys Pro
 565
 20 (2) INFORMATION FOR SEQ ID NO:508:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..776
 30 (D) OTHER INFORMATION: / Ceres Seq. ID 1941142
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:
 agtcgcctcc ttctgcgcc gccgcgcgc cgcgcgcgc cgctaccacc gcctcgcggc 60
 cgctcgcggc tccgcgtttc cgcacggaag ttggtgaagg tttcttgagg ctgagaacat 120
 ggtgctgaag acggaacttt gccgcttcag cggccagaag atttatcctg ggaaaggcat 180
 35 tagatttatc cgtgctgatt ctcaggtctt cttttttgcc aactcgaaat gcaagcgcta 240
 cttccacaac cgctgaagc ctgcaaagct tacctggaca gcaatgtaca ggaagcagca 300
 caagaaggat atccatgctg aagcggtaaa gaagaggcgc cgcgccacca agaagccata 360
 ctccagggtca attgtgggtg cttccttgga agtaatccag aagaagagag ctgagaagcc 420
 agagggtccgc gatgctgcta gagaggctgc tcttcgtgag atcaaggagc gcatcaagaa 480
 40 gaccaaggat gagaagaaa cgaagaaggc ggagggtgagc aagtcccaga agacgcagac 540
 aaagggtgcg gtccagaagg gttccaagg ccccaagttg ggcggcggtg gtgggaagcg 600
 ctgaaagaac ttagtgtcgt ttctcgacat tgcagtcgtt ccttagccaa agccactttc 660
 gtagaacctg tgttgaaattt gcaagactta ttcaagcgtt gcttgtgcgt gctaaatacc 720
 atggcaagag aacggattta tatttatgcc tgaaaaaaat gaccgttcat attctt
 45 (2) INFORMATION FOR SEQ ID NO:509:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 50 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 55 (D) OTHER INFORMATION: / Ceres Seq. ID 1941143
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:
 Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr
 1 5 10 15
 60 Pro Gly Lys Gly Ile Arg Phe Ile Arg Ala Asp Ser Gln Val Phe Leu
 20 25 30
 Phe Ala Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Arg Leu Lys Pro
 35 40 45

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Ala Lys Leu Thr Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp
 50 55 60
 Ile His Ala Glu Ala Val Lys Lys Arg Arg Arg Ala Thr Lys Lys Pro
 65 70 75 80
 5 Tyr Ser Arg Ser Ile Val Gly Ala Ser Leu Glu Val Ile Gln Lys Lys
 85 90 95
 Arg Ala Glu Lys Pro Glu Val Arg Asp Ala Ala Arg Glu Ala Ala Leu
 100 105 110
 Arg Glu Ile Lys Glu Arg Ile Lys Lys Thr Lys Asp Glu Lys Lys Ala
 115 120 125
 10 Lys Lys Ala Glu Val Ser Lys Ser Gln Lys Thr Gln Thr Lys Gly Ala
 130 135 140
 Val Gln Lys Gly Ser Lys Gly Pro Lys Leu Gly Gly Gly Gly Lys
 145 150 155 160
 15 Arg

(2) INFORMATION FOR SEQ ID NO:510:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 106 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25 (A) NAME/KEY: peptide
 (B) LOCATION: 1..106
 (D) OTHER INFORMATION: / Ceres Seq. ID 1941144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:

30 Met Tyr Arg Lys Gln His Lys Lys Asp Ile His Ala Glu Ala Val Lys
 1 5 10 15
 Lys Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
 20 25 30
 Ala Ser Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
 35 40 45
 Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
 50 55 60
 Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Ala Glu Val Ser Lys
 65 70 75 80
 Ser Gln Lys Thr Gln Thr Lys Gly Ala Val Gln Lys Gly Ser Lys Gly
 40 85 90 95
 Pro Lys Leu Gly Gly Gly Gly Gly Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:511:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1024 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

50 (A) NAME/KEY: -
 (B) LOCATION: 1..1024
 (D) OTHER INFORMATION: / Ceres Seq. ID 1942975

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:

55 ataaattcct ccgctcccct tcgcgcgttc ctgtcgcgcc gccgctcccc tcccaaccca 60
 ctagctcaaa accctagagc tctcgcctgc tcgcctccgc cgccggagcg agctccccat 120
 cttcatccgt caaccatggc gacccagatc agcaagaaga agaagttcgt cagcgacggt 180
 gttttctacg ccgagctcaa tgagatgctg acgcgggagc tggcggagga cggctactct 240
 ggcgtggagg tcgcgcgtcac gccgatgcgc acggagatca tcatccgcgc cacgcgcacg 300
 60 cagaacgtgc tcggcgagaa gggccgtagg atcagggagc tcacctcgt cgtccagaag 360
 aggttcaact tccctgagaa tggcggttag ctttatgccg agaaggtcgt caaccgtggg 420
 ctctgtgcca tcgcgcaggc cgagtccctc cgttacaagc tcctcggtgg ccttgccgtc 480

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5 cgcagggcctt gctacgggtgt tcttcgttat gttatggaga gtggtgccaa gggttgtgag 540
 gtgatcgtga gtggaaagct cagggcccaa agagccaagt ccatgaagtt caaggatggc 600
 tacatgatct catctgggtca accagtgaac gagtacattg actcggctgt gagacacgtt 660
 cttctcagac aggggtgttct tggcatcaag gtgaagatca tgcttgactg ggacccgaag 720
 ggcaagggtg gcccgatcac tcctcttccg gacctgggtga ccatccacac cccgaaggac 780
 gaggacgagc cgcgccctcc ggtcttggca cctcctgagg tgtaagggtcc caactgtgtc 840
 cttgaaatgg cagtttgatc gggtcctaga taggtttcta tcttacgata aggacaatgc 900
 taaggcagtt ggttacctta atctttatgg acagatgcta tgtgttgctt ctgtggcact 960
 10 tttgtttaag ctaagttttg cggagacaag atacttatat atgttcccga tgaaattatg 1020
 gttc

(2) INFORMATION FOR SEQ ID NO:512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1942976

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:

Ile Asn Ser Ser Ala Pro Leu Arg Arg Phe Leu Ser Arg Arg Arg Ser
 1 5 10 15
 25 Pro Pro Asn Pro Leu Ala Gln Asn Pro Arg Ala Leu Ala Cys Ser Pro
 20 25 30
 Pro Pro Pro Glu Arg Ala Pro His Leu His Pro Ser Thr Met Ala Thr
 35 40 45
 30 Gln Ile Ser Lys Lys Lys Lys Phe Val Ser Asp Gly Val Phe Tyr Ala
 50 55 60
 Glu Leu Asn Glu Met Leu Thr Arg Glu Leu Ala Glu Asp Gly Tyr Ser
 65 70 75 80
 Gly Val Glu Val Arg Val Thr Pro Met Arg Thr Glu Ile Ile Ile Arg
 85 90 95
 35 Ala Thr Arg Thr Gln Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg
 100 105 110
 Glu Leu Thr Ser Val Val Gln Lys Arg Phe Asn Phe Pro Glu Asn Gly
 115 120 125
 Val Glu Leu Tyr Ala Glu Lys Val Val Asn Arg Gly Leu Cys Ala Ile
 130 135 140
 40 Ala Gln Ala Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly Leu Ala Val
 145 150 155 160
 Arg Arg Ala Cys Tyr Gly Val Leu Arg Tyr Val Met Glu Ser Gly Ala
 165 170 175
 45 Lys Gly Cys Glu Val Ile Val Ser Gly Lys Leu Arg Ala Gln Arg Ala
 180 185 190
 Lys Ser Met Lys Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly Gln Pro
 195 200 205
 Val Asn Glu Tyr Ile Asp Ser Ala Val Arg His Val Leu Leu Arg Gln
 210 215 220
 50 Gly Val Leu Gly Ile Lys Val Lys Ile Met Leu Asp Trp Asp Pro Lys
 225 230 235 240
 Gly Lys Val Gly Pro Ile Thr Pro Leu Pro Asp Leu Val Thr Ile His
 245 250 255
 55 Thr Pro Lys Asp Glu Asp Glu Pro Arg Pro Pro Val Leu Ala Pro Pro
 260 265 270
 Glu Val

(2) INFORMATION FOR SEQ ID NO:513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

5 (A) NAME/KEY: peptide

(B) LOCATION: 1..229

(D) OTHER INFORMATION: / Ceres Seq. ID 1942977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:

10 Met Ala Thr Gln Ile Ser Lys Lys Lys Lys Phe Val Ser Asp Gly Val
 1 5 10 15
 Phe Tyr Ala Glu Leu Asn Glu Met Leu Thr Arg Glu Leu Ala Glu Asp
 20 25 30
 Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Met Arg Thr Glu Ile
 35 40 45
 15 Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu Gly Glu Lys Gly Arg
 50 55 60
 Arg Ile Arg Glu Leu Thr Ser Val Val Gln Lys Arg Phe Asn Phe Pro
 65 70 75 80
 Glu Asn Gly Val Glu Leu Tyr Ala Glu Lys Val Val Asn Arg Gly Leu
 85 90 95
 20 Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly
 100 105 110
 Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu Arg Tyr Val Met Glu
 115 120 125
 25 Ser Gly Ala Lys Gly Cys Glu Val Ile Val Ser Gly Lys Leu Arg Ala
 130 135 140
 Gln Arg Ala Lys Ser Met Lys Phe Lys Asp Gly Tyr Met Ile Ser Ser
 145 150 155 160
 Gly Gln Pro Val Asn Glu Tyr Ile Asp Ser Ala Val Arg His Val Leu
 165 170 175
 30 Leu Arg Gln Gly Val Leu Gly Ile Lys Val Lys Ile Met Leu Asp Trp
 180 185 190
 Asp Pro Lys Gly Lys Val Gly Pro Ile Thr Pro Leu Pro Asp Leu Val
 195 200 205
 35 Thr Ile His Thr Pro Lys Asp Glu Asp Glu Pro Arg Pro Pro Val Leu
 210 215 220
 Ala Pro Pro Glu Val
 225

(2) INFORMATION FOR SEQ ID NO:514:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..206

(D) OTHER INFORMATION: / Ceres Seq. ID 1942978

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:

Met Leu Thr Arg Glu Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu Val
 1 5 10 15
 Arg Val Thr Pro Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr
 20 25 30
 55 Gln Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser
 35 40 45
 Val Val Gln Lys Arg Phe Asn Phe Pro Glu Asn Gly Val Glu Leu Tyr
 50 55 60
 Ala Glu Lys Val Val Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu
 65 70 75 80
 60 Ser Leu Arg Tyr Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys
 85 90 95

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Tyr Gly Val Leu Arg Tyr Val Met Glu Ser Gly Ala Lys Gly Cys Glu
 100 105 110
 Val Ile Val Ser Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met Lys
 115 120 125
 5 Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly Gln Pro Val Asn Glu Tyr
 130 135 140
 Ile Asp Ser Ala Val Arg His Val Leu Leu Arg Gln Gly Val Leu Gly
 145 150 155 160
 Ile Lys Val Lys Ile Met Leu Asp Trp Asp Pro Lys Gly Lys Val Gly
 10 165 170 175
 Pro Ile Thr Pro Leu Pro Asp Leu Val Thr Ile His Thr Pro Lys Asp
 180 185 190
 Glu Asp Glu Pro Arg Pro Pro Val Leu Ala Pro Pro Glu Val
 195 200 205
 15 (2) INFORMATION FOR SEQ ID NO:515:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1069 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 20 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (iix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..1069
 25 (D) OTHER INFORMATION: / Ceres Seq. ID 1944349
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:
 acttcggttc tgcctttgac cagctcttgc gctcggttta tctcgtgcgg ttgttgctag 60
 aaccgtccct aattccattc ccgtgatctg gtttagtcat ttcattggtt tatttggtgc 120
 atctgtggtg aatctgtggt cacttagatc aacataggaa gatgtacgcc cagttgagtt 180
 30 ttgagtcggc tggttggtgt tccctaacta gggactgagg gtctgaagct ctataacctgt 240
 tgcaatcgcg tagttgtgcg tgctagatgt atcagagaat ccctttgagt agaaagcaca 300
 cgcacacagc tgccacggta ttggcattcg taggtatctg ttctactgac gtgctacctg 360
 caccaggata gcacctgata tttgtgcgct ttttttggtg aagatttttt gaagctgaga 420
 agatggtgct gaagacggaa ctctgccgct tcagtggcca gaagatctat cctgggaaag 480
 35 gcatccggtt tattcgtgct gattctcagg ttttcctttt tgccaactct aaatgcaagc 540
 gctacttcca caaccgctg aagcctgcaa agcttacctg gacagcaatg tacaggaagc 600
 agcacaagaa ggacatccat gctgaagctg tcaagaagag gcgccgcgcc accaagaagc 660
 cataactcgag gtccattgtg ggtgcttcct tggaagtgat ccagaagaag agagctgaga 720
 agcctgaggt ccgtgatgct gctagagaag ctgctcttcg tgagatcaag gagcgcacatca 780
 40 agaagaccaa ggacgagaag aaggcgaaga aggctgaggt gtccaagtcc cagaaggcgc 840
 agacgaaggc cgctgtccag aagggttcca agggcccca gttgggcggc ggcggtggca 900
 aacgctgaaa aggaacgaag tgtcatttcg agacctcacc aaagtcacct ttgtagtacc 960
 tgggttaatt ttgcattttc gttcagagtt acttgtgact cttaactacc atgtcaagag 1020
 aatggattcg ttatttttat atattgggag aaatgatcgc cgttccttc
 45 (2) INFORMATION FOR SEQ ID NO:516:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 50 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (iix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..161
 55 (D) OTHER INFORMATION: / Ceres Seq. ID 1944350
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:
 Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr
 1 5 10 15
 Pro Gly Lys Gly Ile Arg Phe Ile Arg Ala Asp Ser Gln Val Phe Leu
 20 25 30
 60 Phe Ala Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Arg Leu Lys Pro
 35 40 45

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Ala Lys Leu Thr Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp
 50 55 60
 Ile His Ala Glu Ala Val Lys Lys Arg Arg Arg Ala Thr Lys Lys Pro
 65 70 75 80
 5 Tyr Ser Arg Ser Ile Val Gly Ala Ser Leu Glu Val Ile Gln Lys Lys
 85 90 95
 Arg Ala Glu Lys Pro Glu Val Arg Asp Ala Ala Arg Glu Ala Ala Leu
 100 105 110
 Arg Glu Ile Lys Glu Arg Ile Lys Lys Thr Lys Asp Glu Lys Lys Ala
 115 120 125
 10 Lys Lys Ala Glu Val Ser Lys Ser Gln Lys Ala Gln Thr Lys Gly Ala
 130 135 140
 Val Gln Lys Gly Ser Lys Gly Pro Lys Leu Gly Gly Gly Gly Lys
 145 150 155 160
 15 Arg

(2) INFORMATION FOR SEQ ID NO:517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1944351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:

Met Tyr Arg Lys Gln His Lys Lys Asp Ile His Ala Glu Ala Val Lys
 1 5 10 15
 Lys Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
 20 25 30
 Ala Ser Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
 35 40 45
 35 Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
 50 55 60
 Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Ala Glu Val Ser Lys
 65 70 75 80
 Ser Gln Lys Ala Gln Thr Lys Gly Ala Val Gln Lys Gly Ser Lys Gly
 85 90 95
 40 Pro Lys Leu Gly Gly Gly Gly Lys Arg
 100 105

(2) INFORMATION FOR SEQ ID NO:518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..89

(D) OTHER INFORMATION: / Ceres Seq. ID 1944352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:

Met Leu Leu Glu Lys Leu Leu Phe Val Arg Ser Arg Ser Ala Ser Arg
 1 5 10 15
 Arg Pro Arg Thr Arg Arg Arg Arg Arg Arg Leu Arg Cys Pro Ser Pro
 20 25 30
 Arg Arg Arg Arg Arg Arg Ala Leu Ser Arg Arg Val Pro Arg Ala Pro
 35 40 45
 60 Ser Trp Ala Ala Ala Val Ala Asn Ala Glu Lys Glu Arg Ser Val Ile
 50 55 60

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Ser Arg Pro His Gln Ser His Leu Cys Ser Thr Trp Val Asn Phe Ala
 65 70 75 80
 Phe Ser Phe Arg Val Thr Cys Asp Ser
 85

(2) INFORMATION FOR SEQ ID NO:519:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1035 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1035

(D) OTHER INFORMATION: / Ceres Seq. ID 1964011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:

```

aacatataaaa ttacgtgctc cctcttcgcc gccgtctctc gcgcgccac ttccctcccg      60
accactcgc ccaaaaccgt agcgccctcg cctgctcgcc gccgcgctcg ttgcgagctc      120
cccatcttcc tccgttaacc atggcgaccc agatcagcaa gaagaagaag ttcgtcagcg      180
20 acggcgtggt ctacqccgag ctcaatgaga tgctgacgcg ggagctcgcg gaggacggct      240
actccggcgt ggaggtgctg gtcacaccga tgcgcacgga gatcatcatc cgcgcaacgc      300
GCacgcagaa cgtgctcggc gagaagggcc gcagGatcag ggagctcacg tctgtggtcc      360
agaagagggt caacttccc gagaacggcg tcgagctcta cgcgagaag gtcgtcaacc      420
gcggcctctg cgcctcgcg caggctgagt cctccgcta caagctcctc ggaggccttg      480
25 ccgtccggag ggctgctat ggtgttcttc gctttgttat ggagagtggg gccgagggtt      540
gtgaggtcat tgtgagtga aagctcaggg ctcaaagagc caagtccatg aagttcaagg      600
atggctacat gatctcatct ggtcagccag tgaatgagta catcgactca gctgtgagac      660
acgtcctcct cagacagggt gttctgggta tcaaggtgaa gatcatgctt gactgggacc      720
cgaagggcaa ggttgcccc atcacccctc ttccggacct ggtgaccatc cataccccga      780
30 aggaggagga cgagctgcgc cctcctgtct tggcagctga ggtctaaggc cccaacagcg      840
tcttcgaaat ggcagtttga tcgggtccta gctaggtttg atcttatgat aagggcagtg      900
ctaagacagt tcgttcgctg tcacttctgt ttaaaattaa gttttgccga gacaagctat      960
atgtaccgga tgaagtggtg gttccrtatt gtatgctctg gaattttatt tttggtatgt      1020
ttattttttt gccct

```

(2) INFORMATION FOR SEQ ID NO:520:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..274

(D) OTHER INFORMATION: / Ceres Seq. ID 1964012

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:

```

His Ile Asn Tyr Val Leu Pro Leu Arg Arg Arg Leu Ser Arg Arg His
1      5      10      15
Phe Pro Pro Asp Pro Leu Ala Gln Asn Arg Ser Ala Leu Ala Cys Ser
20      25      30
Pro Pro Pro Ser Leu Arg Ala Pro His Leu Pro Pro Leu Thr Met Ala
35      40      45
Thr Gln Ile Ser Lys Lys Lys Lys Phe Val Ser Asp Gly Val Phe Tyr
50      55      60
55 Ala Glu Leu Asn Glu Met Leu Thr Arg Glu Leu Ala Glu Asp Gly Tyr
65      70      75      80
Ser Gly Val Glu Val Arg Val Thr Pro Met Arg Thr Glu Ile Ile Ile
85      90      95
Arg Ala Thr Arg Thr Gln Asn Val Leu Gly Glu Lys Gly Arg Arg Ile
100      105      110
60 Arg Glu Leu Thr Ser Val Val Gln Lys Arg Phe Asn Phe Pro Glu Asn
115      120      125

```

598

Gly Val Glu Leu Tyr Ala Glu Lys Val Val Asn Arg Gly Leu Cys Ala
 130 135 140
 Ile Ala Gln Ala Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly Leu Ala
 145 150 155 160
 5 Val Arg Arg Ala Cys Tyr Gly Val Leu Arg Phe Val Met Glu Ser Gly
 165 170 175
 Ala Glu Gly Cys Glu Val Ile Val Ser Gly Lys Leu Arg Ala Gln Arg
 180 185 190
 10 Ala Lys Ser Met Lys Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly Gln
 195 200 205
 Pro Val Asn Glu Tyr Ile Asp Ser Ala Val Arg His Val Leu Leu Arg
 210 215 220
 Gln Gly Val Leu Gly Ile Lys Val Lys Ile Met Leu Asp Trp Asp Pro
 225 230 235 240
 15 Lys Gly Lys Val Gly Pro Ile Thr Pro Leu Pro Asp Leu Val Thr Ile
 245 250 255
 His Thr Pro Lys Glu Glu Asp Glu Leu Arg Pro Pro Val Leu Ala Ala
 260 265 270
 Glu Val

(2) INFORMATION FOR SEQ ID NO:521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..228

(D) OTHER INFORMATION: / Ceres Seq. ID 1964013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:

Met Ala Thr Gln Ile Ser Lys Lys Lys Lys Phe Val Ser Asp Gly Val
 1 10 15
 35 Phe Tyr Ala Glu Leu Asn Glu Met Leu Thr Arg Glu Leu Ala Glu Asp
 20 25 30
 Gly Tyr Ser Gly Val Glu Val Arg Val Thr Pro Met Arg Thr Glu Ile
 35 40 45
 40 Ile Ile Arg Ala Thr Arg Thr Gln Asn Val Leu Gly Glu Lys Gly Arg
 50 55 60
 Arg Ile Arg Glu Leu Thr Ser Val Val Gln Lys Arg Phe Asn Phe Pro
 65 70 75 80
 Glu Asn Gly Val Glu Leu Tyr Ala Glu Lys Val Val Asn Arg Gly Leu
 85 90 95
 45 Cys Ala Ile Ala Gln Ala Glu Ser Leu Arg Tyr Lys Leu Leu Gly Gly
 100 105 110
 Leu Ala Val Arg Arg Ala Cys Tyr Gly Val Leu Arg Phe Val Met Glu
 115 120 125
 50 Ser Gly Ala Glu Gly Cys Glu Val Ile Val Ser Gly Lys Leu Arg Ala
 130 135 140
 Gln Arg Ala Lys Ser Met Lys Phe Lys Asp Gly Tyr Met Ile Ser Ser
 145 150 155 160
 Gly Gln Pro Val Asn Glu Tyr Ile Asp Ser Ala Val Arg His Val Leu
 165 170 175
 55 Leu Arg Gln Gly Val Leu Gly Ile Lys Val Lys Ile Met Leu Asp Trp
 180 185 190
 Asp Pro Lys Gly Lys Val Gly Pro Ile Thr Pro Leu Pro Asp Leu Val
 195 200 205
 60 Thr Ile His Thr Pro Lys Glu Glu Asp Glu Leu Arg Pro Pro Val Leu
 210 215 220
 Ala Ala Glu Val
 225

599

(2) INFORMATION FOR SEQ ID NO:522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 205 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..205

(D) OTHER INFORMATION: / Ceres Seq. ID 1964014

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:

```

Met Leu Thr Arg Leu Ala Glu Asp Gly Tyr Ser Gly Val Glu Val
1           5           10           15
Arg Val Thr Pro Met Arg Thr Glu Ile Ile Ile Arg Ala Thr Arg Thr
15          20          25          30
Gln Asn Val Leu Gly Glu Lys Gly Arg Arg Ile Arg Glu Leu Thr Ser
35          40          45
Val Val Gln Lys Arg Phe Asn Phe Pro Glu Asn Gly Val Glu Leu Tyr
20          50          55          60
Ala Glu Lys Val Val Asn Arg Gly Leu Cys Ala Ile Ala Gln Ala Glu
65          70          75          80
Ser Leu Arg Tyr Lys Leu Leu Gly Gly Leu Ala Val Arg Arg Ala Cys
85          90          95
Tyr Gly Val Leu Arg Phe Val Met Glu Ser Gly Ala Glu Gly Cys Glu
25          100         105         110
Val Ile Val Ser Gly Lys Leu Arg Ala Gln Arg Ala Lys Ser Met Lys
115         120         125
Phe Lys Asp Gly Tyr Met Ile Ser Ser Gly Gln Pro Val Asn Glu Tyr
30          130         135         140
Ile Asp Ser Ala Val Arg His Val Leu Leu Arg Gln Gly Val Leu Gly
145         150         155         160
Ile Lys Val Lys Ile Met Leu Asp Trp Asp Pro Lys Glu Lys Val Gly
165         170         175
Pro Ile Thr Pro Leu Pro Asp Leu Val Thr Ile His Thr Pro Lys Glu
35          180         185         190
Glu Asp Glu Leu Arg Pro Pro Val Leu Ala Ala Glu Val
195         200         205

```

(2) INFORMATION FOR SEQ ID NO:523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..818

(D) OTHER INFORMATION: / Ceres Seq. ID 1983854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:

```

gatataagaa accctagcgg agccactaac acagtcgcct ccttcctgcr ccgccgccgc      60
cgccgccgcc gccgctacca ccgcctcgcg gccgcctgcg gctccgcgtt tccgcacgga      120
agttggtgaa ggtttcttga ggctgagaac atggtgctga agacggaact ttgccgcttc      180
agcgscagaa gatttatcct gggaaaggca ttagatttat ccgtgctgat tctcaggtct      240
tcctttttgc caactcgaaa tgcaagcgct acttccacaa ccgcctgaag cctgcaaagc      300
ttacctggac agcaatgtac aggaagcagc acaagaagga tatccatgct gaagcggtaa      360
agaagaggcg ccgcgccacc aagaagccat actccaggtc aattgtgggt gcttccttgg      420
aagtaatcca gaagaagaga gctgagaagc cagaggtccg cgatgctgct agagaagctg      480
ctcttcgtga gatcaaggag cgcatacaaga agaccaagga tgagaagaaa gcgaagaagg      540
cggaggtgag caagtcccag aagacgcaga caaagggtgc ggtccagaag ggttccaagg      600
gccccaagtt gggcggcggt ggtgggaagc gctgaaagaa cttagtgtcg tttctcgaca      660
ttgcagtcgt tccttagcca aagccacttt cgtagaacct gtgttgaatt tgcaagactt      720

```

600

attcaagcgt tgcttgtgcg tgctaaatac catggcaaga gaacggattt atatttatgc
ctgaaaaaaaa tgaccgttca tattcttaac tcattctg

780

(2) INFORMATION FOR SEQ ID NO:524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 1983855

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:

Met Tyr Arg Lys Gln His Lys Lys Asp Ile His Ala Glu Ala Val Lys
1 5 10 15
Lys Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
20 25 30
Ala Ser Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
35 40 45
Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
50 55 60
Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Ala Glu Val Ser Lys
65 70 75 80
Ser Gln Lys Thr Gln Thr Lys Gly Ala Val Gln Lys Gly Ser Lys Gly
85 90 95
Pro Lys Leu Gly Gly Gly Gly Gly Lys Arg
100 105

(2) INFORMATION FOR SEQ ID NO:525:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
(B) LOCATION: 1..802

(D) OTHER INFORMATION: / Ceres Seq. ID 1990261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:

gatataagaa accctagcgg mscactaaya cagtgcgctc cttcctgcgc cgccgcccgc 60
gccgcccgtc ccaccgcctc gcgccgcctc gcggtccgc gtttccgcac ggaagtgtgt 120
gaaggtttct tgaggctgag aacatggtgc tgaagacgga actttgccgc ttcagcggcc 180
agaagattta tcctgggaaa ggcattagat ttatccgtgc tgattctcag gtcttccttt 240
45 ttgccaactc gaaatgcaag cgctacttcc acaaccgcct gaagcctgca aagcttacct 300
ggacagcaat gtacaggaag cagcacaaga aggatatcca tgctgaagcg gtaaagaaga 360
ggcgcgcgcg caccaagaag ccatactcca ggtcaattgt ggggtgcttc ttggaagtaa 420
tccagaagaa gagagctgag aagccagagg tccgcgatgc tgctagagaa gctgctcttc 480
gtgagatcaa ggagcgcac aagaagacca aggatgagaa gaaagcgaag aaggcggagg 540
50 tgagcaagtc ccagaagacg cagacaaagg gtgcggtcca gaagggttcc aagggcccca 600
agttgggctg cgggtggtggg aagcgttgaa agaacttagt gtcgtttctc gacattgcag 660
tcgttcctta gccaaagcca ctttcgtaga acctgtgttg aatttgcaag acttattcaa 720
gcgttgcttg tgcgtgctaa ataccatggc aagagaacgg atttatattt atgcctgaaa 780
aaaaatgacc gttcatattc tt

(2) INFORMATION FOR SEQ ID NO:526:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

601

(A) NAME/KEY: peptide

(B) LOCATION: 1..161

(D) OTHER INFORMATION: / Ceres Seq. ID 2061972

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:

5 Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr
 1 5 10 15
 Pro Gly Lys Gly Ile Arg Phe Ile Arg Ala Asp Ser Gln Val Phe Leu
 20 25 30
 Phe Ala Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Arg Leu Lys Pro
 35 40 45
 10 Ala Lys Leu Thr Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp
 50 55 60
 Ile His Ala Glu Ala Val Lys Lys Arg Arg Arg Ala Thr Lys Lys Pro
 65 70 75 80
 15 Tyr Ser Arg Ser Ile Val Gly Ala Ser Leu Glu Val Ile Gln Lys Lys
 85 90 95
 Arg Ala Glu Lys Pro Glu Val Arg Asp Ala Ala Arg Glu Ala Ala Leu
 100 105 110
 Arg Glu Ile Lys Glu Arg Ile Lys Lys Thr Lys Asp Glu Lys Lys Ala
 115 120 125
 20 Lys Lys Ala Glu Val Ser Lys Ser Gln Lys Thr Gln Thr Lys Gly Ala
 130 135 140
 Val Gln Lys Gly Ser Lys Gly Pro Lys Leu Gly Gly Gly Gly Lys
 145 150 155 160
 25 Arg

(2) INFORMATION FOR SEQ ID NO:527:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 2061973

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:

40 Met Tyr Arg Lys Gln His Lys Lys Asp Ile His Ala Glu Ala Val Lys
 1 5 10 15
 Lys Arg Arg Arg Ala Thr Lys Lys Pro Tyr Ser Arg Ser Ile Val Gly
 20 25 30
 Ala Ser Leu Glu Val Ile Gln Lys Lys Arg Ala Glu Lys Pro Glu Val
 35 40 45
 45 Arg Asp Ala Ala Arg Glu Ala Ala Leu Arg Glu Ile Lys Glu Arg Ile
 50 55 60
 Lys Lys Thr Lys Asp Glu Lys Lys Ala Lys Lys Ala Glu Val Ser Lys
 65 70 75 80
 Ser Gln Lys Thr Gln Thr Lys Gly Ala Val Gln Lys Gly Ser Lys Gly
 85 90 95
 50 Pro Lys Leu Gly Gly Gly Gly Gly Lys Arg
 100 105

SEQ TABLE 2

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 494 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

602

(A) NAME/KEY: -

(B) LOCATION: 1..494

(D) OTHER INFORMATION: / Ceres Seq. ID 1007802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

5  aacaatcggg agaaaggaga agacgaagat gtcgttggtg tgggttggaag cgatggttgcc      60
   tctcgggaatc atcgggtggga tgctctgtat catgggcaat tctcagtact acatccacaa      120
   agcttatcat ggccgtccta agcacatcgg ccacgatgaa tgggatgttg ctatggaaa      180
   acgcgacaag aaagtcgtcg agaaagctgc agtccttcc tcatgattcg ctttatctct      240
   tttgtgttcc ttaggggctt aaggtgacca cttgtggtga caaataaagt gcattccaga      300
10 agaagaagaa gctgggggat ctagtacttt cattcccatt tgattttcc tggacatatt      360
   aaagctttca gaaatcagac ctcaataaca tttggtttat caatatttct ctattcgtga      420
   tattttgtat gcttttaagt tgcatgatac actgaactac tctcttgctg tgtgagtgaa      480
   taaatgaata tctc

```

(2) INFORMATION FOR SEQ ID NO:2:

```

15  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 94 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear

```

20 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..94

(D) OTHER INFORMATION: / Ceres Seq. ID 1007803

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Gln Ser Glu Glu Arg Arg Arg Arg Arg Cys Arg Trp Tyr Gly Trp Lys
1      5      10      15
Arg Cys Cys Leu Ser Glu Ser Ser Val Gly Cys Ser Val Ser Trp Ala
      20      25      30
30  Ile Leu Ser Thr Thr Ser Thr Lys Leu Ile Met Ala Val Leu Ser Thr
      35      40      45
Ser Ala Thr Met Asn Gly Met Leu Leu Trp Lys Asp Ala Thr Arg Lys
      50      55      60
35  Ser Ser Arg Lys Leu Gln Leu Leu Pro His Asp Ser Leu Tyr Leu Phe
      65      70      75      80
Cys Val Pro Gln Gly Leu Lys Val Thr Thr Cys Gly Asp Lys
      85      90

```

(2) INFORMATION FOR SEQ ID NO:3:

```

40  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 74 amino acids
      (B) TYPE: amino acid
      (C) STRANDEDNESS:
      (D) TOPOLOGY: linear

```

45 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1007804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

50  Thr Ile Gly Arg Lys Glu Lys Thr Lys Met Ser Leu Val Trp Leu Glu
      1      5      10      15
Ala Met Leu Pro Leu Gly Ile Ile Gly Gly Met Leu Cys Ile Met Gly
      20      25      30
55  Asn Ser Gln Tyr Tyr Ile His Lys Ala Tyr His Gly Arg Pro Lys His
      35      40      45
Ile Gly His Asp Glu Trp Asp Val Ala Met Glu Arg Arg Asp Lys Lys
      50      55      60
Val Val Glu Lys Ala Ala Pro Ser Ser
      65      70

```

60 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

603

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..65
 (D) OTHER INFORMATION: / Ceres Seq. ID 1007805
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

10	Met	Ser	Leu	Val	Trp	Leu	Glu	Ala	Met	Leu	Pro	Leu	Gly	Ile	Ile	Gly
	1			5					10				15			
	Gly	Met	Leu	Cys	Ile	Met	Gly	Asn	Ser	Gln	Tyr	Tyr	Ile	His	Lys	Ala
			20					25					30			
	Tyr	His	Gly	Arg	Pro	Lys	His	Ile	Gly	His	Asp	Glu	Trp	Asp	Val	Ala
15		35				40				45						
	Met	Glu	Arg	Arg	Asp	Lys	Lys	Val	Val	Glu	Lys	Ala	Ala	Ala	Pro	Ser
		50				55				60						
	Ser															
	65															

20 (2) INFORMATION FOR SEQ ID NO:5:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 700 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..700
 (D) OTHER INFORMATION: / Ceres Seq. ID 1008556
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

	aaaagaaaac	tgaagaaccc	caaaaatccc	agtgaaaga	aaacgttatc	cacttcgaga	60
	gagtgcacgc	tcacgaagca	aatccaaatt	caaaaactttt	ccataaaaaat	caaatacactt	120
	cttcttatta	cttccccaaa	tcgaaatcag	tcacttatta	aaaccctaaa	tcatagcacgat	180
35	cgcaccggca	ttgcagacga	cgttcgtgtc	atcaaccaac	ttcctgaaac	attcttcttc	240
	gtggggatca	tcatacccaa	acaatgtgat	tcttcccaaa	aacaagagat	cttctacctc	300
	cgtagtgtgc	gccgcgcgtc	gtgatgtctc	ttctgacgga	acaatctact	taatcggcgg	360
	agccatcgcc	gttgcaactgc	tcggaactgc	atttccgatc	ctcttcaaac	gcaaagacac	420
	gtgtccggaa	tgtgatggag	caggatattgt	gaggaaagga	ggagtgcactc	tgagagccaa	480
40	cgccgcacgg	aaggatcttc	ctcagatcgt	ttgtgctaata	tgcaatggac	tcggaaagct	540
	taaccagatt	gataaatcat	aagtcttctt	catatatatg	taaaaagctc	catttctcat	600
	tcctcttctt	atctacaata	tacctctgta	agagtagata	gcttcgaatg	atcaatgggt	660
	gcttggagat	ggatggatat	atatatacaa	ttgctttttt			

45 (2) INFORMATION FOR SEQ ID NO:6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..129
 (D) OTHER INFORMATION: / Ceres Seq. ID 1008557
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

55	Met	Thr	Ile	Ala	Pro	Ala	Leu	Gln	Thr	Thr	Phe	Val	Ser	Ser	Thr	Asn
	1				5				10					15		
	Phe	Leu	Lys	His	Ser	Ser	Ser	Trp	Gly	Ser	Ser	Ser	Pro	Asn	Asn	Val
			20					25					30			
60	Ile	Leu	Pro	Lys	Asn	Lys	Arg	Ser	Ser	Thr	Ser	Val	Val	Val	Ala	Ala
		35				40				45						
	Val	Gly	Asp	Val	Ser	Ser	Asp	Gly	Thr	Ile	Tyr	Leu	Ile	Gly	Gly	Ala

604

50 55 60
 Ile Ala Val Ala Leu Val Gly Thr Ala Phe Pro Ile Leu Phe Lys Arg
 65 70 75 80
 Lys Asp Thr Cys Pro Glu Cys Asp Gly Ala Gly Phe Val Arg Lys Gly
 5 85 90 95
 Gly Val Thr Leu Arg Ala Asn Ala Ala Arg Lys Asp Leu Pro Gln Ile
 100 105 110
 Val Cys Ala Asn Cys Asn Gly Leu Gly Lys Leu Asn Gln Ile Asp Lys
 115 120 125
 10 Ser

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 665 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

20 (A) NAME/KEY: -
 (B) LOCATION: 1..665
 (D) OTHER INFORMATION: / Ceres Seq. ID 1008628

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

25 atgttactct tctcagatct cttgttcggt ttgatgtaca atggcgctcct tggtagcagc 60
 tcctatctct ttctcaggtg actctcatgt caaagcacac cgaaacttca atgcgattcg 120
 caagagctct acattgactg ttcaaacaaa atcaaaccgc agtcacaaac tctcggtttc 180
 tgcaggttac cgtgggggaa gtaagggtgg tggaagtagt gattttgtta ccggttttct 240
 tctaggaagt gctgtgttcg gaactctggc ttatatcttt gctccacaga tccgaagatc 300
 agtgctgagc gagaatgaat atggtttcaa gaaaccggag cagccgatgt actatgacga 360
 30 aggcctagag gagagaagag agatattgaa tgagaaaatc ggccaactca attccgccat 420
 tgacaagggt tcgtcgcgtc tgaaaggagg tcggagcggg agcagcaaga acacttcttc 480
 gccgtctgtc ccagttgaaa ccgacgcaga agcagaagct actgcatgat tgaatgtaat 540
 cctctgctct attttaccaa ttcaaaactg ccttccattg gttctgtggt tttttttttt 600
 35 tttttgttg aaccattagg ggcttttctg acttttagat attgaaagaa aaagacaatc 660
 gtcgc

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

45 (A) NAME/KEY: peptide
 (B) LOCATION: 1..162
 (D) OTHER INFORMATION: / Ceres Seq. ID 1008629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ser Leu Val Ala Ala Pro Ile Ser Phe Ser Gly Asp Ser His
 1 5 10 15
 50 Val Lys Ala His Arg Asn Phe Asn Ala Ile Arg Lys Ser Ser Thr Leu
 20 25 30
 Thr Val Gln Thr Lys Ser Asn Arg Ser His Lys Leu Ser Val Ser Ala
 35 40 45
 Gly Tyr Arg Gly Gly Ser Lys Gly Gly Gly Ser Ser Asp Phe Val Thr
 50 55 60
 Gly Phe Leu Leu Gly Ser Ala Val Phe Gly Thr Leu Ala Tyr Ile Phe
 65 70 75 80
 Ala Pro Gln Ile Arg Arg Ser Val Leu Ser Glu Asn Glu Tyr Gly Phe
 85 90 95
 60 Lys Lys Pro Glu Gln Pro Met Tyr Tyr Asp Glu Gly Leu Glu Glu Arg
 100 105 110
 Arg Glu Ile Leu Asn Glu Lys Ile Gly Gln Leu Asn Ser Ala Ile Asp

605

115 120 125
 Lys Val Ser Ser Arg Leu Lys Gly Gly Arg Ser Gly Ser Ser Lys Asn
 130 135 140
 Thr Ser Ser Pro Ser Val Pro Val Glu Thr Asp Ala Glu Ala Glu Ala
 5 145 150 155 160
 Thr Ala

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..1101
 (D) OTHER INFORMATION: / Ceres Seq. ID 1009376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

cttcttttctt ctttcttctt tctgttttct ggtcgctcgt taccocccaag acctcgtcga 60
 gggtttctttc tctctgaaaa agtgcttttg ctgcggttcc atgctctcgg aaggaacttg 120
 gctgaatcgt tggaggatta tcgatctggc gtcgttggtg catctctagc tgcgccaatt 180
 catcggtacc gggttgattt ctccttttcg cgaatctagc cttccgtgat cttagccatg 240
 ttctatggca cagctgtatg ggacccttgg cttatcgttg gccagattat ttgcctccaa 300
 25 tgccttact atctactct tggactcttc accatggtct ttcttggcct tcgtgttctt 360
 cgccttagtc ttgtctactt cttcgattac gctactctca ctacttcac cttcaccggt 420
 tggctcgtta ttgcctcatt cctcttctct tcaactcgct gggctgtgta catgatattt 480
 ttgggtggagc gagcacggaa atgcttagat ttctctgcaa ctctctacat catacatctc 540
 ttcttttgca tcatgtatgg aggatggcct tctctatagg cgtgggtgggt tgtaaatgga 600
 30 accggactcg ctgttatggc ttgtctagct gagtacttgt gcattaaacg cgaacagcga 660
 gagatcccta tggatcgctt ccactcaagg gtttgaagat tggtgaaaga acaagtgatg 720
 aagattcttg tgggttagca gcgcgactcg tagagcctag tagagcctag tactcttaac 780
 aattgtgatg tacagagatg aaatcagagg agtagaatgg gcgaaaggaa gttcagctag 840
 ccaagcaaca atgttggaca ctggtgcacc aactctgact gcaattttta gtgacttcaa 900
 35 atactaagac ttggaatac gtttcaattt gttcttttgt atgaaaaaaa cattagactc 960
 gaataggtta ttgatttcat gttgcttctt ttttttgttt atactggatt ttctcttcta 1020
 tctctactt ggtgcagctt tgtgtgtttt aaaaccagtg tctcattcat catactcttt 1080
 taccaccaat tgaatccttc c

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..152
 (D) OTHER INFORMATION: / Ceres Seq. ID 1009377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Phe Tyr Gly Thr Ala Val Trp Asp Pro Trp Leu Ile Val Gly Gln
 1 5 10 15
 Ile Ile Cys Leu Gln Cys Ser Tyr Tyr Leu Thr Leu Gly Leu Phe Thr
 20 25 30
 55 Met Val Phe Leu Gly Leu Arg Val Pro Arg Leu Ser Leu Val Tyr Phe
 35 40 45
 Phe Asp Tyr Ala Thr Leu Thr Ser Thr Phe Thr Gly Trp Ser Val
 50 55 60
 60 Ile Ala Ser Phe Leu Phe Ser Ser Leu Ala Gly Ala Val Tyr Met Ile
 65 70 75 80
 Phe Leu Val Glu Arg Ala Arg Lys Cys Leu Asp Phe Ser Ala Thr Leu
 85 90 95

606

Tyr Ile Ile His Leu Phe Phe Cys Ile Met Tyr Gly Gly Trp Pro Ser
 100 105 110
 Ser Met Ala Trp Trp Val Val Asn Gly Thr Gly Leu Ala Val Met Ala
 115 120 125
 5 Leu Leu Ala Glu Tyr Leu Cys Ile Lys Arg Glu Gln Arg Glu Ile Pro
 130 135 140
 Met Asp Arg Phe His Ser Arg Val
 145 150

(2) INFORMATION FOR SEQ ID NO:11:

10 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1009378

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Val Phe Leu Gly Leu Arg Val Pro Arg Leu Ser Leu Val Tyr Phe
 1 5 10 15
 Phe Asp Tyr Ala Thr Leu Thr Thr Ser Thr Phe Thr Gly Trp Ser Val
 20 25 30
 25 Ile Ala Ser Phe Leu Phe Ser Ser Leu Ala Gly Ala Val Tyr Met Ile
 35 40 45
 Phe Leu Val Glu Arg Ala Arg Lys Cys Leu Asp Phe Ser Ala Thr Leu
 50 55 60
 Tyr Ile Ile His Leu Phe Phe Cys Ile Met Tyr Gly Gly Trp Pro Ser
 30 65 70 75 80
 Ser Met Ala Trp Trp Val Val Asn Gly Thr Gly Leu Ala Val Met Ala
 85 90 95
 Leu Leu Ala Glu Tyr Leu Cys Ile Lys Arg Glu Gln Arg Glu Ile Pro
 100 105 110
 35 Met Asp Arg Phe His Ser Arg Val
 115 120

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1009379

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ala Gln Leu Tyr Gly Thr Leu Gly Leu Ser Leu Ala Arg Leu Phe
 50 1 5 10 15
 Ala Ser Asn Ala Leu Thr Ile Ser Leu Leu Asp Ser Ser Pro Trp Ser
 20 25 30
 Phe Leu Ala Phe Val Phe Leu Ala Leu Val Leu Ser Thr Ser Ser Ile
 35 40 45
 55 Thr Leu Leu Ser Leu Leu Pro Pro Ser Pro Val Gly Leu Leu Leu Pro
 50 55 60
 His Ser Ser Ser Leu His Ser Leu Gly Leu Cys Thr
 65 70 75

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 398 base pairs

(B) TYPE: nucleic acid

607

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 5 (A) NAME/KEY: -
 (B) LOCATION: 1..398
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011128
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
 10 aaatcaatag cttatctagt tcttgactgt tcaacgatca atggcaccat ccgctgcaat 60
 gctcatactc tcacatcctc tagttagcca caaagctaag aatcaatctc tgtcatcgcc 120
 gtcgtctgtt aagtcgacac gtgtcttcgg ttttctttgg ccttggaagg cattagacaa 180
 tgaggatcat tccgcggttg ttctaggccg gctctttggc gatccggcta ctatcgagaa 240
 gcgcttccaa gaagctcttg aacaaagctg ttggttaatt gtacaatgtt tggttgggtt 300
 tattgattgt ttttacgtta aaatcgcttt tataaattgg aaattgaagt actgtaaaat 360
 15 gtaaaaattg actatatata attaaaggta cattatgc
 (2) INFORMATION FOR SEQ ID NO:14:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 25 (B) LOCATION: 1..78
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011129
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
 Met Ala Pro Ser Ala Ala Met Leu Ile Leu Ser His Pro Leu Val Ser
 1 5 10 15
 30 His Lys Ala Lys Asn Gln Ser Leu Ser Ser Pro Ser Ser Val Lys Ser
 20 25 30
 Thr Arg Val Phe Gly Phe Leu Trp Pro Trp Lys Ala Leu Asp Asn Glu
 35 35 40 45
 Asp His Ser Ala Val Val Leu Gly Arg Leu Phe Gly Asp Pro Ala Thr
 50 55 60
 35 Ile Glu Lys Arg Phe Gln Glu Ala Leu Glu Gln Ser Cys Trp
 65 70 75
 (2) INFORMATION FOR SEQ ID NO:15:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 45 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..72
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011130
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
 50 Met Leu Ile Leu Ser His Pro Leu Val Ser His Lys Ala Lys Asn Gln
 1 5 10 15
 Ser Leu Ser Ser Pro Ser Ser Val Lys Ser Thr Arg Val Phe Gly Phe
 20 25 30
 Leu Trp Pro Trp Lys Ala Leu Asp Asn Glu Asp His Ser Ala Val Val
 55 35 40 45
 Leu Gly Arg Leu Phe Gly Asp Pro Ala Thr Ile Glu Lys Arg Phe Gln
 50 55 60
 Glu Ala Leu Glu Gln Ser Cys Trp
 65 70
 60 (2) INFORMATION FOR SEQ ID NO:16:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 549 base pairs

608

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -
 (B) LOCATION: 1..549
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011718

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

agggatgtag taggcccaata ggcaaatcag agaatcacaa atggtatctg gtcaagaaga      60
ttcctgtttg tctgcagatg catgtgtgta atctagggtta tatgtttttg tccatttggt      120
ttcataaggc aataaagatc cagctattta ctacttggtg agaaaaaagt gagggaaaac      180
agagtcaagt ccgattactt ttctgggaaa gctgaggatt ttgtgttctt agagagcaga      240
tgaagaggtg actggtgttt ctggtgagat agaagttggc atctaaattt gctttctctg      300
gaccagtgaa atcaattgca gtctcctata tattgtagta ggcgatgtat cagtggtgaa      360
gcgaggatga catctgtggg tacttgttct taatccttca ctctgatatc tatgctttag      420
aagcgtttca agttcatgaa gctgatttga tgttgagttt ttaacaacaa gaatcaattc      480
actccaaaaa tatgtaaact ctgccatgcc ttgagctgct ttttggatta tccactgttt      540
tggtttgtg

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
 (B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1011719

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```

Gly Cys Ser Arg Pro Ile Gly Lys Ser Glu Asn His Lys Trp Tyr Leu
1           5           10           15
Val Lys Lys Ile Pro Val Cys Leu Gln Met His Val Cys Asn Leu Gly
35          20          25          30
Tyr Met Phe Leu Ser Ile Trp Phe His Lys Ala Ile Lys Ile Gln Leu
35          40          45
Phe Thr Thr Cys Glu Glu Lys Ser Glu Gly Lys Gln Ser Gln Val Arg
50          55          60
Leu Leu Phe Trp Glu Ser
65          70

```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
 (B) LOCATION: 1..45

(D) OTHER INFORMATION: / Ceres Seq. ID 1011720

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Met His Val Cys Asn Leu Gly Tyr Met Phe Leu Ser Ile Trp Phe His
55 1           5           10           15
Lys Ala Ile Lys Ile Gln Leu Phe Thr Thr Cys Glu Glu Lys Ser Glu
20          25          30
Gly Lys Gln Ser Gln Val Arg Leu Leu Phe Trp Glu Ser
35          40          45

```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

609

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..37
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011721

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

10 Met Phe Leu Ser Ile Trp Phe His Lys Ala Ile Lys Ile Gln Leu Phe
 1 5 10 15
 Thr Thr Cys Glu Glu Lys Ser Glu Gly Lys Gln Ser Gln Val Arg Leu
 20 25 30
 Leu Phe Trp Glu Ser
 15 35

(2) INFORMATION FOR SEQ ID NO:20:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 25 (B) LOCATION: 1..417
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011735

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

aattccttct ttttcacatc tacccaaaat tccaaaacac catcgatttt ttgctctctt 60
 gaaatgctct ttttatgtcc aattcttctc ttccaactaa accgaaccgg aaaaccaggt 120
 30 tcggagatcg gtgtttactg atggccaaac agcaacgaac ccgactttac atactccgaa 180
 gatgtgtctc catgctgctt tgctggcacg accactctat ttctgattag ttgcagtc 240
 tgaaccggac tgaccaagaa gtagcaatca gaagaatgtg atgtcattta gagttttttc 300
 ttgttttctt ttagaactct cttcagggaa tcttttgtaa ttgaagaaga ctctaaggat 360
 tgggcctttt gggcctttgt acatattgtg taaataacat atgaactttt tttaccc

35 (2) INFORMATION FOR SEQ ID NO:21:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 40 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..51
 45 (D) OTHER INFORMATION: / Ceres Seq. ID 1011736

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Ser Asn Ser Ser Leu Pro Thr Lys Pro Asn Arg Lys Thr Arg Phe
 1 5 10 15
 Gly Asp Arg Cys Leu Leu Met Ala Lys Gln Gln Arg Thr Arg Leu Tyr
 50 20 25 30
 Ile Leu Arg Arg Cys Val Ser Met Leu Leu Cys Trp His Asp His Ser
 35 40 45
 Ile Ser Asp
 50

55 (2) INFORMATION FOR SEQ ID NO:22:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 46 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 60 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

610

(A) NAME/KEY: peptide

(B) LOCATION: 1..46

(D) OTHER INFORMATION: / Ceres Seq. ID 1011737

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

5 Asn Ser Phe Phe Thr Ser Thr Gln Asn Ser Lys Thr Pro Ser Ile
 1 5 10 15
 Phe Cys Ser Leu Glu Met Leu Phe Leu Cys Pro Ile Leu Leu Phe Gln
 20 25 30
 10 Leu Asn Arg Thr Gly Lys Pro Gly Ser Glu Ile Gly Val Tyr
 35 40 45

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

15 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

20 (B) LOCATION: 1..32

(D) OTHER INFORMATION: / Ceres Seq. ID 1011738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ile Pro Ser Phe Ser His Leu Pro Lys Ile Pro Lys His His Arg Phe
 1 5 10 15
 25 Phe Ala Leu Leu Lys Cys Ser Phe Tyr Val Gln Phe Phe Ser Ser Asn
 20 25 30

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

30 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

35 (A) NAME/KEY: -

(B) LOCATION: 1..712

(D) OTHER INFORMATION: / Ceres Seq. ID 1011755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

actcaaatag atgaagaaat ggcgagctta agcaccgagct tgctcggaat aagacgaggg 60
 40 tcaagtaaca agaacaaggc agaagataag accaaaaacc agtggtttgc aagaagcatc 120
 caaagcatag acaatcacct ggtgtttgtt ctctttgtct taacgagagg ctctctcttt 180
 ttatcaaagc agcttcttca cgtagaccaa gatctcgtca aatcttgtct acttcttctt 240
 caactacttc ctctctttca tctgacgggt cttcttctgt ctcttcttgt ccttctctta 300
 ttgttgatcg ccgacgatac ttgttaatgt ccggaggcag cggtagagga gagaaagtga 360
 45 tttcgtggat gacgaaaagc cgatccgtag cttataaagt ggatgatgag aaaagaagga 420
 agaagaagac aaagacgaat agtggtttct tttttggtt ggtaatgggc acaaagaaga 480
 gacaataaga tagtcagtct tgtagatttg ttagattaga ttgttcttga ttgtgtattt 540
 tcttgattct ttcatttttag attgattgct acatatagat gactagatca gtttggtggg 600
 tacgtgcaag tgagagagat tctttatacg tattcttgtg attgattccc taagcttgta 660
 50 gtttagtgtg gtaacataaa atgtgataat ccagatttaa tatgcgttga ac

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

55 (C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

60 (B) LOCATION: 1..108

(D) OTHER INFORMATION: / Ceres Seq. ID 1011756

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

611

Thr Gln Ile Asp Glu Glu Met Ala Ser Leu Ser Thr Ser Leu Leu Gly
 1 5 10 15
 Ile Arg Arg Gly Ser Ser Asn Lys Asn Lys Ala Glu Asp Lys Thr Lys
 20 25 30
 5 Asn Gln Cys Phe Ala Arg Ser Ile Gln Ser Ile Asp Asn His Leu Val
 35 40 45
 Phe Val Leu Phe Val Leu Thr Arg Gly Ser Leu Phe Leu Ser Lys Gln
 50 55 60
 10 Leu Leu His Val Asp Gln Asp Leu Val Lys Ser Cys Leu Leu Leu Pro
 65 70 75 80
 Gln Leu Leu Pro Leu Phe His Leu Thr Val Leu Leu Leu Ser Leu Leu
 85 90 95
 Val Leu Leu Leu Leu Ile Ala Asp Asp Thr Cys
 100 105

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1011757

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ala Ser Leu Ser Thr Ser Leu Leu Gly Ile Arg Arg Gly Ser Ser
 1 5 10 15
 Asn Lys Asn Lys Ala Glu Asp Lys Thr Lys Asn Gln Cys Phe Ala Arg
 20 25 30
 Ser Ile Gln Ser Ile Asp Asn His Leu Val Phe Val Leu Phe Val Leu
 35 40 45
 Thr Arg Gly Ser Leu Phe Leu Ser Lys Gln Leu Leu His Val Asp Gln
 50 55 60
 35 Asp Leu Val Lys Ser Cys Leu Leu Leu Pro Gln Leu Leu Pro Leu Phe
 65 70 75 80
 His Leu Thr Val Leu Leu Leu Ser Leu Leu Val Leu Leu Leu Leu Leu
 85 90 95
 Ile Ala Asp Asp Thr Cys
 100

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 422 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..422

(D) OTHER INFORMATION: / Ceres Seq. ID 1011832

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

aataacaata tcaaaagata aaaacagagt ttgcttttat aagatcaaag aaggtaaaaa 60
 aaaaaagtgg caaaatggag tgcgatcgta ttgataatga tggatgatgat tgttgcggtc 120
 55 acaatagaag cacaagaaga aagtgggttg actatttgtt ttcgccaatg ttctcagcct 180
 tgtcgcagtg acgacggtag ttgctatgaa aactgtaaaa tcgaatgcgg tgggtcccaag 240
 cctcccttat ctgctctacg aagctcacat gcatgagatg gcatcatcaa tggaagttcg 300
 cggaaggata ggatgataaa aagagatttg tagcggattt ttgatcatct ctactgtttt 360
 taacttcacg ttttatatta taagagtttc attaaaaaga tcaataaaac gagaaaatgt 420
 gg

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

612

- (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..59
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011833
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:
 Met Met Val Met Ile Val Ala Val Thr Ile Glu Ala Gln Glu Glu Ser
 1 5 10 15
 Gly Trp Thr Ile Cys Phe Arg Gln Cys Ser Gln Pro Cys Arg Ser Asp
 20 25 30
 15 Asp Gly Ser Cys Tyr Glu Asn Cys Lys Ile Glu Cys Gly Gly Pro Lys
 35 40 45
 Pro Pro Leu Ser Arg Leu Arg Ser Ser His Ala
 50 55
- (2) INFORMATION FOR SEQ ID NO:29:
 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..58
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011834
- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:
 Met Val Met Ile Val Ala Val Thr Ile Glu Ala Gln Glu Glu Ser Gly
 1 5 10 15
 Trp Thr Ile Cys Phe Arg Gln Cys Ser Gln Pro Cys Arg Ser Asp Asp
 20 25 30
 35 Gly Ser Cys Tyr Glu Asn Cys Lys Ile Glu Cys Gly Gly Pro Lys Pro
 35 40 45
 Pro Leu Ser Arg Leu Arg Ser Ser His Ala
 50 55
- (2) INFORMATION FOR SEQ ID NO:30:
 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- 45 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..56
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011835
- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
 Met Ile Val Ala Val Thr Ile Glu Ala Gln Glu Glu Ser Gly Trp Thr
 1 5 10 15
 Ile Cys Phe Arg Gln Cys Ser Gln Pro Cys Arg Ser Asp Asp Gly Ser
 20 25 30
 55 Cys Tyr Glu Asn Cys Lys Ile Glu Cys Gly Gly Pro Lys Pro Pro Leu
 35 40 45
 Ser Arg Leu Arg Ser Ser His Ala
 50 55
- (2) INFORMATION FOR SEQ ID NO:31:
 60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 713 base pairs
 (B) TYPE: nucleic acid

613

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..713

(D) OTHER INFORMATION: / Ceres Seq. ID 1011907

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

aattctgggtt tttcttgcaa tgcttcttcc atttctctcc tcctctctcc tcctccgtct      60
10 ctcttctccg atcatgtccc ctgatcccaa atccaatacc ttcttcttct ctttttccaa      120
ttgattaccg gagaatttca gatcgcgatc tccgatttat taataattac agaaaaaaat      180
aattaaacc tagagagaga gagagatata tatatacatg gagagttcat taggtttcat      240
ggcgggtttc gccgtctcag gaagcgttgt gttcttagcg agtcaatttc acaagcgtct      300
tctctccgat tacatggaca agttcgaatt cgaaatccga gcgcagaaaa aaatgggtgat      360
15 gaagaagaag gtgagattcg cggcggatgt ggtggagccg tcggggaata acaaagagta      420
tcgccggaga cattcttcca aggctaaatc gaattcgaag atggcggcaa ctatttgact      480
ttaaggtttt ttgtacaaaa tttaatgtgt aatttattca tttgggtttt tgtgatttga      540
aattcgtaaa ttttaatttcg gaatctgaat ctgggctaaa cttttcaagt cttccccagg      600
gtcaattctt tttcttcttc ttttttttct tgaggggttt tttttgttg ttgtgacctg      660
20 taaataaatg tgttgtttgt gtatatacaa aatgtgattg ctaattacct ttt

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..86

(D) OTHER INFORMATION: / Ceres Seq. ID 1011908

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Met Glu Ser Ser Leu Gly Phe Met Ala Val Phe Ala Val Ser Gly Ser
1          5          10          15
35 Val Val Phe Leu Ala Ser Gln Phe His Lys Arg Leu Leu Ser Asp Tyr
    20          25          30
Met Asp Lys Phe Glu Phe Glu Ile Arg Ala Gln Lys Lys Met Val Met
    35          40          45
40 Lys Lys Lys Val Arg Phe Ala Ala Asp Val Val Glu Pro Ser Gly Asn
    50          55          60
Asn Lys Glu Tyr Arg Arg Arg His Ser Ser Lys Ala Lys Ser Asn Ser
65          70          75          80
Lys Met Ala Ala Thr Ile
    85

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..79

(D) OTHER INFORMATION: / Ceres Seq. ID 1011909

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

Met Ala Val Phe Ala Val Ser Gly Ser Val Val Phe Leu Ala Ser Gln
1          5          10          15
60 Phe His Lys Arg Leu Leu Ser Asp Tyr Met Asp Lys Phe Glu Phe Glu
    20          25          30
Ile Arg Ala Gln Lys Lys Met Val Met Lys Lys Lys Val Arg Phe Ala
    35          40          45

```

614

Ala Asp Val Val Glu Pro Ser Gly Asn Asn Lys Glu Tyr Arg Arg Arg
 50 55 60
 His Ser Ser Lys Ala Lys Ser Asn Ser Lys Met Ala Ala Thr Ile
 65 70 75

5 (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..59

15

(D) OTHER INFORMATION: / Ceres Seq. ID 1011910

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Phe Trp Phe Phe Leu Gln Cys Phe Phe His Phe Ser Pro Pro Leu Ser
 1 5 10 15
 Ser Ser Val Ser Leu Leu Arg Ser Cys Pro Leu Ile Pro Asn Pro Ile
 20 25 30
 Pro Ser Ser Ser Leu Phe Pro Ile Asp Tyr Arg Arg Ile Ser Asp Arg
 35 40 45
 Asp Leu Arg Phe Ile Asn Asn Tyr Arg Lys Lys
 50 55

25 (2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 (B) LOCATION: 1..580

35

(D) OTHER INFORMATION: / Ceres Seq. ID 1011911

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

aattgtttta aaattacaaa ttagtccggt cttttattcc cgtactcgtt cttctttctt 60
 cttcttcctc tcatcgatcat tttctcgatt ctactcttc cggtcaccga ctaattctga 120
 ataagggttta tcaaaagaat aagaataagt ggataaaaag ctagctttga aagagttatt 180
 40 gcagagaaaa aaaatgggat cgagagggat tatcaacgat aagtgggtcaa tgaggattct 240
 atgggggttgt gctatcggaa gtgctatttg tttatacatg gttgctgtag agagacaaac 300
 tcagaacagg gctcgtgcta tggctgagag tttgagagct gctgaatcac aaggtgatgg 360
 tgataatgtc taatatctac caagttagtc tcagttgaat actctcagtt gagttttttt 420
 ttttggtgtt tgtttttgtt ataatgactt cttctgccaa gatgggtgtg atgtagtttc 480
 45 ttttttgcaa ataatcgtaa taaggtttcg aaacttgag agttgaagtt gctgaacata 540
 cgatttgtgt tatcgcaaaa aaagttattt cttatgcctg

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..59

55

(D) OTHER INFORMATION: / Ceres Seq. ID 1011912

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Met Gly Ser Arg Gly Ile Ile Asn Asp Lys Trp Ser Met Arg Ile Leu
 1 5 10 15
 Trp Gly Cys Ala Ile Gly Ser Ala Ile Gly Leu Tyr Met Val Ala Val
 20 25 30

60

615

Glu Arg Gln Thr Gln Asn Arg Ala Arg Ala Met Ala Glu Ser Leu Arg
 35 40 45
 Ala Ala Glu Ser Gln Gly Asp Gly Asp Asn Val
 50 55

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1011913

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Met Arg Ile Leu Trp Gly Cys Ala Ile Gly Ser Ala Ile Gly Leu Tyr
 1 5 10 15
 Met Val Ala Val Glu Arg Gln Thr Gln Asn Arg Ala Arg Ala Met Ala
 20 25 30
 Glu Ser Leu Arg Ala Ala Glu Ser Gln Gly Asp Gly Asp Asn Val
 35 40 45

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1011914

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ile Val Leu Lys Leu Gln Ile Ser Pro Phe Phe Tyr Ser Arg Thr Arg
 1 5 10 15
 Ser Phe Phe Phe Phe Phe Leu Ser Ser Ser Phe Ser Arg Phe Ser Leu
 20 25 30
 Phe Arg Ser Pro Thr Asn Ser Glu
 35 40

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -

(B) LOCATION: 1..415

(D) OTHER INFORMATION: / Ceres Seq. ID 1011954

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

tcacaaaacc tgattgttct gtttcgaacc gatagattcg aaccttggtt taagttgccg 60
 gcttcgagga atctccggtg tggactttca ctctgtttc ttcttcatga cgcaagctgt 120
 tttctctaga atacgctttc ttagaaccct ggaaaacgtt acccagcttc ctcaatcctc 180
 tagctctagc tcgaagaaca tcctttgaaa cacttggtatc tttaagcacc gcttggcaga 240
 caccagataa ggttgattcg atgtcaacaa catttatttg ccaaagggat tgaagcattg 300
 catccttttt agcttcaatg gctttctgaa tatgtctctg atctttgtga ttgtgatgat 360
 catgcatgtc ctatcggttc gatgtatttt ataatgttc gtctgtaagt tattt

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids

616

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..42
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011955
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
 10 Ser Gln Asn Leu Ile Val Leu Phe Arg Thr Asp Arg Phe Glu Pro Trp
 1 5 10 15
 Phe Lys Leu Pro Ala Ser Arg Asn Leu Arg Cys Gly Leu Ser Leu Leu
 20 25 30
 Phe Leu Leu His Asp Ala Ser Cys Phe Leu
 15 35 40
 (2) INFORMATION FOR SEQ ID NO:41:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 20 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 25 (B) LOCATION: 1..33
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011956
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:
 Met Thr Gln Ala Val Phe Ser Arg Ile Arg Phe Leu Arg Thr Leu Glu
 1 5 10 15
 30 Asn Val Thr Gln Leu Pro Gln Ser Ser Ser Ser Ser Lys Asn Ile
 20 25 30
 Leu
 (2) INFORMATION FOR SEQ ID NO:42:
 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..440
 (D) OTHER INFORMATION: / Ceres Seq. ID 1011960
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:
 gacagtcagt cactgtaaca ttttagatct ttcccgaaga agaaaacgaa gaagagacga 60
 agagagaaat gaggccgatg cagctggata tggtatcgga gatggatgat gcaggttctt 120
 cgatggccat ggacgttgat gacctcgaag ccatggagat actcaacgaa ggaggacttg 180
 tctcagataa caagctcgcc gacgccgatt tcttcaacaa attcgatgat gatttcgatg 240
 50 acaccgatat caactaaatc cggttaagtt ttctctttaa gatttcagtt ttttttccta 300
 aacttgatgt aatttggtga gaaacctatg tagtaagtgt gtaataagtt ctgggatttt 360
 tatgtttgtg gtatgtaaca atgtttttct tcatttggat tactaaaaca tttgatttgt 420
 gtgttattgt gctttgtctg
 (2) INFORMATION FOR SEQ ID NO:43:
 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 60 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide

617

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 1011961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

5 Met Arg Pro Met Gln Leu Asp Met Leu Ser Glu Met Asp Asp Ala Gly
 1 5 10 15
 Ser Ser Met Ala Met Asp Val Asp Asp Leu Glu Ala Met Glu Ile Leu
 20 25 30
 Asn Glu Gly Gly Leu Val Ser Asp Asn Lys Leu Ala Asp Ala Asp Phe
 35 40 45
 10 Phe Asn Lys Phe Asp Asp Asp Phe Asp Asp Thr Asp Ile Asn
 50 55 60

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20 (A) NAME/KEY: peptide
 (B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1011962

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

25 Met Gln Leu Asp Met Leu Ser Glu Met Asp Asp Ala Gly Ser Ser Met
 1 5 10 15
 Ala Met Asp Val Asp Asp Leu Glu Ala Met Glu Ile Leu Asn Glu Gly
 20 25 30
 Gly Leu Val Ser Asp Asn Lys Leu Ala Asp Ala Asp Phe Phe Asn Lys
 35 40 45
 30 Phe Asp Asp Asp Phe Asp Asp Thr Asp Ile Asn
 50 55

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 55 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

40 (A) NAME/KEY: peptide
 (B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1011963

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

45 Met Leu Ser Glu Met Asp Asp Ala Gly Ser Ser Met Ala Met Asp Val
 1 5 10 15
 Asp Asp Leu Glu Ala Met Glu Ile Leu Asn Glu Gly Gly Leu Val Ser
 20 25 30
 Asp Asn Lys Leu Ala Asp Ala Asp Phe Phe Asn Lys Phe Asp Asp Asp
 35 40 45
 50 Phe Asp Asp Thr Asp Ile Asn
 50 55

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 193 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

60 (A) NAME/KEY: -
 (B) LOCATION: 1..193
 (D) OTHER INFORMATION: / Ceres Seq. ID 1014075

618

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

aaaaccctta agctaagcaa atttcaaagc aattcaaaaa ccctagcctc tctctcttta 60
 tctctcacaa caaatctttt gaaatggcga tctctaaggc ttccattgtt gttctcatga 120
 5 tggtgattat ctccgtcggt gcatcggcac agtctgaggc accagcacca agtcctactt 180
 ctggatctag tcg

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 10 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 15 (B) LOCATION: 1..39
 (D) OTHER INFORMATION: / Ceres Seq. ID 1014076

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Lys Thr Leu Lys Leu Ser Lys Phe Gln Ser Asn Ser Lys Thr Leu Ala
 1 5 10 15
 20 Ser Leu Ser Leu Ser Leu Thr Thr Lys Ser Leu Lys Trp Arg Ser Leu
 25 30
 Arg Leu Pro Leu Leu Phe Ser
 35

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
 (B) LOCATION: 1..36
 (D) OTHER INFORMATION: / Ceres Seq. ID 1014077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met Ala Ile Ser Lys Ala Ser Ile Val Val Leu Met Met Val Ile Ile
 1 5 10 15
 Ser Val Val Ala Ser Ala Gln Ser Glu Ala Pro Ala Pro Ser Pro Thr
 20 25 30
 40 Ser Gly Ser Ser
 35

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 711 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
 50 (B) LOCATION: 1..711
 (D) OTHER INFORMATION: / Ceres Seq. ID 1015865

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

actcttccgg tcaccgacta attctgggta gctcacattc cttatgctca ttcattccaca 60
 55 gttccctaata taacgctacg aattttgttt ctctctttat ttcttctttc ctcttgtaga 120
 ataagggttta tcaaaagaat aagaataagg tttatctctt aaatctccga taattagcag 180
 agtttttttca ggattgagtt tgatttgctg ttttggaatc ataaattttg cgtttttagtg 240
 gataaaaagc tagcttaaag agttattgca gagaaaaaaa atgggatcga gagggattat 300
 caacgataag tgggtcaatga ggattctatg gggttggtgct atcggaagtg ctattgggtt 360
 60 atacatgggtt gctgtagaga gacaaactca gaacagggct cgtgctatgg ctgagagttt 420
 gagagctgct gaatcacaag gtgatgggtga taatgtctaa tatctaccaa gtatggtcga 480
 gttgaataact ctcatgttag tttttttttt tgggtgtttgt ttttggtata atgacttctt 540

619

ctgccaaagat ggtgttgatg tagtttcttt tttgcaaata atcgtaataa ggttttcgaaa 600
 ctggagagt tgaagttgct gaacatacga tttgtgttat cgcaaaaaaa gttatttctt 660
 atgcctgtca tgctatgttt gtgaattcga tttttaatgc gtattttcag c

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1015866

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Met Gly Ser Arg Gly Ile Ile Asn Asp Lys Trp Ser Met Arg Ile Leu
 1 5 10 15
 Trp Gly Cys Ala Ile Gly Ser Ala Ile Gly Leu Tyr Met Val Ala Val
 20 25 30
 Glu Arg Gln Thr Gln Asn Arg Ala Arg Ala Met Ala Glu Ser Leu Arg
 35 40 45
 Ala Ala Glu Ser Gln Gly Asp Gly Asp Asn Val
 50 55

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1015867

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Arg Ile Leu Trp Gly Cys Ala Ile Gly Ser Ala Ile Gly Leu Tyr
 1 5 10 15
 Met Val Ala Val Glu Arg Gln Thr Gln Asn Arg Ala Arg Ala Met Ala
 20 25 30
 Glu Ser Leu Arg Ala Ala Glu Ser Gln Gly Asp Gly Asp Asn Val
 35 40 45

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..38

(D) OTHER INFORMATION: / Ceres Seq. ID 1015868

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ser Ser Gly His Arg Leu Ile Leu Val Ser Ser His Ser Leu Cys Ser
 1 5 10 15
 Phe Ile His Ser Ser Leu Ile Asn Ala Thr Asn Phe Val Ser Pro Leu
 20 25 30
 Ile Ser Ser Phe Leu Leu
 35

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 432 base pairs

620

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 5 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..432
 (D) OTHER INFORMATION: / Ceres Seq. ID 1021371
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:
 10 gtcatttttct cgattctcac ttttccggtc accgactaat tctgagaaaa aaaatgggat 60
 cgagaggggat tatcaacgat aagtgggtcaa tgaggattct atgggggttgt gctatcggaa 120
 gtgctatttgg tttatacatg gttgctgtag agagacaaac tcagaacagg gctcgtgcta 180
 tggctgagag tttgagagct gctgaatcac aaggtgatgg tgataatgtc taatatctac 240
 caagtagtgc tcagttgaat actctcagtt gagttttttt ttttgggtgtt tgtttttgtt 300
 15 ataatgactt cttctgccaa gatgggtgttg atgtagtttc ttttttgcaa ataatcgtaa 360
 taaggtttcg aaacttgag agttgaagtt gctgaacata cgatttgtgt tatcgcaaaa 420
 aaagttattt cc
 (2) INFORMATION FOR SEQ ID NO:54:
 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 25 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..76
 (D) OTHER INFORMATION: / Ceres Seq. ID 1021372
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:
 30 His Phe Leu Asp Ser His Ser Ser Gly His Arg Leu Ile Leu Arg Lys
 1 5 10 15
 Lys Met Gly Ser Arg Gly Ile Ile Asn Asp Lys Trp Ser Met Arg Ile
 20 25 30
 35 Leu Trp Gly Cys Ala Ile Gly Ser Ala Ile Gly Leu Tyr Met Val Ala
 35 40 45
 Val Glu Arg Gln Thr Gln Asn Arg Ala Arg Ala Met Ala Glu Ser Leu
 50 55 60
 Arg Ala Ala Glu Ser Gln Gly Asp Gly Asp Asn Val
 65 70 75
 40 (2) INFORMATION FOR SEQ ID NO:55:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 45 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..59
 (D) OTHER INFORMATION: / Ceres Seq. ID 1021373
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
 Met Gly Ser Arg Gly Ile Ile Asn Asp Lys Trp Ser Met Arg Ile Leu
 1 5 10 15
 Trp Gly Cys Ala Ile Gly Ser Ala Ile Gly Leu Tyr Met Val Ala Val
 55 20 25 30
 Glu Arg Gln Thr Gln Asn Arg Ala Arg Ala Met Ala Glu Ser Leu Arg
 35 40 45
 Ala Ala Glu Ser Gln Gly Asp Gly Asp Asn Val
 50 55
 60 (2) INFORMATION FOR SEQ ID NO:56:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 47 amino acids

621

(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..47
 (D) OTHER INFORMATION: / Ceres Seq. ID 1021374

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

10 Met Arg Ile Leu Trp Gly Cys Ala Ile Gly Ser Ala Ile Gly Leu Tyr
 1 5 10 15
 Met Val Ala Val Glu Arg Gln Thr Gln Asn Arg Ala Arg Ala Met Ala
 20 25 30
 Glu Ser Leu Arg Ala Ala Glu Ser Gln Gly Asp Gly Asp Asn Val
 15 35 40 45

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..286
 (D) OTHER INFORMATION: / Ceres Seq. ID 1022578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

caccattgga tggttcggct atacaagctg aaacctccca ggaacaggat tcgtggtaaa 60
 gcaaagaaac tgaaatcgaa aacaagctct ggattgagtt caaaatcagc gaagaagaac 120
 30 ccgtgggtct agaaatccta gaattttcaa tgttgatgg tgagttatat gtcaactctt 180
 aggtctcttt attatcgaga aagttgttgc agacgcagtc aagtttcttg tgtaggattc 240
 gtaaaaattt tgttaacttt attcgaattt catgtttatt gcggag

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

40 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: / Ceres Seq. ID 1022579

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

45 His His Trp Met Val Arg Leu Tyr Lys Leu Lys Pro Pro Arg Asn Arg
 1 5 10 15
 Ile Arg Gly Lys Ala Lys Lys Leu Lys Ser Lys Thr Ser Ser Gly Leu
 20 25 30
 Ser Ser Lys Ser Ala Lys Lys Asn Pro Trp Val
 50 35 40

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..43
 (D) OTHER INFORMATION: / Ceres Seq. ID 1022580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

60

622

Met Val Ser Tyr Met Ser Thr Leu Arg Ser Leu Tyr Tyr Arg Glu Ser
 1 5 10 15
 Cys Cys Arg Arg Ser Gln Val Ser Gly Val Gly Phe Val Lys Ile Leu
 20 25 30

5 Leu Thr Leu Phe Glu Phe His Val Tyr Cys Gly
 35 40

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..40

(D) OTHER INFORMATION: / Ceres Seq. ID 1022581

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Met Val Arg Leu Tyr Lys Leu Lys Pro Pro Arg Asn Arg Ile Arg Gly
 1 5 10 15
 Lys Ala Lys Lys Leu Lys Ser Lys Thr Ser Ser Gly Leu Ser Ser Lys
 20 25 30

Ser Ala Lys Lys Asn Pro Trp Val
 35 40

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 643 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..643

(D) OTHER INFORMATION: / Ceres Seq. ID 1024240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

agactcagtg aggatcttct aggcgatttt ctcgagaaaa tcgtttgagg aaaatggaga 60
 cttctatgag gtataccagc aattccaagt ctatgaagat tcatgccaaa gagaagggtc 120
 cgggtgaactc aaaaacccat ttacagcttc atggagagtt agatactgga actggggctc 180
 40 cgagttactt ctgtgcgatg attagacact tttttcctga ggccttgggg taggattgca 240
 ttatgataag cgccaaaagc ttcgggtgtc tgtacgcgga aaaaaagagt ttcctgtaag 300
 agctgataag cgtgtaacct ttaatatata agggcggtgt gatattgatc aggacttaaa 360
 tcagaagaac cccaaaggag cagcagaatt tgcctggaac ataatggatt tcaaggaaga 420
 tcaggatgta cggatcaaag ttggctacga aatgtttgat aagggtccctt atatgcagat 480
 45 tagagaaaac aattggactc tcaacgcgaa catgaaggga aaatggaact tgcggtatga 540
 cctgtaactg catttttttc aatcatcatc tgagaaatgt attgatacca ctgctgatga 600
 acacatttta attctaccaa ttaatcaaatt tcagagatct tcc

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 1024241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Glu Thr Ser Met Arg Tyr Thr Ser Asn Ser Lys Ser Met Lys Ile
 1 5 10 15
 His Ala Lys Glu Lys Val Pro Val Asn Ser Lys Thr His Leu Gln Leu

623

20 25 30
 His Gly Glu Leu Asp Thr Gly Thr Gly Ala Pro Ser Tyr Phe Cys Ala
 35 40 45
 Met Ile Arg His Phe Phe Pro Glu Ala Leu Gly

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..55

(D) OTHER INFORMATION: / Ceres Seq. ID 1024242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Met Arg Tyr Thr Ser Asn Ser Lys Ser Met Lys Ile His Ala Lys Glu
 1 5 10 15
 Lys Val Pro Val Asn Ser Lys Thr His Leu Gln Leu His Gly Glu Leu
 20 25 30
 Asp Thr Gly Thr Gly Ala Pro Ser Tyr Phe Cys Ala Met Ile Arg His
 35 40 45
 Phe Phe Pro Glu Ala Leu Gly
 50 55

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 1024243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Met Asp Phe Lys Glu Asp Gln Asp Val Arg Ile Lys Val Gly Tyr Glu
 1 5 10 15
 Met Phe Asp Lys Val Pro Tyr Met Gln Ile Arg Glu Asn Asn Trp Thr
 20 25 30
 Leu Asn Ala Asn Met Lys Gly Lys Trp Asn Leu Arg Tyr Asp Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 729 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..729

(D) OTHER INFORMATION: / Ceres Seq. ID 1026562

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

gttaatcata taaatttgac cctaaaatct atctcattct ctcacatcaatc ttcttccttt 60
 aaatccctaa atcttcacgt tactttttcta tctacatttt cacttttcaat ggcttttgatt 120
 atcacctgct ccgctctacc cacgatccga gcattcttcg gatccggatc ccttaaccgg 180
 gatcaaaacc gtaagaaatc tgctgcttgg tgggctcctc tcttcgggtt accctccgat 240
 ccagattacc tcaacatcga aagctcatgc tccaccgtga atccggataa aaccgatatt 300
 tccgggtcgg gtcaaaaagt tcgtcgcggg tgttttacgg aggagaaagc taagcagttg 360
 aggaggaaaa ccgcagaagc ttccacgttc catgacgtaa tgtatcactc cgccattgct 420

624

tctcgacttg cgtctgatat caccggccga gtcgaggatt gaaacggatt cgggtcagat 480
 ctggagacga atcaattaat gaataatgaa ttaatctttt ttttcttaat tcagtggttct 540
 tgtaggatgc agaccatctt ctatcggtgc tcctttttca tttgaaccgt tggtttgtgt 600
 ttgggtctttg tgtgttgtaa actctgggtc cctttctgtt tcttctgtaa tcaaccgttg 660
 5 gatttcact tgttattttt agacatgtgt tccctagtta gctcttttat cttatctcaa 720
 atttaaggc

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..153

(D) OTHER INFORMATION: / Ceres Seq. ID 1026563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Val Asn His Ile Asn Leu Thr Leu Lys Ser Ile Ser Phe Ser His Gln
 1 5 10 15
 Ser Ser Ser Phe Lys Ser Leu Asn Leu His Val Thr Phe Leu Ser Thr
 20 25 30
 Phe Ser Leu Ser Met Ala Leu Ile Thr Cys Ser Ala Leu Pro Thr
 35 40 45
 25 Ile Arg Ala Ser Ser Gly Ser Gly Ser Leu Asn Pro Asp Gln Asn Arg
 50 55 60
 Lys Lys Ser Ala Ala Trp Trp Ala Pro Leu Phe Gly Leu Pro Ser Asp
 65 70 75 80
 Pro Asp Tyr Leu Asn Ile Glu Ser Ser Cys Ser Thr Val Asn Pro Asp
 30 85 90 95
 Lys Thr Asp Ile Ser Gly Ser Gly Gln Lys Phe Arg Arg Gly Cys Phe
 100 105 110
 Thr Glu Glu Lys Ala Lys Gln Leu Arg Arg Lys Thr Ala Glu Ala Ser
 115 120 125
 35 Thr Phe His Asp Val Met Tyr His Ser Ala Ile Ala Ser Arg Leu Ala
 130 135 140
 Ser Asp Ile Thr Gly Arg Val Glu Asp
 145 150

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..117

(D) OTHER INFORMATION: / Ceres Seq. ID 1026564

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Ala Leu Ile Ile Thr Cys Ser Ala Leu Pro Thr Ile Arg Ala Ser
 1 5 10 15
 Ser Gly Ser Gly Ser Leu Asn Pro Asp Gln Asn Arg Lys Lys Ser Ala
 20 25 30
 55 Ala Trp Trp Ala Pro Leu Phe Gly Leu Pro Ser Asp Pro Asp Tyr Leu
 35 40 45
 Asn Ile Glu Ser Ser Cys Ser Thr Val Asn Pro Asp Lys Thr Asp Ile
 50 55 60
 Ser Gly Ser Gly Gln Lys Phe Arg Arg Gly Cys Phe Thr Glu Glu Lys
 60 65 70 75 80
 Ala Lys Gln Leu Arg Arg Lys Thr Ala Glu Ala Ser Thr Phe His Asp
 85 90 95

625

Val Met Tyr His Ser Ala Ile Ala Ser Arg Leu Ala Ser Asp Ile Thr
 100 105 110
 Gly Arg Val Glu Asp
 115

5 (2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..484

15 (D) OTHER INFORMATION: / Ceres Seq. ID 1026648

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

aaggatcaca aaattaggggt tttaatttga tagagaagat gaatttcaga agctttgagg 60
 agttctggcc tttctacatg atgcaacact cgaatccatc gacgcgaagg ttgcacttca 120
 taggtatcat cgcgagcatc gttgctttga tatgttcgat tttgatcaac tggtggttct 180
 20 tagctctgggt gcctctgctt gggtacggat tcgcgtggta tagccacttc ttcgtggaag 240
 ggaatgttcc ggcgagcttt gggcatccgc tttggtcggt tctctgcgat ctcaagatgt 300
 ttagtctgat gctcacagga agcatggaga gagagatgaa gagacttggt aagaggccat 360
 tggtgcagct ctcttgaagc agcagcagat atctctatag aattgttctt gattcttctt 420
 attgcgttct gcgattggat tttagactcc agtttgtaat tacttcatgg aatcgttggt 480
 25 tgcg

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..112

35 (D) OTHER INFORMATION: / Ceres Seq. ID 1026649

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Asn Phe Arg Ser Phe Glu Glu Phe Trp Pro Phe Tyr Met Met Gln
 1 5 10 15
 40 His Ser Asn Pro Ser Thr Arg Arg Leu His Phe Ile Gly Ile Ile Ala
 20 25 30
 Ser Ile Val Ala Leu Ile Cys Ser Ile Leu Ile Asn Trp Trp Phe Leu
 35 40 45
 45 Ala Leu Val Pro Leu Leu Gly Tyr Gly Phe Ala Trp Tyr Ser His Phe
 50 55 60
 Phe Val Glu Gly Asn Val Pro Ala Ser Phe Gly His Pro Leu Trp Ser
 65 70 75 80
 Phe Leu Cys Asp Leu Lys Met Phe Ser Leu Met Leu Thr Gly Ser Met
 85 90 95
 50 Glu Arg Glu Met Lys Arg Leu Gly Lys Arg Pro Leu Leu Gln Leu Ser
 100 105 110

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

60 (D) OTHER INFORMATION: / Ceres Seq. ID 1026650

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Met Met Gln His Ser Asn Pro Ser Thr Arg Arg Leu His Phe Ile Gly
 1 5 10 15
 Ile Ile Ala Ser Ile Val Ala Leu Ile Cys Ser Ile Leu Ile Asn Trp
 5 20 25 30
 Trp Phe Leu Ala Leu Val Pro Leu Leu Gly Tyr Gly Phe Ala Trp Tyr
 35 40 45
 Ser His Phe Phe Val Glu Gly Asn Val Pro Ala Ser Phe Gly His Pro
 50 55 60
 10 Leu Trp Ser Phe Leu Cys Asp Leu Lys Met Phe Ser Leu Met Leu Thr
 65 70 75 80
 Gly Ser Met Glu Arg Glu Met Lys Arg Leu Gly Lys Arg Pro Leu Leu
 85 90 95
 Gln Leu Ser

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1026651

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Gln His Ser Asn Pro Ser Thr Arg Arg Leu His Phe Ile Gly Ile
 1 5 10 15
 30 Ile Ala Ser Ile Val Ala Leu Ile Cys Ser Ile Leu Ile Asn Trp Trp
 20 25 30
 Phe Leu Ala Leu Val Pro Leu Leu Gly Tyr Gly Phe Ala Trp Tyr Ser
 35 35 40 45
 His Phe Phe Val Glu Gly Asn Val Pro Ala Ser Phe Gly His Pro Leu
 50 55 60
 35 Trp Ser Phe Leu Cys Asp Leu Lys Met Phe Ser Leu Met Leu Thr Gly
 65 70 75 80
 Ser Met Glu Arg Glu Met Lys Arg Leu Gly Lys Arg Pro Leu Leu Gln
 85 90 95
 40 Leu Ser

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 563 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..563

(D) OTHER INFORMATION: / Ceres Seq. ID 1027881

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

aaaacacaga gaggtagcag agagagagag tgaatatgga gaagtacttt ggaaatgcgt 60
 55 acaggggaga tccaggagtg ccacatgcag atgcagatcg tttcatgaat atatggattg 120
 gttctgctgc tttctccgtt cttacctggg ttaatcctta catgtggcag ctctctaacc 180
 agttcaatta ccatgacaag tggatgctgt ttgagcagta ccaactggaaa aaagcaaggg 240
 caaagaagca accttatgaa ttcaagtggg ataagatacc caaagaagtc agggactcgt 300
 actattacaa ctggccagtc tacttcccat agaagtgtct ctgtgttgct gtgaatcaga 360
 60 agagaaacca aacacttggt gaacttctat ggaatctatc tctatctctt cttgatctgt 420
 tattcgtagc acttttggat tttaagtttt ttcttttgta atgatcaatc tctcaactct 480
 tcactgtttc atctcctcta gttgactctc ttatggaaat attgaatctc tttgaagagc 540

627

agaaccagaa tctgtctgtt atg

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..109

(D) OTHER INFORMATION: / Ceres Seq. ID 1027882

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

Asn Thr Glu Ser Asp Glu Arg Glu Arg Val Lys Met Glu Lys Tyr Phe
1      5      10      15
Gly Asn Ala Tyr Arg Gly Asp Pro Gly Val Pro His Ala Asp Ala Asp
      20      25      30
Arg Phe Met Asn Ile Trp Ile Gly Ser Ala Ala Phe Ser Val Leu Thr
      35      40      45
Trp Val Asn Pro Tyr Met Trp Gln Leu Ser Asn Gln Phe Asn Tyr His
      50      55      60
Asp Lys Trp Met Leu Phe Glu Gln Tyr His Trp Lys Lys Ala Arg Ala
65      70      75      80
Lys Lys Gln Pro Tyr Glu Phe Lys Trp Asn Lys Ile Pro Lys Glu Val
      85      90      95
Arg Asp Ser Tyr Tyr Tyr Asn Trp Pro Val Tyr Phe Pro
      100     105

```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..98

(D) OTHER INFORMATION: / Ceres Seq. ID 1027883

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```

Met Glu Lys Tyr Phe Gly Asn Ala Tyr Arg Gly Asp Pro Gly Val Pro
1      5      10      15
His Ala Asp Ala Asp Arg Phe Met Asn Ile Trp Ile Gly Ser Ala Ala
      20      25      30
Phe Ser Val Leu Thr Trp Val Asn Pro Tyr Met Trp Gln Leu Ser Asn
45      35      40      45
Gln Phe Asn Tyr His Asp Lys Trp Met Leu Phe Glu Gln Tyr His Trp
      50      55      60
Lys Lys Ala Arg Ala Lys Lys Gln Pro Tyr Glu Phe Lys Trp Asn Lys
65      70      75      80
Ile Pro Lys Glu Val Arg Asp Ser Tyr Tyr Tyr Asn Trp Pro Val Tyr
      85      90      95
Phe Pro

```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

628

(B) LOCATION: 1..75

(D) OTHER INFORMATION: / Ceres Seq. ID 1027884

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

5 Met Asn Ile Trp Ile Gly Ser Ala Ala Phe Ser Val Leu Thr Trp Val
 1 5 10 15
 Asn Pro Tyr Met Trp Gln Leu Ser Asn Gln Phe Asn Tyr His Asp Lys
 20 25 30
 Trp Met Leu Phe Glu Gln Tyr His Trp Lys Lys Ala Arg Ala Lys Lys
 35 40 45
 10 Gln Pro Tyr Glu Phe Lys Trp Asn Lys Ile Pro Lys Glu Val Arg Asp
 50 55 60
 Ser Tyr Tyr Tyr Asn Trp Pro Val Tyr Phe Pro
 65 70 75

(2) INFORMATION FOR SEQ ID NO:76:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..305

(D) OTHER INFORMATION: / Ceres Seq. ID 1381797

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

gagggttttg ttttggtgac tcagtgagga ttttctaggc gattttctcg agaaaatcgt 60
 ttgaggaaaa tggagacttc tatgaggtat accagcaatt ccaagtctat gaagattcat 120
 gccaaagaga aggttcgggt gaactcaaaa acccatttac agcttcatgg agagtttagat 180
 actggaactg gggctccgag ttacttctgt gcgatgatta gacacttttt tcttgaggct 240
 30 tcaacaggcc ttggggtagg attgcattat gataagcgcc aaaagcttcg gtgtcttgta 300
 cgcg

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..78

(D) OTHER INFORMATION: / Ceres Seq. ID 1381798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

45 Met Glu Thr Ser Met Arg Tyr Thr Ser Asn Ser Lys Ser Met Lys Ile
 1 5 10 15
 His Ala Lys Glu Lys Val Pro Val Asn Ser Lys Thr His Leu Gln Leu
 20 25 30
 His Gly Glu Leu Asp Thr Gly Thr Gly Ala Pro Ser Tyr Phe Cys Ala
 35 40 45
 50 Met Ile Arg His Phe Phe Pro Glu Ala Ser Thr Gly Leu Gly Val Gly
 50 55 60
 Leu His Tyr Asp Lys Arg Gln Lys Leu Arg Cys Leu Val Arg
 65 70 75

(2) INFORMATION FOR SEQ ID NO:78:

55 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

60 (ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

629

(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1381799

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

5 Met Arg Tyr Thr Ser Asn Ser Lys Ser Met Lys Ile His Ala Lys Glu
 1 5 10 15
 Lys Val Pro Val Asn Ser Lys Thr His Leu Gln Leu His Gly Glu Leu
 20 25 30
 Asp Thr Gly Thr Gly Ala Pro Ser Tyr Phe Cys Ala Met Ile Arg His
 35 40 45
 10 Phe Phe Pro Glu Ala Ser Thr Gly Leu Gly Val Gly Leu His Tyr Asp
 50 55 60
 Lys Arg Gln Lys Leu Arg Cys Leu Val Arg
 65 70

(2) INFORMATION FOR SEQ ID NO:79:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:

(A) NAME/KEY: peptide
 (B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1381800

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

25 Met Lys Ile His Ala Lys Glu Lys Val Pro Val Asn Ser Lys Thr His
 1 5 10 15
 Leu Gln Leu His Gly Glu Leu Asp Thr Gly Thr Gly Ala Pro Ser Tyr
 20 25 30
 30 Phe Cys Ala Met Ile Arg His Phe Pro Glu Ala Ser Thr Gly Leu
 35 40 45
 Gly Val Gly Leu His Tyr Asp Lys Arg Gln Lys Leu Arg Cys Leu Val
 50 55 60
 Arg
 65

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 840 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..840

(D) OTHER INFORMATION: / Ceres Seq. ID 1442747

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

acacgaaacg attccgcttc tccgcttcct tcataaatat ctcaactcgc gtcactacat 60
 tgttctttca cagcaatttt tcatttctct cttaaccgta aacgaatctc tcttctcaaa 120
 50 gttttatttt ctctctgcga tggctcaaga agatgttact gctgttgcta ctaacggtgc 180
 tgggtccggtg gagacgcac ttgtcttcac tgagttcaag cagatgttgc tcgttgaagc 240
 tcaaaaggctc ggtgacgctg ttactttcta caaatctgct tttgggtgcga tcgagtctgg 300
 tcattctctt taccctaagc gtaacttgac caagagcttc ctcatgttct ctctctcgag 360
 cttaatctcg ctggctcttc ctctgttgtt tgcgacgttt cctctctccc tgggttttct 420
 55 actgcgaaat cggaaggctt gggagtgcact tttcttctcg gaactaagga tgctgaagcc 480
 gccgttgcca aagctgttga cgccggagct gtgaaagtgg aggttacgga ggcagaagtt 540
 gaactgggat tcaaaggaaa agttacggat ccttttggtg tcacttggat ctctcgcgag 600
 aagaagaccg tgatcaccga cgagaacaaa gaggtttaga atctgtcgtc ggatctaatt 660
 ctctgctcgg ttctgaacaa aaaaaaatta tctattatcc taggtttatg cttttatttt 720
 60 gtcttttgtg gaatccggtg atcagtaaac cggatcgagt aggctaata ctttcggatt 780
 ctaatttcac cccttttgac aaactctaatt ctgggtgaaa ttgcatatta atctcgggct 840

(2) INFORMATION FOR SEQ ID NO:81:

630

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..148

(D) OTHER INFORMATION: / Ceres Seq. ID 1442748

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

His Glu Thr Ile Pro Leu Leu Arg Phe Leu His Lys Tyr Leu Thr His
 1 5 10 15
 Arg His Tyr Ile Val Leu Ser His Ala Ile Phe Ile Ser Leu Leu Thr
 20 25 30
 Val Asn Glu Ser Leu Phe Ser Lys Phe Tyr Phe Leu Ser Ala Met Ala
 35 40 45
 Gln Glu Asp Val Thr Ala Val Ala Thr Asn Gly Ala Gly Pro Val Glu
 50 55 60
 Thr His Leu Val Phe Thr Glu Phe Lys Gln Met Leu Leu Val Glu Ala
 65 70 75 80
 Gln Lys Val Gly Asp Ala Val Thr Phe Tyr Lys Ser Ala Phe Gly Ala
 85 90 95
 Ile Glu Ser Gly His Ser Leu Tyr Pro Lys Arg Asn Leu Thr Lys Ser
 100 105 110
 Phe Leu Met Phe Ser Leu Leu Ser Leu Ile Ser Leu Ala Leu Pro Ser
 115 120 125
 Leu Phe Ala Thr Phe Pro Leu Ser Leu Val Phe Leu Leu Arg Asn Arg
 130 135 140
 Lys Val Arg Glu
 145

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..102

(D) OTHER INFORMATION: / Ceres Seq. ID 1442749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Met Ala Gln Glu Asp Val Thr Ala Val Ala Thr Asn Gly Ala Gly Pro
 1 5 10 15
 Val Glu Thr His Leu Val Phe Thr Glu Phe Lys Gln Met Leu Leu Val
 20 25 30
 Glu Ala Gln Lys Val Gly Asp Ala Val Thr Phe Tyr Lys Ser Ala Phe
 35 40 45
 Gly Ala Ile Glu Ser Gly His Ser Leu Tyr Pro Lys Arg Asn Leu Thr
 50 55 60
 Lys Ser Phe Leu Met Phe Ser Leu Leu Ser Leu Ile Ser Leu Ala Leu
 65 70 75 80
 Pro Ser Leu Phe Ala Thr Phe Pro Leu Ser Leu Val Phe Leu Leu Arg
 85 90 95
 Asn Arg Lys Val Arg Glu
 100

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

631

(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide
(ix) FEATURE:

5

(A) NAME/KEY: peptide
(B) LOCATION: 1..74

(D) OTHER INFORMATION: / Ceres Seq. ID 1442750

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Met Leu Leu Val Glu Ala Gln Lys Val Gly Asp Ala Val Thr Phe Tyr
1 5 10 15
10 Lys Ser Ala Phe Gly Ala Ile Glu Ser Gly His Ser Leu Tyr Pro Lys
20 25 30
Arg Asn Leu Thr Lys Ser Phe Leu Met Phe Ser Leu Leu Ser Leu Ile
35 40 45
15 Ser Leu Ala Leu Pro Ser Leu Phe Ala Thr Phe Pro Leu Ser Leu Val
50 55 60
Phe Leu Leu Arg Asn Arg Lys Val Arg Glu
65 70

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 513 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

25

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..513

(D) OTHER INFORMATION: / Ceres Seq. ID 1459199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

30 aacttgatc ttaacacaga gaagaagcac aatcggaaga aaggagaaga cgaagatgct 60
gttggtatgg ctggaagcga tgttgccctc cggaatcatc ggtgggatgc tctgtatcat 120
gggcaattct cagtactaca tccacaaagc ttatcatggc cgctcctaagc acatcggcca 180
cgatgaatgg gatgttgcta tggaaagacg cgacaagaaa gtcgtcgaga aagctgcagc 240
tccttcctca tgattcgctt tatctctttt gtgttcctca ggtgaccact tgtggtgaca 300
35 aataaagtgc attccagaag aagaagaagc tgggggatct agtactttca ttcccatttg 360
attttccttg gacatattaa agctttcaga aatcagacct caataacatt tggtttatca 420
atatttctct attcgtgata ttttgtatgc ttttaagttg catgatacac tgaactactc 480
tcttgctgtg tgagtgaata aatgaatc tgc

(2) INFORMATION FOR SEQ ID NO:85:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..83

(D) OTHER INFORMATION: / Ceres Seq. ID 1459200

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

50 Thr Trp Ile Leu Thr Gln Arg Arg Ser Thr Ile Gly Arg Lys Glu Lys
1 5 10 15
Thr Lys Met Ser Leu Val Trp Leu Glu Ala Met Leu Pro Leu Gly Ile
20 25 30
55 Ile Gly Gly Met Leu Cys Ile Met Gly Asn Ser Gln Tyr Ile His
35 40 45
Lys Ala Tyr His Gly Arg Pro Lys His Ile Gly His Asp Glu Trp Asp
50 55 60
60 Val Ala Met Glu Arg Arg Asp Lys Lys Val Val Glu Lys Ala Ala Ala
65 70 75 80
Pro Ser Ser

632

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..65

(D) OTHER INFORMATION: / Ceres Seq. ID 1459201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

Met Ser Leu Val Trp Leu Glu Ala Met Leu Pro Leu Gly Ile Ile Gly
1          5          10          15
Gly Met Leu Cys Ile Met Gly Asn Ser Gln Tyr Tyr Ile His Lys Ala
15          20          25          30
Tyr His Gly Arg Pro Lys His Ile Gly His Asp Glu Trp Asp Val Ala
35          40          45
Met Glu Arg Arg Asp Lys Lys Val Val Glu Lys Ala Ala Ala Pro Ser
20 50          55          60
Ser
65

```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1459202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

Met Leu Pro Leu Gly Ile Ile Gly Gly Met Leu Cys Ile Met Gly Asn
1          5          10          15
Ser Gln Tyr Tyr Ile His Lys Ala Tyr His Gly Arg Pro Lys His Ile
20          25          30
Gly His Asp Glu Trp Asp Val Ala Met Glu Arg Arg Asp Lys Lys Val
40 35          40          45
Val Glu Lys Ala Ala Ala Pro Ser Ser
50          55

```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1140

(D) OTHER INFORMATION: / Ceres Seq. ID 1565605

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

atgatttggt tacatttttt cgtggtgttc ttgatttttt tctttgatca aaactagtag      60
aaattttcca atttcgtcct gccttgat tagtagtaga tattttggaa tttgattagt      120
aggtagaaga agatggggac gacgttagat gtatcaagag cagagctagc acttggtgta      180
atgtatttga acaaagcaga ggcaagagat aagtatatga gagctataca gtatggttcc      240
aagttcttga tgggtggaca acctgtact gctcaaaatg ttgacaaatc tactagctta      300
gcaagaaaag tcttcggtct tttcaagttt gtgaatgact tgcatggtct tatcagtcct      360
gtgcctaaag gaactcctct tctcttgtt ttacttgga agtcgaagaa cgcactttta      420
tctacattct tgttcctgga tcaaattgtc tggcttggga gatcaggaat atataagaac      480

```


633

```

aaagaacgag ctgagttact tggacgtata tctctcttct gctggatggg atcttctgtc 540
tgcacaactt tagtcgaggt tggtagatg ggaaggcttt cttcatcaat gaagaagatc 600
gaaaagggac tcaagaatgg aaacaagtat caggatgagg attatcgtgc taagctaaaa 660
aaatcaaacg agaggtcact tgctttgatc aaatcagcta tggacattgt tgtagcagct 720
5 ggtcttcttc agttagctcc aacgaagatc actcctcgtg tcaccggagc ttttggattc 780
atcacctcca tcatttcttg ttaccagttg cttccgacac gcccgaagat caaaacaccc 840
tgaagtcaat cgaggaagct ggtgttaagg agaaagtcac ttcagaaagt ttctgttctt 900
cttattatta aggaaattca ctgctgttat aaaacatcgt ataaaatact tatttgcagg 960
10 aattacggtt attataaatt tatgcctcag attcttgata cacaagtctt aatactcaat 1020
agtattgcat tattatgaga tgttgtttct Gctacgcaat aactagaggc aaaatccaac 1080
tacatatatg ttttgatctg attattataa tagactttgg gcttcattcc gcctaaagct 1140

```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 236 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```

20 (A) NAME/KEY: peptide
    (B) LOCATION: 1..236

```

(D) OTHER INFORMATION: / Ceres Seq. ID 1565606

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

25 Met Gly Thr Thr Leu Asp Val Ser Arg Ala Glu Leu Ala Leu Val Val
    1           5           10           15
Met Tyr Leu Asn Lys Ala Glu Ala Arg Asp Lys Leu Cys Arg Ala Ile
    20           25           30
Gln Tyr Gly Ser Lys Phe Leu Ser Gly Gly Gln Pro Gly Thr Ala Gln
    35           40           45
30 Asn Val Asp Lys Ser Thr Ser Leu Ala Arg Lys Val Phe Arg Leu Phe
    50           55           60
Lys Phe Val Asn Asp Leu His Gly Leu Ile Ser Pro Val Pro Lys Gly
    65           70           75           80
Thr Pro Leu Pro Leu Val Leu Leu Gly Lys Ser Lys Asn Ala Leu Leu
    85           90           95
35 Ser Thr Phe Leu Phe Leu Asp Gln Ile Val Trp Leu Gly Arg Ser Gly
    100          105          110
Ile Tyr Lys Asn Lys Glu Arg Ala Glu Leu Leu Gly Arg Ile Ser Leu
    115          120          125
40 Phe Cys Trp Met Gly Ser Ser Val Cys Thr Thr Leu Val Glu Val Gly
    130          135          140
Glu Met Gly Arg Leu Ser Ser Ser Met Lys Lys Ile Glu Lys Gly Leu
    145          150          155          160
Lys Asn Gly Asn Lys Tyr Gln Asp Glu Asp Tyr Arg Ala Lys Leu Lys
    165          170          175
45 Lys Ser Asn Glu Arg Ser Leu Ala Leu Ile Lys Ser Ala Met Asp Ile
    180          185          190
Val Val Ala Ala Gly Leu Leu Gln Leu Ala Pro Thr Lys Ile Thr Pro
    195          200          205
50 Arg Val Thr Gly Ala Phe Gly Phe Ile Thr Ser Ile Ile Ser Cys Tyr
    210          215          220
Gln Leu Leu Pro Thr Arg Pro Lys Ile Lys Thr Pro
    225          230          235

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

```

55 (A) LENGTH: 220 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

634

(B) LOCATION: 1..220

(D) OTHER INFORMATION: / Ceres Seq. ID 1565607

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

5 Met Tyr Leu Asn Lys Ala Glu Ala Arg Asp Lys Leu Cys Arg Ala Ile
 1 5 10 15
 Gln Tyr Gly Ser Lys Phe Leu Ser Gly Gly Gln Pro Gly Thr Ala Gln
 20 25 30
 Asn Val Asp Lys Ser Thr Ser Leu Ala Arg Lys Val Phe Arg Leu Phe
 35 40 45
 10 Lys Phe Val Asn Asp Leu His Gly Leu Ile Ser Pro Val Pro Lys Gly
 50 55 60
 Thr Pro Leu Pro Leu Val Leu Leu Gly Lys Ser Lys Asn Ala Leu Leu
 65 70 75 80
 Ser Thr Phe Leu Phe Leu Asp Gln Ile Val Trp Leu Gly Arg Ser Gly
 85 90 95
 15 Ile Tyr Lys Asn Lys Glu Arg Ala Glu Leu Leu Gly Arg Ile Ser Leu
 100 105 110
 Phe Cys Trp Met Gly Ser Ser Val Cys Thr Thr Leu Val Glu Val Gly
 115 120 125
 20 Glu Met Gly Arg Leu Ser Ser Ser Met Lys Lys Ile Glu Lys Gly Leu
 130 135 140
 Lys Asn Gly Asn Lys Tyr Gln Asp Glu Asp Tyr Arg Ala Lys Leu Lys
 145 150 155 160
 Lys Ser Asn Glu Arg Ser Leu Ala Leu Ile Lys Ser Ala Met Asp Ile
 165 170 175
 25 Val Val Ala Ala Gly Leu Leu Gln Leu Ala Pro Thr Lys Ile Thr Pro
 180 185 190
 Arg Val Thr Gly Ala Phe Gly Phe Ile Thr Ser Ile Ile Ser Cys Tyr
 195 200 205
 30 Gln Leu Leu Pro Thr Arg Pro Lys Ile Lys Thr Pro
 210 215 220

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 533 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

40 (A) NAME/KEY: -
 (B) LOCATION: 1..533
 (D) OTHER INFORMATION: / Ceres Seq. ID 1566686

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

45 atgattggtg gtttcttcgc cgatgttaaa ttcaacagat cgagagagaa aaaactctct 60
 ctccctctc cgttcaccgt cgcgactcgg ctctacagta cattttgttg agcaatctcg 120
 tatttagagg attccaatgt ctggcgaga ggataataaa tcttcccatg ctgagctttc 180
 gtcccaaatt tttcttgatc ttgtggattc ggtgatagct gatgtagcat ctgagtgatca 240
 tcgggtagca cgactaggac ttgatcgtga ttgggatata gtagaagaag agttgagatt 300
 gtcagtggaa gcgcgtgcga agatcgctga tcctagcaac aacctcgaaa ccaacaccaa 360
 50 atatgttggt gatataattg ggcagactca cctcctgta gctagtgaag tggtcaattg 420
 catgaactgt gggcgacaaa ttgttgcagg aaggtttgct cctcatctgg aaaaatgcat 480
 gggaaaggga agaaaggctc gtgGccaagG actaccagaa gcacaacggc tgc

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 132 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

60 (A) NAME/KEY: peptide
 (B) LOCATION: 1..132

635

(D) OTHER INFORMATION: / Ceres Seq. ID 1566687

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Met Ser Gly Ala Glu Asp Asn Lys Ser Ser His Ala Gln Leu Ser Ser
 1 5 10 15
 5 Gln Ile Phe Leu Asp Leu Val Asp Ser Val Ile Ala Asp Val Ala Ser
 20 25 30
 Glu Cys His Arg Val Ala Arg Leu Gly Leu Asp Arg Asp Leu Asp Ile
 35 40 45
 Val Glu Glu Glu Leu Arg Leu Ser Val Glu Ala Arg Ala Lys Ile Ala
 50 55 60
 10 Asp Pro Ser Asn Asn Leu Glu Thr Asn Thr Lys Tyr Val Val Asp Ile
 65 70 75 80
 Phe Gly Gln Thr His Pro Pro Val Ala Ser Glu Val Phe Asn Cys Met
 85 90 95
 15 Asn Cys Gly Arg Gln Ile Val Ala Gly Arg Phe Ala Pro His Leu Glu
 100 105 110
 Lys Cys Met Gly Lys Gly Arg Lys Ala Arg Gly Gln Gly Leu Pro Glu
 115 120 125
 Ala Gln Arg Leu
 130

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 815 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..815

(D) OTHER INFORMATION: / Ceres Seq. ID 1567367

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

gaaacaagac acgaaagaat ctctaaagaa atcattttca tcgcttcgct tcgatttttc 60
 ttcaatggct gtcgtcggcg ctccaatatc gtctccggcg gctcagctgc agacacaatt 120
 35 tctctccaat cccattctcc ccgcttttcg ccggtctttc tccaccggaa aatcaccagc 180
 aactttctcc gtcgtagcta tggctcccca gaaaaagggtg aacaaatatg atgccaagtg 240
 gaagaaacaa tggtagcgag ctggattggt tttcgaaggg agtgagcaaa taaacgttga 300
 tgttttcaag aagctggaga agcgaaaagt gttgagcaac gttgagaaat ctggcctgct 360
 gtaaaagcag aggggttggg actcacattg tcatctcttg agaagcttaa agtcttctcc 420
 40 aaagcagagg accttgggtc tctcagcttc cttgagaact tagctggamG AACatcgccct 480
 gcggtcttag cctcggctgc attaccagct ctcacggctg ctattgtagc cgtggtgttg 540
 atcccgaatg actcaactac tctagtgtgt gctcaggcgg ttttggccgg tgctcttgcg 600
 cttacagggg ttgttttgtt gggtgttctt gttgttttgg atggacttca agaagctgac 660
 tgattctttc tctgtaaacc aaacataaac ccatgtcttg tccaattgat ttttgtcagt 720
 45 tgctgattta tagctgtatg gttcagttgt ttatggttag tccaagacat aagctgagtg 780
 atagaaagaa gctttataat aattaaacaa atatt

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..76

(D) OTHER INFORMATION: / Ceres Seq. ID 1567368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Glu Thr Arg His Glu Arg Ile Ser Lys Glu Ile Ile Phe Ile Ala Ser
 1 5 10 15
 60 Leu Arg Phe Phe Phe Asn Gly Cys Arg Arg Arg Ser Asn Ile Val Ser
 20 25 30

636

Gly Gly Ser Ala Ala Asp Thr Ile Ser Leu Gln Ser His Ser Pro Pro
 35 40 45
 Leu Ser Pro Val Phe Leu His Arg Lys Ile Thr Ser Asn Phe Leu Arg
 50 55 60
 5 Arg Ser Tyr Gly Ser Pro Glu Lys Gly Glu Gln Ile
 65 70 75

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..120

(D) OTHER INFORMATION: / Ceres Seq. ID 1567369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Lys Gln Asp Thr Lys Glu Ser Leu Lys Lys Ser Phe Ser Ser Leu Arg
 1 5 10 15
 Phe Asp Phe Ser Ser Met Ala Val Val Gly Ala Pro Ile Ser Ser Pro
 20 25 30
 Ala Ala Gln Leu Gln Thr Gln Phe Leu Ser Asn Pro Ile Leu Pro Arg
 35 40 45
 25 Phe Arg Arg Ser Phe Ser Thr Gly Lys Ser Pro Ala Thr Phe Ser Val
 50 55 60
 Val Ala Met Ala Pro Gln Lys Lys Val Asn Lys Tyr Asp Ala Lys Trp
 65 70 75 80
 Lys Lys Gln Trp Tyr Gly Ala Gly Leu Phe Phe Glu Gly Ser Glu Gln
 85 90 95
 30 Ile Asn Val Asp Val Phe Lys Lys Leu Glu Lys Arg Lys Val Leu Ser
 100 105 110
 Asn Val Glu Lys Ser Gly Leu Leu
 115 120

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1567370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Met Ala Val Val Gly Ala Pro Ile Ser Ser Pro Ala Ala Gln Leu Gln
 1 5 10 15
 Thr Gln Phe Leu Ser Asn Pro Ile Leu Pro Arg Phe Arg Arg Ser Phe
 20 25 30
 Ser Thr Gly Lys Ser Pro Ala Thr Phe Ser Val Val Ala Met Ala Pro
 35 40 45
 Gln Lys Lys Val Asn Lys Tyr Asp Ala Lys Trp Lys Lys Gln Trp Tyr
 50 55 60
 55 Gly Ala Gly Leu Phe Phe Glu Gly Ser Glu Gln Ile Asn Val Asp Val
 65 70 75 80
 Phe Lys Lys Leu Glu Lys Arg Lys Val Leu Ser Asn Val Glu Lys Ser
 85 90 95
 Gly Leu Leu

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

637

- (A) LENGTH: 541 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..541
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570101

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```

aaaMcttttac gttggtatta tctggtttca ctttttctta accctctttg gtgaatgcgt      60
cattgaaacg ccattatccg ccgtgcta atgatctcct cccccgtcgg aaaaaatggc      120
cactggtgga aaagtctcct tcaaagtcac tctgacttcg gatcctaagc ttcttttcaa      180
agtttttcagc gtaccagaag gagctccggt cacggcgggt ctgaaattcg cagcagaaga      240
15 gttcaaggtt cctccacaaa ccagcgccat catcactaat gatgggatcg ggatcaatcc      300
tcaacagagt gcaggaaacg tttttctgaa gcacggatct gaactaagat tgatcccgcg      360
tgatagagtt ggagctgtgt ttgtgatgga tccatagatg atgtgtaagc aatgattaaa      420
aactcagttc caaaaaaaaa acataataat atactgaaat gcttatgtat caactTcgtt      480
gaataaatat gtaatcgtca catcctttta cggattgaag tgagttgaat ttggtcaagt      540

```

20

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: peptide
- (B) LOCATION: 1..93
- (D) OTHER INFORMATION: / Ceres Seq. ID 1570102

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```

Met Ala Thr Gly Lys Lys Val Ser Phe Lys Val Thr Leu Thr Ser Asp
1           5           10           15
35 Pro Lys Leu Pro Phe Lys Val Phe Ser Val Pro Glu Gly Ala Pro Phe
           20           25           30
Thr Ala Val Leu Lys Phe Ala Ala Glu Glu Phe Lys Val Pro Pro Gln
           35           40           45
40 Thr Ser Ala Ile Ile Thr Asn Asp Gly Ile Gly Ile Asn Pro Gln Gln
           50           55           60
Ser Ala Gly Asn Val Phe Leu Lys His Gly Ser Glu Leu Arg Leu Ile
65           70           75           80
Pro Arg Asp Arg Val Gly Ala Val Phe Val Met Asp Pro
           85           90

```

45

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: -
- (B) LOCATION: 1..418
- (D) OTHER INFORMATION: / Ceres Seq. ID 1571051

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

aaaaggaaga cgacgatgca gagtttaacg tcaaacgaag tTgcggggtt ggcagttggg      60
gctctgcttc ttggtgccac catcgctgct cctaaagtgt atgcttttat cgctgcttct      120
cagagaagat ctctttggcat gtgtcgaaaa tgtggagatc ttaagaatgt agcttggtgc      180
60 cgttgcaaag gaacaggaac aatcaaatca ggaggattct ttggtttcag tgactcatca      240
aacacaagat cagtggtgtt cgataattgc caagccaaag gttgtttccc ttgccctgaa      300
tgctcaaaat cttgaccatt ttctcggtat tttatagttg tttcatcttc ttgacactat      360

```

638

gataagtgtgta atcggtccat tggtaatggt aatgttaaag ttgaagaatg tcttggtt

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..104

(D) OTHER INFORMATION: / Ceres Seq. ID 1571052

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Lys Arg Lys Thr Thr Met Gln Ser Leu Thr Ser Asn Glu Val Ala Gly
 1 5 10 15
 Leu Ala Val Gly Ala Leu Leu Leu Gly Ala Thr Ile Ala Ala Pro Lys
 20 25 30
 Val Asp Ala Phe Ile Ala Ala Ser Gln Arg Arg Ser Leu Gly Met Cys
 35 40 45
 Arg Lys Cys Gly Asp Leu Lys Asn Val Ala Cys Gly Arg Cys Lys Gly
 50 55 60
 Thr Gly Thr Ile Lys Ser Gly Gly Phe Phe Gly Phe Ser Asp Ser Ser
 65 70 75 80
 Asn Thr Arg Ser Val Ala Cys Asp Asn Cys Gln Ala Lys Gly Cys Phe
 85 90 95
 Pro Cys Pro Glu Cys Ser Lys Ser
 100

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..99

(D) OTHER INFORMATION: / Ceres Seq. ID 1571053

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Met Gln Ser Leu Thr Ser Asn Glu Val Ala Gly Leu Ala Val Gly Ala
 1 5 10 15
 Leu Leu Leu Gly Ala Thr Ile Ala Ala Pro Lys Val Asp Ala Phe Ile
 20 25 30
 Ala Ala Ser Gln Arg Arg Ser Leu Gly Met Cys Arg Lys Cys Gly Asp
 35 40 45
 Leu Lys Asn Val Ala Cys Gly Arg Cys Lys Gly Thr Gly Thr Ile Lys
 50 55 60
 Ser Gly Gly Phe Phe Gly Phe Ser Asp Ser Ser Asn Thr Arg Ser Val
 65 70 75 80
 Ala Cys Asp Asn Cys Gln Ala Lys Gly Cys Phe Pro Cys Pro Glu Cys
 85 90 95
 Ser Lys Ser

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

639

(B) LOCATION: 1..58

(D) OTHER INFORMATION: / Ceres Seq. ID 1571054

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

5 Met Cys Arg Lys Cys Gly Asp Leu Lys Asn Val Ala Cys Gly Arg Cys
 1 5 10 15
 Lys Gly Thr Gly Thr Ile Lys Ser Gly Gly Phe Phe Gly Phe Ser Asp
 20 25 30
 Ser Ser Asn Thr Arg Ser Val Ala Cys Asp Asn Cys Gln Ala Lys Gly
 35 40 45
 10 Cys Phe Pro Cys Pro Glu Cys Ser Lys Ser
 50 55

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 444 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

20 (A) NAME/KEY: -
 (B) LOCATION: 1..444
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

25 aatctacttt tgagttctct ggagcagctt tggctctttc tctcttcagt tacagctcgc 60
 gatccagatc catatccagt catggcgggt gtagtagcaa gaattgtgga aaagtttggt 120
 aaacgtgata tttggtatcg aatatcggtg atatcaattc cagtctctag tgtcctaata 180
 gtactaggga atatggagct tgctcgtatc agagaggaga agaagctttt gaaggagagg 240
 tttgatcaac tgagggctag aggaataatc agagatcagt aatccaaaag tgtgtttagg 300
 ctttggtttt ttgtttcttt tctatgaatt taatttttta tttctccttt ccatgaatta 360
 30 accaactcta tgtaacgaga tgatttatcc ttgtctctct aagactcgag atgattcgct 420
 attgataaaa cttctattat tScC

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 93 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

40 (A) NAME/KEY: peptide
 (B) LOCATION: 1..93
 (D) OTHER INFORMATION: / Ceres Seq. ID 1571101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

45 Asn Leu Leu Leu Ser Ser Leu Glu Gln Leu Trp Ser Phe Leu Ser Ser
 1 5 10 15
 Val Thr Ala Arg Asp Pro Asp Pro Tyr Pro Val Met Ala Gly Val Val
 20 25 30
 Ala Arg Ile Val Glu Lys Phe Gly Lys Arg Asp Ile Trp Tyr Arg Ile
 35 40 45
 50 Ser Leu Ile Ser Ile Pro Val Ser Ser Val Leu Ile Val Leu Gly Asn
 50 55 60
 Met Glu Leu Ala Arg Ile Arg Glu Glu Lys Lys Leu Leu Lys Glu Arg
 65 70 75 80
 Phe Asp Gln Leu Arg Ala Arg Gly Ile Ile Arg Asp Gln
 55 85 90

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

640

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..66

(D) OTHER INFORMATION: / Ceres Seq. ID 1571102

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Met Ala Gly Val Val Ala Arg Ile Val Glu Lys Phe Gly Lys Arg Asp
 1 5 10 15
 Ile Trp Tyr Arg Ile Ser Leu Ile Ser Ile Pro Val Ser Ser Val Leu
 20 25 30
 10 Ile Val Leu Gly Asn Met Glu Leu Ala Arg Ile Arg Glu Glu Lys Lys
 35 40 45
 Leu Leu Lys Glu Arg Phe Asp Gln Leu Arg Ala Arg Gly Ile Ile Arg
 50 55 60
 Asp Gln
 15 65

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 636 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..636

(D) OTHER INFORMATION: / Ceres Seq. ID 1665272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

cagaataaaa atctatttct tgtgtttgtg ttatatttac ttaaaaaaat aaaggagatc 60
 agtttgggag aaagcagcaa agaagaaaaa tggcagcaac atttgcaaca ccatcgacgg 120
 30 tgataggcct cggaggatca tccatcacca ccaaaccctt ctcttcatcc tttttaaaac 180
 caacattaag cgccaagaac cctttgagac tcgccggtgc atcgggagga agagtcactt 240
 gctttgagag gaactggttg aggagagatt tgaacgtggt aggatttggg ctgacggat 300
 ggctagctcc gtcgagcatt ccagcgataa atgggaagag cctgacgggt ctcttcttcg 360
 atagcatcgg aactgagctc gctcacttcc cgactcctcc agctctcact tcacagtctt 420
 35 ggttgtggtt ggttacgtgg cacttaggcc tcttctctcg cctcactttc ggacaaatcg 480
 gattcaaggg caggactgag gattacttct aaggataact attcttggtt tcgtttgtac 540
 tatatgctct ctcttggtta tgtgtaatat tatcaatcaa aacaaagctt tctttgctat 600
 ttgatgtttc attctatatc tcgacaAgtc tttctt

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 1665273

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Ala Ala Thr Phe Ala Thr Pro Ser Thr Val Ile Gly Leu Gly Gly
 1 5 10 15
 Ser Ser Ile Thr Thr Lys Pro Phe Ser Ser Ser Phe Leu Lys Pro Thr
 20 25 30
 55 Leu Ser Ala Lys Asn Pro Leu Arg Leu Ala Gly Ala Ser Gly Gly Arg
 35 40 45
 Val Thr Cys Phe Glu Arg Asn Trp Leu Arg Arg Asp Leu Asn Val Val
 50 55 60
 Gly Phe Gly Leu Ile Gly Trp Leu Ala Pro Ser Ser Ile Pro Ala Ile
 60 65 70 75 80
 Asn Gly Lys Ser Leu Thr Gly Leu Phe Phe Asp Ser Ile Gly Thr Glu
 85 90 95

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Leu Ala His Phe Pro Thr Pro Pro Ala Leu Thr Ser Gln Phe Trp Leu
 100 105 110
 Trp Leu Val Thr Trp His Leu Gly Leu Phe Leu Cys Leu Thr Phe Gly
 115 120 125
 5 Gln Ile Gly Phe Lys Gly Arg Thr Glu Asp Tyr Phe
 130 135 140

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 522 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- 15 (A) NAME/KEY: -
 (B) LOCATION: 1..522
 (D) OTHER INFORMATION: / Ceres Seq. ID 1713895

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

20 aaacttggat cttaacacag agaagaagca caatcggaag aaaggagaag acgaagatgt 60
 cgttgggtatg gctggaagcg atgttgccctc tcggaatcat cggtgggatg ctctgtatca 120
 tgggcaaatc tcagtactac atccacaaag cttatcatgg ccgtcctaag cacatcggcc 180
 acgatgaatg ggatgttgct atggaaagac gcgacaagaa agtcgtcgag aaagctgcag 240
 ctcccttcctc atgattcgct ttatctcttt tgtgttcctc aggggcttaa ggtgaccact 300
 25 tgtggtgaca aataaagtgc attccagaag aagaagaagc tgggggatct agtactttca 360
 ttcccatttg attttccttg gacatattaa agctttcaga aatcagacct caataacatt 420
 tgggtttatca atatttctct attcgtgata ttttgtatgc ttttaagttg catgatacac 480
 tgaactactc tcttgctgtg tgagtgaata aatgaatatc tg

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 83 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 35 (A) NAME/KEY: peptide
 (B) LOCATION: 1..83
 (D) OTHER INFORMATION: / Ceres Seq. ID 1713896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

40 Thr Trp Ile Leu Thr Gln Arg Arg Ser Thr Ile Gly Arg Lys Glu Lys
 1 5 10 15
 Thr Lys Met Ser Leu Val Trp Leu Glu Ala Met Leu Pro Leu Gly Ile
 20 25 30
 45 Ile Gly Gly Met Leu Cys Ile Met Gly Asn Ser Gln Tyr Tyr Ile His
 35 40 45
 Lys Ala Tyr His Gly Arg Pro Lys His Ile Gly His Asp Glu Trp Asp
 50 55 60
 Val Ala Met Glu Arg Arg Asp Lys Lys Val Val Glu Lys Ala Ala Ala
 65 70 75 80
 50 Pro Ser Ser

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 65 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- 60 (A) NAME/KEY: peptide
 (B) LOCATION: 1..65
 (D) OTHER INFORMATION: / Ceres Seq. ID 1713897

642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Met Ser Leu Val Trp Leu Glu Ala Met Leu Pro Leu Gly Ile Ile Gly
 1 5 10 15
 Gly Met Leu Cys Ile Met Gly Asn Ser Gln Tyr Tyr Ile His Lys Ala
 5 20 25 30
 Tyr His Gly Arg Pro Lys His Ile Gly His Asp Glu Trp Asp Val Ala
 35 40 45
 Met Glu Arg Arg Asp Lys Lys Val Val Glu Lys Ala Ala Ala Pro Ser
 50 55 60
 10 Ser
 65

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1713898

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Met Leu Pro Leu Gly Ile Ile Gly Gly Met Leu Cys Ile Met Gly Asn
 25 1 5 10 15
 Ser Gln Tyr Tyr Ile His Lys Ala Tyr His Gly Arg Pro Lys His Ile
 20 25 30
 Gly His Asp Glu Trp Asp Val Ala Met Glu Arg Arg Asp Lys Lys Val
 35 40 45
 30 Val Glu Lys Ala Ala Ala Pro Ser Ser
 50 55

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 745 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..745

(D) OTHER INFORMATION: / Ceres Seq. ID 1923752

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

acgcttagga ttaaggact atcggttcttg gttgtggatt ctgcccacc gtcttgctta 60
 45 cgagtcacac accaccgtcc ttggatcgag tcttcaactt aagctctgat gctaattcac 120
 atcaaagctg acttgctctg actttgtctc tcaaggattt gaggcgtgat tcaagaacaa 180
 aacaaattaa agaacaactt ttctttatatt attagaaac tactcaaaac taaatctctc 240
 taggtcttta gaacaactct cttaaagcctc tcaatctctt tcttgagact tatggaacaa 300
 ctctccatag tctctctata tagaactgag ctaccocctaa gtctatatct catgaagtct 360
 50 ctctcgactc gcatgtttat ctcatgaggt ctctctcgac tctaaggaga tctctcttga 420
 ctcacatctt gagctctctc ttgtatcctc ttggatgctt tagctctctt gtgttatctt 480
 cttcttcttc atagagatca tatatatact aggaccaaac acctcctttc cctattgtga 540
 ataggaatac ttacaaatct tatccaactt gacattatct gtatttcttt ttttcttgat 600
 ttctttctt gaatttcttt tctgtatct cttctagcat cttctagaag gagataactt 660
 55 gtcctcaag taagttgtaa ttatccaaca cgcattgtgat ctttaatgat cgtggggatt 720
 atttagtggc agagatgaat actct

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

643

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..35

(D) OTHER INFORMATION: / Ceres Seq. ID 1923753

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg Leu Gly Phe Lys Asp Tyr Arg Ser Trp Leu Trp Ile Leu Ala His
 1 5 10 15
 Arg Leu Ala Tyr Glu Ser His Thr Thr Val Leu Gly Ser Ser Leu Gln
 20 25 30
 Leu Lys Leu
 35

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..31

(D) OTHER INFORMATION: / Ceres Seq. ID 1923754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Glu Gln Leu Ser Ile Val Ser Leu Tyr Arg Thr Glu Leu Pro Leu
 1 5 10 15
 Ser Leu Tyr Leu Met Lys Ser Leu Ser Thr Arg Met Phe Ile Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..36

(D) OTHER INFORMATION: / Ceres Seq. ID 1923755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Arg Ser Leu Ser Thr Leu Arg Arg Ser Leu Leu Thr His Ile Leu
 1 5 10 15
 Ser Ser Leu Phe Asp Pro Leu Gly Cys Phe Ser Ser Leu Val Leu Ser
 20 25 30
 Ser Ser Ser Ser
 35

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 487 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..487

(D) OTHER INFORMATION: / Ceres Seq. ID 1976816

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

aaaccctagc aaaaacctct ctctctctct caattcactt ctctctctac aatggcttgg 60
 cgcaacgcag gatctgctgc tcgttctttc gtctccgcca ccgcaagatc accatctctc 120
 cgttctccca ccacggcgct tctcgcctc cgctctctc aatctctctt acctagccgt 180
 cgcttcacct tctcgtcacc ttccaggaat ctaggagccc taggttgac acagtcgttc 240

644

ttgcctctgt acagtgttgt ggctacttct caactgacat ctcaccttaa cgtaaatttg 300
 cgagctttct gcgagctgtc taacgggtact tgaagaggca aaagagtgtg atttcactgc 360
 gcatgcgtga atcagtactt tgaagggatg tgagatcgaa attgtgggat tacctcagca 420
 aaaacttgct taatgtgttg cctgttttag aagtttttagt ttcacaatgt gtggatttat 480
 tagttgt

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..70

(D) OTHER INFORMATION: / Ceres Seq. ID 1976817

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Asn Pro Ser Lys Asn Leu Ser Leu Ser Leu Asn Ser Leu Leu Leu Leu
 1 5 10 15
 20 Gln Trp Leu Gly Ala Thr Gln Asp Leu Leu Leu Val Leu Ser Ser Pro
 25 30
 Pro Pro Gln Asp His His Leu Ser Val Leu Pro Pro Arg Arg Phe Leu
 35 40 45
 25 Ala Ser Val Leu Leu Asn Pro Pro Tyr Leu Ala Val Ala Ser Pro Ser
 50 55 60
 Arg His Leu Pro Gly Ile
 65 70

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..57

(D) OTHER INFORMATION: / Ceres Seq. ID 1976818

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Thr Leu Ala Lys Thr Ser Leu Ser Leu Ser Ile His Phe Ser Ser Tyr
 1 5 10 15
 Asn Gly Leu Ala Gln Arg Arg Ile Cys Ser Phe Phe Arg Leu Arg
 20 25 30
 45 His Arg Lys Ile Thr Ile Ser Pro Phe Ser His His Gly Ala Ser Ser
 35 40 45
 Pro Pro Ser Ser Ser Ile Leu Leu Thr
 50 55

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..93

(D) OTHER INFORMATION: / Ceres Seq. ID 1976819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Met Ala Trp Arg Asn Ala Gly Ser Ala Arg Ser Phe Val Ser Ala
 1 5 10 15
 Thr Ala Arg Ser Pro Ser Leu Arg Ser Pro Thr Thr Ala Leu Pro Arg

645

20 25 30
 Leu Arg Pro Pro Gln Ser Ser Leu Pro Ser Arg Arg Phe Thr Phe Ser
 35 40 45
 Ser Pro Ser Arg Asn Leu Gly Ala Leu Gly Cys Thr Gln Ser Phe Leu
 5 50 55 60
 Pro Leu Tyr Ser Val Val Ala Thr Ser Gln Leu Thr Ser His Leu Asn
 65 70 75 80
 Val Asn Leu Arg Ala Phe Cys Glu Leu Ser Asn Gly Thr
 85 90

10 (2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 566 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..566

20 (D) OTHER INFORMATION: / Ceres Seq. ID 2025128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

atgaatcttc	ttcgcttcgg	ctccgcctct	tattctcgag	aaagctcatc	ttgcttctca	60
catctaaaca	aatatctcat	ctcttctatt	ctactttatc	acttcattctc	cgtacgctct	120
tctttcttcg	ttgcttcttc	ttttgattta	taaattggat	ccaaaacatc	ataggctctc	180
gtcatcctta	tatacaagca	ttgttacttt	gtgatataaa	gaacgaagaa	ttgtacgaag	240
gcaacgagca	agatgagtag	caaggcgaat	gagggtttaa	agagtagcaa	ggcgaatgaa	300
gttgaaagga	ggaagatgaa	tagcacggcc	aatgacgatg	aaaggatgaa	taggatcatc	360
agagatggcc	gtcgtcgtta	cgtcacctgg	agccgcagcc	gcaacccctc	ggcagctcat	420
atcttttggg	caaaacccta	atattttcta	gggttgggct	attagttttt	gttttgggct	480
tttttgaatt	gtattttggg	ctttttatta	atttgtagtg	ggttaattgt	ttggattagg	540
atttttggtg	gtgtaatttt	tttttt				

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..50

(D) OTHER INFORMATION: / Ceres Seq. ID 2025129

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Met Asn Leu Leu Arg Phe Gly Ser Ala Ser Tyr Ser Arg Glu Ser Ser	
1 5 10 15	
Ser Cys Phe Ser His Leu Asn Lys Tyr Leu Ile Ser Ser Ile Leu Leu	
20 25 30	
Tyr His Phe Ile Ser Val Arg Ser Phe Phe Val Ala Ser Ser Phe	
35 40 45	

50 Asp Leu
50

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 2025130

646

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Glu Ser Ser Ser Arg Leu Arg Leu Leu Phe Ser Arg Lys Leu Ile
 1 5 10 15
 Leu Leu Leu Thr Ser Lys Gln Ile Ser His Leu Phe Tyr Ser Thr Leu
 5 20 25 30
 Ser Leu His Leu Arg Thr Leu Phe Phe Leu Arg Cys Phe Phe Phe
 35 40 45

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..41

(D) OTHER INFORMATION: / Ceres Seq. ID 2025131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Met Asn Ser Thr Ala Asn Asp Asp Glu Arg Met Asn Arg Ile Ile Arg
 1 5 10 15
 Asp Gly Arg Arg Arg Tyr Val Thr Trp Ser Arg Ser Arg Asn Pro Ser
 20 25 30
 Ala Ala His Ile Phe Trp Ser Lys Pro
 35 40

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 545 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..545

(D) OTHER INFORMATION: / Ceres Seq. ID 2025402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

tttttttttt ttttgcgaaa ttgaaatgat ctacataaaa aactcaattg ataattttac 60
 aaaggagaaa aatttgtcaa tcaaagaaga agagaaagat tgaactttta acctcacttg 120
 40 gtcataactt caacgccatt ctttccagcg ataatgacag aagtagccat tccgagaaac 180
 agaccatgct ccaccactcc ttgaaacttc ccaatctctt tagccgcagc gaatccatcc 240
 ttcaaaggag tcttaaaata caaatcaata atgtaattac tggtatcagt cacataaggc 300
 ttgccatcac catcaactct aagctttgat tcacatccaa attccttgaa gaggtcttgc 360
 aatctaataca aattaaagtt ccagcagaat tgaacaactt ccaccggcat agctaatacca 420
 45 cttccaccga gtccgtgaac gagtttggtg tcatcagcca caacaataaa cttgtcagcc 480
 acagcttcca ccattacctt gaacatccta atcgaaaaat tatccaatcc aatccattac 540
 ttact

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..47

(D) OTHER INFORMATION: / Ceres Seq. ID 2025403

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Met Leu His His Ser Leu Lys Leu Pro Asn Leu Phe Ser Arg Ser Glu
 1 5 10 15
 Ser Ile Leu Gln Arg Ser Leu Lys Ile Gln Ile Asn Asn Val Ile Thr

647

20 25 30
Val Ile Ser His Ile Arg Leu Ala Ile Thr Ile Asn Ser Lys Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide
(B) LOCATION: 1..33

(D) OTHER INFORMATION: / Ceres Seq. ID 2025404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Phe Phe Phe Phe Cys Glu Ile Glu Met Ile Ser His Lys Asn Ser Ile
1 5 10 15
Asp Asn Phe Thr Lys Glu Lys Asn Leu Ser Ile Lys Glu Glu Glu Lys
20 25 30
Asp

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1954 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1954

(D) OTHER INFORMATION: / Ceres Seq. ID 2025479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

atggaacctt	atataaccag	aagagataca	gttaatacaag	tgttacatgc	agaagaagaa	60
gaagaataca	atgattgtga	attggatcaa	ctcttccttg	tgcattctga	tattagatct	120
gttcttctcc	agattgatga	gcttggtgtt	gaagccacaa	agcgtaagac	cgtgagcaag	180
cacgggttaa	tagaagttga	atctttcaga	actgtgttgt	ctgatatgct	ttcctcacta	240
aagccatggt	ttcctcgatt	gcaagaagcg	atgtctgatt	ttcagttgct	tccagaggat	300
caggaagaac	agtctttgat	gagcacaac	gaagaagaag	atttgtttga	tgttgagagt	360
cctgagccta	ctcaatttga	gcccttagtc	tctccttctc	ctcttgtgca	ttggcgtggt	420
gatcataacg	cagacaagg	tagacaactc	tttcttttga	caccactacc	cttaggaaaa	480
tctgaattcc	taaaacacca	gaatgcatct	aagcttacag	ctaaaaggat	ttttccagac	540
actgttgcaa	atgaaccgct	tgaagcttct	aaagaaacaa	gtgatgatgt	tttaggaggt	600
gagtcgttga	aaactgcagg	acttggtaaa	tcttttagtcc	atgccatgga	tttctctgaa	660
aatttgggtg	agtataagcc	atgttcttca	ccagttctca	ggagaaagat	tctgtctgag	720
cttctaata	gaccttgctt	gaagctgtcg	cctccgaaat	cgtgtacaat	gtttaaaccg	780
gttcttgaat	cttctcaact	gggaaagcaa	ggggcttgta	agtctacctg	ctctgaattg	840
ggatcatctg	gtattgaaaa	aacagacaat	ctctgctcga	agtatcctga	gctcttgagg	900
atacaacatg	ctccgataac	tagaaaaacg	gatcttgaat	cctcgccggt	ttggtgggtt	960
tctcctccta	aaacatgtgt	tttaattggag	cctgtgaatg	agaagaaacc	aattgatgaa	1020
actggtggat	cttttgatgt	tccaaacatt	ataccagaag	caaaacacac	tacagaggga	1080
agcatgtcaa	tgggtggttga	gagtactcca	ttgttttaaag	aaccagagag	cataatgacg	1140
agaaacagaa	caaaagcagg	tgagagtact	ctgaagaaag	agctatggac	aagatttgaa	1200
gaagcaacga	ttcatgacag	tcggttcaac	tcgatgacaa	caacaacaac	agtgagagga	1260
aataataaga	aatgtttcat	ggaaatgtta	gaagaagtga	gtggcaatga	ggaagatcat	1320
gagttaagt	gagagtttgt	ggctctaaaa	ccttatcaag	tactcatatc	ggaactgagc	1380
ataacaaaac	cttttcattg	tctgtctact	cttattagct	gctacataac	tcaaagtaac	1440
aaacatacac	atataacata	tagaaaagatc	gaaaacaaaa	gatcgggatg	agtatggctc	1500
caaagacctc	aactacactt	gctttatttc	ttgtgaccaa	tattctcttc	ctcaacctca	1560
ttaccctgag	ttgcgcagac	aatacttgcc	caagagacgt	tctcaaactt	tcgacatgct	1620
cgaatgttct	caacctcatc	aacttgaagc	tcggggcacc	agctatgagg	ccttggttgc	1680
ctattctctt	tgggtctaatt	gatctcgatg	ttgcgggttg	cctttgcacc	gcgctcaagc	1740

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tcagccttct tggcatcacc atcgacactc ctattcacct taacttggct cttaacgcct 1800
 gtggaggtac ccttcctgat ggattccgtt gcccaacata gctacaatat attcatattt 1860
 tctatctatg ttcttgaatt ggtttTgtct aacatccaaa ttcaaaccta aattcatgta 1920
 taagcaaata acaagtaaaa ttaagacttt tatg

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 496 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..496

(D) OTHER INFORMATION: / Ceres Seq. ID 2025480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Met	Glu	Pro	Tyr	Ile	Thr	Arg	Arg	Asp	Thr	Val	Asn	Gln	Val	Leu	His
1				5					10					15	
Ala	Glu	Glu	Glu	Glu	Glu	Tyr	Asn	Asp	Cys	Glu	Leu	Asp	Gln	Leu	Phe
			20					25					30		
Leu	Val	His	Ser	Asp	Ile	Arg	Ser	Val	Leu	Leu	Gln	Ile	Asp	Glu	Leu
		35					40					45			
Val	Val	Glu	Ala	Thr	Lys	Arg	Lys	Thr	Val	Ser	Lys	His	Gly	Leu	Ile
	50					55					60				
Glu	Val	Glu	Ser	Phe	Arg	Thr	Val	Leu	Ser	Asp	Met	Leu	Ser	Ser	Leu
65					70					75				80	
Lys	Pro	Trp	Phe	Pro	Arg	Leu	Gln	Glu	Ala	Met	Ser	Asp	Phe	Gln	Leu
				85					90					95	
Leu	Pro	Glu	Asp	Gln	Glu	Glu	Gln	Ser	Leu	Met	Ser	Thr	Asn	Glu	Glu
			100					105					110		
Glu	Asp	Leu	Phe	Asp	Val	Glu	Ser	Pro	Glu	Pro	Thr	Gln	Phe	Glu	Pro
		115					120					125			
Leu	Val	Ser	Pro	Ser	Pro	Leu	Val	His	Trp	Arg	Gly	Asp	His	Asn	Ala
	130					135					140				
Asp	Lys	Gly	Arg	Gln	Leu	Phe	Leu	Leu	Thr	Pro	Leu	Pro	Leu	Gly	Lys
145					150					155				160	
Ser	Glu	Phe	Leu	Lys	His	Gln	Asn	Ala	Ser	Lys	Leu	Thr	Ala	Lys	Arg
				165				170						175	
Ile	Phe	Pro	Asp	Thr	Val	Ala	Asn	Glu	Pro	Leu	Glu	Ala	Ser	Lys	Glu
		180						185					190		
Thr	Ser	Asp	Asp	Val	Leu	Gly	Gly	Glu	Ser	Leu	Lys	Thr	Ala	Gly	Leu
		195					200					205			
Gly	Lys	Ser	Leu	Val	His	Ala	Met	Asp	Phe	Ser	Glu	Asn	Leu	Val	Glu
	210					215					220				
Tyr	Lys	Pro	Cys	Ser	Ser	Pro	Val	Leu	Arg	Arg	Lys	Ile	Leu	Ser	Glu
225					230					235				240	
Leu	Leu	Met	Thr	Pro	Cys	Leu	Lys	Leu	Ser	Pro	Pro	Lys	Ser	Cys	Thr
			245						250					255	
Met	Phe	Lys	Pro	Val	Pro	Glu	Ser	Ser	Gln	Leu	Gly	Lys	Gln	Gly	Ala
		260						265					270		
Cys	Lys	Ser	Thr	Cys	Ser	Glu	Leu	Gly	Ser	Ser	Gly	Ile	Glu	Lys	Thr
		275					280					285			
Asp	Asn	Leu	Cys	Ser	Lys	Tyr	Pro	Glu	Leu	Leu	Gly	Ile	Gln	His	Ala
	290					295					300				
Pro	Ile	Thr	Arg	Lys	Thr	Asp	Leu	Glu	Ser	Ser	Pro	Val	Trp	Trp	Phe
305					310					315				320	
Ser	Pro	Pro	Lys	Thr	Cys	Val	Leu	Met	Glu	Pro	Val	Asn	Glu	Lys	Lys
			325						330					335	
Pro	Ile	Asp	Glu	Thr	Gly	Gly	Ser	Phe	Asp	Val	Pro	Asn	Ile	Ile	Pro
		340						345					350		
Glu	Ala	Lys	His	Thr	Thr	Glu	Gly	Ser	Met	Ser	Met	Val	Val	Glu	Ser
		355					360							365	

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Thr Pro Leu Phe Lys Glu Pro Glu Ser Ile Met Thr Arg Asn Arg Thr
 370 375 380
 Lys Ala Gly Glu Ser Thr Leu Lys Lys Glu Leu Trp Thr Arg Phe Glu
 385 390 395 400
 5 Glu Ala Thr Ile His Asp Ser Arg Phe Asn Ser Met Thr Thr Thr Thr
 405 410 415
 Thr Val Arg Gly Asn Asn Lys Lys Cys Phe Met Glu Met Leu Glu Glu
 420 425 430
 10 Val Ser Gly Asn Glu Glu Asp His Glu Leu Ser Gly Glu Phe Val Ala
 435 440 445
 Leu Lys Pro Tyr Gln Val Leu Ile Ser Glu Leu Ser Ile Thr Asn Ala
 450 455 460
 Phe His Cys Leu Ser Thr Leu Ile Ser Cys Tyr Ile Thr Gln Ser Asn
 465 470 475 480
 15 Lys His Thr His Ile Thr Tyr Arg Lys Ile Glu Asn Lys Arg Ser Gly
 485 490 495

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 421 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

25 (A) NAME/KEY: peptide
 (B) LOCATION: 1..421
 (D) OTHER INFORMATION: / Ceres Seq. ID 2025481

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

30 Met Leu Ser Ser Leu Lys Pro Trp Phe Pro Arg Leu Gln Glu Ala Met
 1 5 10 15
 Ser Asp Phe Gln Leu Leu Pro Glu Asp Gln Glu Glu Gln Ser Leu Met
 20 25 30
 Ser Thr Asn Glu Glu Glu Asp Leu Phe Asp Val Glu Ser Pro Glu Pro
 35 35 40 45
 Thr Gln Phe Glu Pro Leu Val Ser Pro Ser Pro Leu Val His Trp Arg
 50 55 60
 Gly Asp His Asn Ala Asp Lys Gly Arg Gln Leu Phe Leu Leu Thr Pro
 65 70 75 80
 40 Leu Pro Leu Gly Lys Ser Glu Phe Leu Lys His Gln Asn Ala Ser Lys
 85 90 95
 Leu Thr Ala Lys Arg Ile Phe Pro Asp Thr Val Ala Asn Glu Pro Leu
 100 105 110
 Glu Ala Ser Lys Glu Thr Ser Asp Asp Val Leu Gly Gly Glu Ser Leu
 115 120 125
 45 Lys Thr Ala Gly Leu Gly Lys Ser Leu Val His Ala Met Asp Phe Ser
 130 135 140
 Glu Asn Leu Val Glu Tyr Lys Pro Cys Ser Ser Pro Val Leu Arg Arg
 145 150 155 160
 50 Lys Ile Leu Ser Glu Leu Leu Met Thr Pro Cys Leu Lys Leu Ser Pro
 165 170 175
 Pro Lys Ser Cys Thr Met Phe Lys Pro Val Pro Glu Ser Ser Gln Leu
 180 185 190
 Gly Lys Gln Gly Ala Cys Lys Ser Thr Cys Ser Glu Leu Gly Ser Ser
 195 200 205
 55 Gly Ile Glu Lys Thr Asp Asn Leu Cys Ser Lys Tyr Pro Glu Leu Leu
 210 215 220
 Gly Ile Gln His Ala Pro Ile Thr Arg Lys Thr Asp Leu Glu Ser Ser
 225 230 235 240
 60 Pro Val Trp Trp Phe Ser Pro Pro Lys Thr Cys Val Leu Met Glu Pro
 245 250 255
 Val Asn Glu Lys Lys Pro Ile Asp Glu Thr Gly Gly Ser Phe Asp Val
 260 265 270

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Pro Asn Ile Ile Pro Glu Ala Lys His Thr Thr Glu Gly Ser Met Ser
 275 280 285
 Met Val Val Glu Ser Thr Pro Leu Phe Lys Glu Pro Glu Ser Ile Met
 290 295 300

5 Thr Arg Asn Arg Thr Lys Ala Gly Glu Ser Thr Leu Lys Lys Glu Leu
 305 310 315 320
 Trp Thr Arg Phe Glu Glu Ala Thr Ile His Asp Ser Arg Phe Asn Ser
 325 330 335

10 Met Thr Thr Thr Thr Thr Val Arg Gly Asn Asn Lys Lys Cys Phe Met
 340 345 350
 Glu Met Leu Glu Glu Val Ser Gly Asn Glu Glu Asp His Glu Leu Ser
 355 360 365
 Gly Glu Phe Val Ala Leu Lys Pro Tyr Gln Val Leu Ile Ser Glu Leu
 370 375 380

15 Ser Ile Thr Asn Ala Phe His Cys Leu Ser Thr Leu Ile Ser Cys Tyr
 385 390 395 400
 Ile Thr Gln Ser Asn Lys His Thr His Ile Thr Tyr Arg Lys Ile Glu
 405 410 415
 Asn Lys Arg Ser Gly
 420

(2) INFORMATION FOR SEQ ID NO:130:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..406
 (D) OTHER INFORMATION: / Ceres Seq. ID 2025482
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Met Ser Asp Phe Gln Leu Leu Pro Glu Asp Gln Glu Glu Gln Ser Leu
 1 5 10 15
 35 Met Ser Thr Asn Glu Glu Glu Asp Leu Phe Asp Val Glu Ser Pro Glu
 20 25 30
 Pro Thr Gln Phe Glu Pro Leu Val Ser Pro Ser Pro Leu Val His Trp
 35 40 45
 Arg Gly Asp His Asn Ala Asp Lys Gly Arg Gln Leu Phe Leu Leu Thr
 50 55 60
 Pro Leu Pro Leu Gly Lys Ser Glu Phe Leu Lys His Gln Asn Ala Ser
 65 70 75 80
 Lys Leu Thr Ala Lys Arg Ile Phe Pro Asp Thr Val Ala Asn Glu Pro
 85 90 95
 45 Leu Glu Ala Ser Lys Glu Thr Ser Asp Asp Val Leu Gly Gly Glu Ser
 100 105 110
 Leu Lys Thr Ala Gly Leu Gly Lys Ser Leu Val His Ala Met Asp Phe
 115 120 125
 Ser Glu Asn Leu Val Glu Tyr Lys Pro Cys Ser Ser Pro Val Leu Arg
 130 135 140
 50 Arg Lys Ile Leu Ser Glu Leu Leu Met Thr Pro Cys Leu Lys Leu Ser
 145 150 155 160
 Pro Pro Lys Ser Cys Thr Met Phe Lys Pro Val Pro Glu Ser Ser Gln
 165 170 175
 55 Leu Gly Lys Gln Gly Ala Cys Lys Ser Thr Cys Ser Glu Leu Gly Ser
 180 185 190
 Ser Gly Ile Glu Lys Thr Asp Asn Leu Cys Ser Lys Tyr Pro Glu Leu
 195 200 205
 60 Leu Gly Ile Gln His Ala Pro Ile Thr Arg Lys Thr Asp Leu Glu Ser
 210 215 220
 Ser Pro Val Trp Trp Phe Ser Pro Pro Lys Thr Cys Val Leu Met Glu
 225 230 235 240

	Pro	Val	Asn	Glu	Lys	Lys	Pro	Ile	Asp	Glu	Thr	Gly	Gly	Ser	Phe	Asp															
				245					250						255																
	Val	Pro	Asn	Ile	Ile	Pro	Glu	Ala	Lys	His	Thr	Thr	Glu	Gly	Ser	Met															
			260						265					270																	
5	Ser	Met	Val	Val	Glu	Ser	Thr	Pro	Leu	Phe	Lys	Glu	Pro	Glu	Ser	Ile															
			275					280					285																		
	Met	Thr	Arg	Asn	Arg	Thr	Lys	Ala	Gly	Glu	Ser	Thr	Leu	Lys	Lys	Glu															
		290					295					300																			
10	Leu	Trp	Thr	Arg	Phe	Glu	Glu	Ala	Thr	Ile	His	Asp	Ser	Arg	Phe	Asn															
	305					310					315					320															
	Ser	Met	Thr	Thr	Thr	Thr	Thr	Val	Arg	Gly	Asn	Asn	Lys	Lys	Cys	Phe															
					325					330					335																
	Met	Glu	Met	Leu	Glu	Glu	Val	Ser	Gly	Asn	Glu	Glu	Asp	His	Glu	Leu															
				340					345					350																	
15	Ser	Gly	Glu	Phe	Val	Ala	Leu	Lys	Pro	Tyr	Gln	Val	Leu	Ile	Ser	Glu															
		355						360					365																		
	Leu	Ser	Ile	Thr	Asn	Ala	Phe	His	Cys	Leu	Ser	Thr	Leu	Ile	Ser	Cys															
		370					375					380																			
20	Tyr	Ile	Thr	Gln	Ser	Asn	Lys	His	Thr	His	Ile	Thr	Tyr	Arg	Lys	Ile															
	385					390					395					400															
	Glu	Asn	Lys	Arg	Ser	Gly																									
						405																									
	(2)	INFORMATION FOR SEQ ID NO:131:																													
		(i)	SEQUENCE CHARACTERISTICS:																												
25			(A)	LENGTH: 609 base pairs																											
			(B)	TYPE: nucleic acid																											
			(C)	STRANDEDNESS: single																											
			(D)	TOPOLOGY: linear																											
		(ii)	MOLECULE TYPE: DNA (genomic)																												
30		(ix)	FEATURE:																												
			(A)	NAME/KEY: -																											
			(B)	LOCATION: 1..609																											
			(D)	OTHER INFORMATION: / Ceres Seq. ID 2032963																											
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:131:																												
35	ttt	gtg	tgg	aatt	aact	gg	tgag																								

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35 40 45
 Ala Ile Ala Gly Ser Leu Val Ser Thr Pro Val Ile Gly Trp Ser Leu
 50 55 60
 Tyr Thr Leu Lys Thr Thr Gly Cys Gly Leu Pro Pro Gly Pro Ala Gly
 5 65 70 75 80
 Leu Ile Gly Ala Leu Glu Gly Val Ser Tyr Leu Val Val Val Gly Ile
 85 90 95
 Val Gly Trp Ser Leu Tyr Thr Lys Thr Lys Thr Gly Ser Gly Leu Pro
 100 105 110
 10 Asn Gly Pro Phe Gly Leu Leu Gly Ala Val Glu Gly Leu Ser Tyr Leu
 115 120 125
 Ser Val Leu Ala Ile Leu Val Val Phe Gly Ile Gln Phe Leu Asp Asn
 130 135 140
 Gly Ser Val Pro Gly Pro Leu Pro Ser Asp Gln Cys Phe Gly
 15 145 150 155
 (2) INFORMATION FOR SEQ ID NO:133:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 25 (B) LOCATION: 1..330
 (D) OTHER INFORMATION: / Ceres Seq. ID 2033706
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:
 atgggccaca gaggtagcag agagagagtg aaaatggaga agtactttgg aaatgcgtac 60
 aggggagatc caggagtgcc acatgcagat gcagatcggt tcgtgaatat atggattggt 120
 30 tctgctgctt tctccgttct tacctgggtt aatccttaca tgtggcagct ctctaaccag 180
 ttcaattacc atgacaagtg gatgctgttt gagcagtacc actggaaaaa agcaagggca 240
 aagaagcaac cttatgaatt caagtggaat aagataccca aagaagtcag ggactcgtac 300
 tattacaact ggccagtcta cttcccatag
 (2) INFORMATION FOR SEQ ID NO:134:
 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..109
 (D) OTHER INFORMATION: / Ceres Seq. ID 2033707
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:
 Met Gly His Arg Val Thr Arg Glu Arg Val Lys Met Glu Lys Tyr Phe
 1 5 10 15
 Gly Asn Ala Tyr Arg Gly Asp Pro Gly Val Pro His Ala Asp Ala Asp
 20 25 30
 50 Arg Phe Val Asn Ile Trp Ile Gly Ser Ala Ala Phe Ser Val Leu Thr
 35 40 45
 Trp Val Asn Pro Tyr Met Trp Gln Leu Ser Asn Gln Phe Asn Tyr His
 50 55 60
 Asp Lys Trp Met Leu Phe Glu Gln Tyr His Trp Lys Lys Ala Arg Ala
 55 65 70 75 80
 Lys Lys Gln Pro Tyr Glu Phe Lys Trp Asn Lys Ile Pro Lys Glu Val
 85 90 95
 Arg Asp Ser Tyr Tyr Tyr Asn Trp Pro Val Tyr Phe Pro
 100 105
 60 (2) INFORMATION FOR SEQ ID NO:135:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..98
 (D) OTHER INFORMATION: / Ceres Seq. ID 2033708
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

10	Met	Glu	Lys	Tyr	Phe	Gly	Asn	Ala	Tyr	Arg	Gly	Asp	Pro	Gly	Val	Pro
	1				5					10					15	
	His	Ala	Asp	Ala	Asp	Arg	Phe	Val	Asn	Ile	Trp	Ile	Gly	Ser	Ala	Ala
			20						25					30		
	Phe	Ser	Val	Leu	Thr	Trp	Val	Asn	Pro	Tyr	Met	Trp	Gln	Leu	Ser	Asn
15			35					40					45			
	Gln	Phe	Asn	Tyr	His	Asp	Lys	Trp	Met	Leu	Phe	Glu	Gln	Tyr	His	Trp
		50					55					60				
	Lys	Lys	Ala	Arg	Ala	Lys	Lys	Gln	Pro	Tyr	Glu	Phe	Lys	Trp	Asn	Lys
	65					70				75					80	
20	Ile	Pro	Lys	Glu	Val	Arg	Asp	Ser	Tyr	Tyr	Asn	Trp	Pro	Val	Tyr	
				85					90					95		
	Phe	Pro														

(2) INFORMATION FOR SEQ ID NO:136:
 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 30 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..56
 (D) OTHER INFORMATION: / Ceres Seq. ID 2033709
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

	Met	Trp	Gln	Leu	Ser	Asn	Gln	Phe	Asn	Tyr	His	Asp	Lys	Trp	Met	Leu
	1				5					10					15	
	Phe	Glu	Gln	Tyr	His	Trp	Lys	Lys	Ala	Arg	Ala	Lys	Lys	Gln	Pro	Tyr
			20						25					30		
40	Glu	Phe	Lys	Trp	Asn	Lys	Ile	Pro	Lys	Glu	Val	Arg	Asp	Ser	Tyr	Tyr
			35					40					45			
	Tyr	Asn	Trp	Pro	Val	Tyr	Phe	Pro								
	50						55									

(2) INFORMATION FOR SEQ ID NO:137:
 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 (A) NAME/KEY: -
 (B) LOCATION: 1..418
 (D) OTHER INFORMATION: / Ceres Seq. ID 2043118
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

	ataacaatat	caaaagataa	aaacagagtt	tgctttttata	agatcaaaga	aggtaaaaaa	60
	agaaatggca	aaatggagtg	cgatcgtatt	gataatgatg	gtgatgattg	ttgcggtcac	120
	aatagaagca	caagaagaaa	gtggtgggac	tattttgtttt	cgccaatgtt	ctcagccttg	180
	tcgcagtgac	gacggtagtt	gctatgaaaa	ctgtaaaaatc	gaatgcggtg	gtcccaagcc	240
60	tcccttatct	cgtctacgaa	gctcacatgc	atgagatggc	atcatcaatg	gaagttcgcg	300
	gaaggatagg	atgataaaaa	gagatttgta	gcggattttt	gatcatctct	actgttttta	360
	acttcacggt	ttatattata	agagtttcat	taaaaagatc	aataaaacga	gaaaatgt	

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(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..69

(D) OTHER INFORMATION: / Ceres Seq. ID 2043119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```

Met Ala Lys Trp Ser Ala Ile Val Leu Ile Met Met Val Met Ile Val
 1             5             10             15
15 Ala Val Thr Ile Glu Ala Gln Glu Glu Ser Gly Gly Thr Ile Cys Phe
      20             25             30
Arg Gln Cys Ser Gln Pro Cys Arg Ser Asp Asp Gly Ser Cys Tyr Glu
      35             40             45
20 Asn Cys Lys Ile Glu Cys Gly Gly Pro Lys Pro Pro Leu Ser Arg Leu
      50             55             60
Arg Ser Ser His Ala
65

```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..62

(D) OTHER INFORMATION: / Ceres Seq. ID 2043120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```

Ile Thr Ile Ser Lys Asp Lys Asn Arg Val Cys Phe Tyr Lys Ile Lys
 1             5             10             15
35 Glu Gly Lys Lys Arg Asn Gly Lys Met Glu Cys Asp Arg Ile Asp Asn
      20             25             30
40 Asp Gly Asp Asp Cys Cys Gly His Asn Arg Ser Thr Arg Arg Lys Trp
      35             40             45
Trp Asp Tyr Leu Phe Ser Pro Met Phe Ser Ala Leu Ser Gln
      50             55             60

```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..59

(D) OTHER INFORMATION: / Ceres Seq. ID 2043121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```

Met Met Val Met Ile Val Ala Val Thr Ile Glu Ala Gln Glu Glu Ser
 1             5             10             15
55 Gly Gly Thr Ile Cys Phe Arg Gln Cys Ser Gln Pro Cys Arg Ser Asp
      20             25             30
60 Asp Gly Ser Cys Tyr Glu Asn Cys Lys Ile Glu Cys Gly Gly Pro Lys
      35             40             45
Pro Pro Leu Ser Arg Leu Arg Ser Ser His Ala
      50             55

```

655

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 838 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..838

(D) OTHER INFORMATION: / Ceres Seq. ID 2047214

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```

acacgaaacg attccgcttc tccgcttcct tcataaatat ctcaactcatc gtctctagat      60
tgttcttttca cagcgaattt tcatttctct cttaaccgta aacgaatctc tcttctcaaa      120
gttttatttt ctctctgcga tggctcaaga agatgttact gctgttgcta ctaacggtgc      180
tggtccggtg gagacgcac ttgtcttcac tgagttcaag cagatgttgc tcgttgaagc      240
tcaaaaggtc ggtgacgctg ttactttcta caaatctgct tttggtgcga tcgagtcctgg      300
tcatttctct taccctaagc gtaagcttga ccaagagctt cctcatgttc tctcttctga      360
gcttaatctc gctggctctt ccttcgttgt ttgcgacgtt tctctctctc ctgggttttc      420
tactgcgaaa tcggaagggt cgggagtgac ttttcttctc ggaactaagg atgctgaagc      480
cgccgtttgc aaagctgttg acgccggagc tgtgaaagtg gaggttacgg aggcagaagt      540
tgaactggga ttcaaaggaa aagttacgga tccttttggt gtcacttgga tcttcgcgga      600
gaagaagacc gtgatcaccg acgagaacaa agaggttttag aatctgtcgt cggatctaata      660
tcttcgtcgg tttctgaaca aaaaaacta tctattatcc taggtttatg cttttatttt      720
gtcttttggt gaatccggtg atcagtaaac cggatcgagt aggctaataa ctttcggatt      780
ctaatttcac cccttttgac aaactctaat cttggtgaaa ttgcatatta atctcggg

```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..166

(D) OTHER INFORMATION: / Ceres Seq. ID 2047215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```

Met Ala Gln Glu Asp Val Thr Ala Val Thr Asn Gly Ala Gly Pro
1      5      10      15
Val Glu Thr His Leu Val Phe Thr Glu Phe Lys Gln Met Leu Leu Val
20     25     30
Glu Ala Gln Lys Val Gly Asp Ala Val Thr Phe Tyr Lys Ser Ala Phe
35     40     45
Gly Ala Ile Glu Ser Gly His Ser Leu Tyr Pro Lys Arg Lys Leu Asp
50     55     60
Gln Glu Leu Pro His Val Leu Ser Ser Glu Leu Asn Leu Ala Gly Ser
65     70     75     80
Ser Phe Val Val Cys Asp Val Ser Ser Leu Pro Gly Phe Ser Thr Ala
85     90     95
Lys Ser Glu Gly Ser Gly Val Thr Phe Leu Leu Gly Thr Lys Asp Ala
100    105    110
Glu Ala Ala Val Ala Lys Ala Val Asp Ala Gly Ala Val Lys Val Glu
115    120    125
Val Thr Glu Ala Glu Val Glu Leu Gly Phe Lys Gly Lys Val Thr Asp
130    135    140
Pro Phe Gly Val Thr Trp Ile Phe Ala Glu Lys Lys Thr Val Ile Thr
145    150    155    160
Asp Glu Asn Lys Glu Val
165

```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

656

- (A) LENGTH: 138 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- 5 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..138
 (D) OTHER INFORMATION: / Ceres Seq. ID 2047216
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:
 Met Leu Leu Val Glu Ala Gln Lys Val Gly Asp Ala Val Thr Phe Tyr
 1 5 10 15
 Lys Ser Ala Phe Gly Ala Ile Glu Ser Gly His Ser Leu Tyr Pro Lys
 20 25 30
 15 Arg Lys Leu Asp Gln Glu Leu Pro His Val Leu Ser Ser Glu Leu Asn
 35 40 45
 Leu Ala Gly Ser Ser Phe Val Val Cys Asp Val Ser Ser Leu Pro Gly
 50 55 60
 Phe Ser Thr Ala Lys Ser Glu Gly Ser Gly Val Thr Phe Leu Leu Gly
 65 70 75 80
 20 Thr Lys Asp Ala Glu Ala Ala Val Ala Lys Ala Val Asp Ala Gly Ala
 85 90 95
 Val Lys Val Glu Val Thr Glu Ala Glu Val Glu Leu Gly Phe Lys Gly
 100 105 110
 25 Lys Val Thr Asp Pro Phe Gly Val Thr Trp Ile Phe Ala Glu Lys Lys
 115 120 125
 Thr Val Ile Thr Asp Glu Asn Lys Glu Val
 130 135
- (2) INFORMATION FOR SEQ ID NO:144:
 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 98 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
- 35 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..98
 (D) OTHER INFORMATION: / Ceres Seq. ID 2047217
- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:
 Met Leu Leu Leu Leu Leu Leu Thr Val Leu Val Arg Trp Arg Arg Ile
 1 5 10 15
 Leu Ser Ser Leu Ser Ser Ser Arg Cys Cys Ser Leu Lys Leu Lys Arg
 20 25 30
 45 Ser Val Thr Leu Leu Leu Ser Thr Asn Leu Leu Leu Val Arg Ser Ser
 35 40 45
 Leu Val Ile Leu Phe Thr Leu Ser Val Ser Leu Thr Lys Ser Phe Leu
 50 55 60
 Met Phe Ser Leu Leu Ser Leu Ile Ser Leu Ala Leu Pro Ser Leu Phe
 65 70 75 80
 50 Ala Thr Phe Pro Leu Ser Leu Val Phe Leu Leu Arg Asn Arg Lys Val
 85 90 95
 Arg Glu
- 55 (2) INFORMATION FOR SEQ ID NO:145:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 682 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
- 60 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

657

(A) NAME/KEY: -

(B) LOCATION: 1..682

(D) OTHER INFORMATION: / Ceres Seq. ID 2047438

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

```

5  atgattggtg gtttcttcgc cgatgtaaaa ttcaacagat cgagagagaa aaaactctct 60
   ctccctcctc cgttcaccgt cgcgactcgg ctctacagta cattttgttg agcaatctcg 120
   tattttagagg attccaatgt ctggcgacaga ggataataaa tcttcccatg ctcagctttc 180
   gtcccaaatt tttcttgatc ttgtggattc ggtgatagct gatgtagcat ctgagtgtca 240
   tcgggtagca cgactaggac ttgatcgtga tttggatata gtagaagaag agttgagatt 300
10 gtcagtggaa gcgcgtgcga agatcgtcga tcctagcaac aacctcgaaa ccaacaccaa 360
   atatgttgtt gatataattg ggcagactca cctcctgtga gctagtgaag tgttcaattg 420
   catgaactgt gggcgacaaa ttgttgacag aaggtttgct cctcatctcg aaaaatgcat 480
   gggaaaggga agaaaggctc gtgccaagac aaccagaagc acaacggctg cacagaaccg 540
   gaatgcacga cgcagcccca atccacgata ttctccttat ccaaattctg ctagtgaaga 600
15 ccagttagca agtggatcac ctggtgttgc aggtgaagac tgctcaaatt tcacagttcg 660
   agagaacgtg aaaggagact ga

```

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..181

(D) OTHER INFORMATION: / Ceres Seq. ID 2047439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

```

30 Met Ser Gly Ala Glu Asp Asn Lys Ser Ser His Ala Gln Leu Ser Ser
   1           5           10           15
   Gln Ile Phe Leu Asp Leu Val Asp Ser Val Ile Ala Asp Val Ala Ser
           20           25           30
   Glu Cys His Arg Val Ala Arg Leu Gly Leu Asp Arg Asp Leu Asp Ile
           35           40           45
35 Val Glu Glu Glu Leu Arg Leu Ser Val Glu Ala Arg Ala Lys Ile Ala
   50           55           60
   Asp Pro Ser Asn Asn Leu Glu Thr Asn Thr Lys Tyr Val Val Asp Ile
   65           70           75           80
   Phe Gly Gln Thr His Pro Pro Val Ala Ser Glu Val Phe Asn Cys Met
   85           90           95
40 Asn Cys Gly Arg Gln Ile Val Ala Gly Arg Phe Ala Pro His Leu Glu
           100          105          110
   Lys Cys Met Gly Lys Gly Arg Lys Ala Arg Ala Lys Thr Thr Arg Ser
           115          120          125
45 Thr Thr Ala Ala Gln Asn Arg Asn Ala Arg Arg Ser Pro Asn Pro Arg
   130          135          140
   Tyr Ser Pro Tyr Pro Asn Ser Ala Ser Glu Asn Gln Leu Ala Ser Gly
   145          150          155          160
   Ser Pro Gly Val Ala Gly Glu Asp Cys Ser Asn Phe Thr Val Arg Glu
   165          170          175
50 Asn Val Lys Gly Asp
   180

```

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 501 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..501

658

(D) OTHER INFORMATION: / Ceres Seq. ID 2049056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```

5 aaacaaaggt gtcaagaaga aggatcaaca tattaattga ctaaaaatga aggcattggat 60
  gataatcttg ttggtgattt gtgtcgtgtt ggtggtggag caatcagagg ctgcgaaagg 120
  tcgaaagtat ttaaattccag gcgtgcttga ccggtgtcgt ggtcctaata ctccagcggg 180
  atgtcatcct cacaattccc accacaaacc tcgcgtccct gttcacaatt atagtcgtgg 240
  ttgtagtaga attacccggg gcagacgaga tgcctagggt taacctcaca tgacgacgac 300
  gtccctttat attgatcctt cttctacatg agacttgcaa tgatattata tattcatata 360
  tatacacatt acgctgtata tgataattcc agttgattaa tatataaatc ttactgattt 420
10 caattcaata cacaagatcc tgtaactgaa ataattttgt ccatgttttg tgcttataat 480
  aatggtatga ctcttattat t

```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

```

15 (A) LENGTH: 76 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```

20 (A) NAME/KEY: peptide
    (B) LOCATION: 1..76

```

(D) OTHER INFORMATION: / Ceres Seq. ID 2049057

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

```

25 Met Lys Ala Trp Met Ile Ile Leu Leu Val Ile Cys Val Ala Val Val
   1           5           10           15
  Val Glu Gln Ser Glu Ala Arg Lys Gly Arg Lys Tyr Leu Asn Pro Gly
           20           25           30
  Val Leu Asp Arg Cys Arg Gly Pro Asn Pro Pro Ala Gly Cys His Pro
           35           40           45
30 His Asn Ser His His Lys Pro Arg Val Pro Val His Asn Tyr Ser Arg
   50           55           60
  Gly Cys Ser Arg Ile Thr Arg Cys Arg Arg Asp Ala
   65           70           75

```

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

```

35 (A) LENGTH: 72 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

```

40 (A) NAME/KEY: peptide
    (B) LOCATION: 1..72

```

(D) OTHER INFORMATION: / Ceres Seq. ID 2049058

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

```

45 Met Ile Ile Leu Val Ile Cys Val Ala Val Val Val Glu Gln Ser
   1           5           10           15
  Glu Ala Arg Lys Gly Arg Lys Tyr Leu Asn Pro Gly Val Leu Asp Arg
           20           25           30
50 Cys Arg Gly Pro Asn Pro Pro Ala Gly Cys His Pro His Asn Ser His
   35           40           45
  His Lys Pro Arg Val Pro Val His Asn Tyr Ser Arg Gly Cys Ser Arg
   50           55           60
  Ile Thr Arg Cys Arg Arg Asp Ala
   65           70

```

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

```

60 (A) LENGTH: 1007 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

```

(ii) MOLECULE TYPE: DNA (genomic)

659

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..1007

(D) OTHER INFORMATION: / Ceres Seq. ID 2050386

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```

ccaaatttct ccatggatcg ttctttgaat ctctctgatt tagccttagg gttcgatgag      60
cagctagcta ttccatcgcc actaaatgga aaagtaatac taatagaaga ctgtgtagag      120
acgagtgggt cctttgtact tcaccagcta atgaaacgtg ttctctcctc taactcctcc      180
gacgcactta tctttctcgc ttttgctcgc cctttctctc attatgatcg aatccttgcgt      240
10 aaactgggat gtaatttagc tacccataag tcgaataatc gattgggtgt ctttgacatg      300
ctcatgggta agtggttcaga tggggatcaa atggaagaca atgtgagtgc agttgcgaaa      360
ctatttcggg agatacaaga aaccgttcga aagctacaga gtgtaacaag tggtaacata      420
actgttatgg tggatgacat gtctctgctg gaaattgcta ctaccggcag caactcagat      480
cacgtattgg acttcttgca ttattgccac acattaagtt ctgaaagcaa ttgttcattg      540
15 gtcactcctca atcatgaaga tatatacgcg agcatggaga gacctgcatt tttgctacag      600
atgggtatgcc ttgcagatgt tgtgataaag gcagagcctt tagcctctgg tttagcaaat      660
gatgtacatg gccaattgac tgttctgaac aaagggataa gcaactcagg tagaggaagc      720
tcgaggaaca agttgcagaa ttttcaattc aggatcaaag aaaatggtat cgactatttc      780
tactctgggt gcagaagctg aggattagac accgttctga gcattagcat ggtagtgaga      840
20 tgtttttcta gacagttttg ttattttgcgt ttaggttaaa cagagacact ctgttaaaca      900
tttttacttt agtgtctctt ctggttgtaa cttgatgact tagctaaagt tgaatgcttg      960
agacacagaa acttgtagac atggaaaatt agtaacattc tatatct

```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..266

(D) OTHER INFORMATION: / Ceres Seq. ID 2050387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```

35 Pro Asn Phe Ser Met Asp Arg Ser Leu Asn Leu Leu Asp Leu Ala Leu
   1           5           10           15
Gly Phe Asp Glu Gln Leu Ala Ile Pro Ser Pro Leu Asn Gly Lys Val
   20           25           30
40 Ile Leu Ile Glu Asp Cys Val Glu Thr Ser Gly Ser Phe Val Leu His
   35           40           45
Gln Leu Met Lys Arg Val Leu Ser Ser Asn Ser Ser Asp Ala Leu Ile
   50           55           60
Phe Leu Ala Phe Ala Arg Pro Phe Ser His Tyr Asp Arg Ile Leu Arg
   65           70           75           80
45 Lys Leu Gly Cys Asn Leu Ala Thr His Lys Ser Asn Asn Arg Leu Val
   85           90           95
Phe Phe Asp Met Leu Met Val Lys Cys Ser Asp Gly Asp Gln Met Glu
  100          105          110
Asp Asn Val Ser Ala Val Ala Lys Leu Phe Arg Glu Ile Gln Glu Thr
  115          120          125
50 Val Arg Lys Leu Gln Ser Val Thr Ser Gly Asn Ile Thr Val Met Val
  130          135          140
Asp Asp Met Ser Leu Leu Glu Ile Ala Thr Thr Gly Ser Asn Ser Asp
  145          150          155          160
55 His Val Leu Asp Phe Leu His Tyr Cys His Thr Leu Ser Ser Glu Ser
  165          170          175
Asn Cys Ser Leu Val Ile Leu Asn His Glu Asp Ile Tyr Ala Ser Met
  180          185          190
Glu Arg Pro Ala Phe Leu Leu Gln Met Val Cys Leu Ala Asp Val Val
  195          200          205
60 Ile Lys Ala Glu Pro Leu Ala Ser Gly Leu Ala Asn Asp Val His Gly
  210          215          220

```

660

Gln Leu Thr Val Leu Asn Lys Gly Ile Ser Asn Ser Gly Arg Gly Ser
 225 230 235 240
 Ser Arg Asn Lys Leu Gln Asn Phe Gln Phe Arg Ile Lys Glu Asn Gly
 245 250 255
 5 Ile Asp Tyr Phe Tyr Pro Gly Cys Arg Ser
 260 265

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..262

(D) OTHER INFORMATION: / Ceres Seq. ID 2050388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Met Asp Arg Ser Leu Asn Leu Leu Asp Leu Ala Leu Gly Phe Asp Glu
 1 5 10 15
 Gln Leu Ala Ile Pro Ser Pro Leu Asn Gly Lys Val Ile Leu Ile Glu
 20 25 30
 Asp Cys Val Glu Thr Ser Gly Ser Phe Val Leu His Gln Leu Met Lys
 35 40 45
 25 Arg Val Leu Ser Ser Asn Ser Ser Asp Ala Leu Ile Phe Leu Ala Phe
 50 55 60
 Ala Arg Pro Phe Ser His Tyr Asp Arg Ile Leu Arg Lys Leu Gly Cys
 65 70 75 80
 Asn Leu Ala Thr His Lys Ser Asn Asn Arg Leu Val Phe Phe Asp Met
 30 85 90 95
 Leu Met Val Lys Cys Ser Asp Gly Asp Gln Met Glu Asp Asn Val Ser
 100 105 110
 Ala Val Ala Lys Leu Phe Arg Glu Ile Gln Glu Thr Val Arg Lys Leu
 115 120 125
 35 Gln Ser Val Thr Ser Gly Asn Ile Thr Val Met Val Asp Asp Met Ser
 130 135 140
 Leu Leu Glu Ile Ala Thr Thr Gly Ser Asn Ser Asp His Val Leu Asp
 145 150 155 160
 Phe Leu His Tyr Cys His Thr Leu Ser Ser Glu Ser Asn Cys Ser Leu
 40 165 170 175
 Val Ile Leu Asn His Glu Asp Ile Tyr Ala Ser Met Glu Arg Pro Ala
 180 185 190
 Phe Leu Leu Gln Met Val Cys Leu Ala Asp Val Val Ile Lys Ala Glu
 195 200 205
 45 Pro Leu Ala Ser Gly Leu Ala Asn Asp Val His Gly Gln Leu Thr Val
 210 215 220
 Leu Asn Lys Gly Ile Ser Asn Ser Gly Arg Gly Ser Ser Arg Asn Lys
 225 230 235 240
 Leu Gln Asn Phe Gln Phe Arg Ile Lys Glu Asn Gly Ile Asp Tyr Phe
 50 245 250 255
 Tyr Pro Gly Cys Arg Ser
 260

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..216

661

(D) OTHER INFORMATION: / Ceres Seq. ID 2050389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Met Lys Arg Val Leu Ser Ser Asn Ser Ser Asp Ala Leu Ile Phe Leu
 1 5 10 15
 5 Ala Phe Ala Arg Pro Phe Ser His Tyr Asp Arg Ile Leu Arg Lys Leu
 20 25 30
 Gly Cys Asn Leu Ala Thr His Lys Ser Asn Asn Arg Leu Val Phe Phe
 35 40 45
 10 Asp Met Leu Met Val Lys Cys Ser Asp Gly Asp Gln Met Glu Asp Asn
 50 55 60
 Val Ser Ala Val Ala Lys Leu Phe Arg Glu Ile Gln Glu Thr Val Arg
 65 70 75 80
 Lys Leu Gln Ser Val Thr Ser Gly Asn Ile Thr Val Met Val Asp Asp
 85 90 95
 15 Met Ser Leu Leu Glu Ile Ala Thr Thr Gly Ser Asn Ser Asp His Val
 100 105 110
 Leu Asp Phe Leu His Tyr Cys His Thr Leu Ser Ser Glu Ser Asn Cys
 115 120 125
 20 Ser Leu Val Ile Leu Asn His Glu Asp Ile Tyr Ala Ser Met Glu Arg
 130 135 140
 Pro Ala Phe Leu Leu Gln Met Val Cys Leu Ala Asp Val Val Ile Lys
 145 150 155 160
 Ala Glu Pro Leu Ala Ser Gly Leu Ala Asn Asp Val His Gly Gln Leu
 165 170 175
 25 Thr Val Leu Asn Lys Gly Ile Ser Asn Ser Gly Arg Gly Ser Ser Arg
 180 185 190
 Asn Lys Leu Gln Asn Phe Gln Phe Arg Ile Lys Glu Asn Gly Ile Asp
 195 200 205
 Tyr Phe Tyr Pro Gly Cys Arg Ser
 210 215

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 634 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: -

(B) LOCATION: 1..634

(D) OTHER INFORMATION: / Ceres Seq. ID 2053353

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

gaataaaaaat ctatttcttg tgtttggtt gtatttactt aaaaaataa aggagatcag 60
 tttgggagaa agcagcaaag aagaaaaatg gcagcaacat ttgcaacacc atcgacggtg 120
 45 ataggcctcg gaggatcatc catcaccacc aaacccttct cttcatcctt tttaaaacca 180
 acattaagcg ccaagaaccc tttgagactc gccggtgcat cgggaggaag agtcacttgc 240
 tttgagagga actggttgag gagagatttg aacgtggtag gatttgggct gatcggtg 300
 ctgactccgt cgagcattcc agcgataaat gggaagagcc tgacgggtct cttcttcgat 360
 agcatcgga ctgagctcgc tcaacttccc actcctccag ctctcacttc acagttctgg 420
 50 ttgtggttg ttacgtggca cttaggcctc ttcctctgcc tcaacttccg acaaatcgga 480
 ttcaagggca ggactgaaga ttacttctaa ggataactat tcttgtttgc gtttgacta 540
 tatgctctct cttggttatg tgtaatatta tcaatcaaaa caaagctttc tttgctattt 600
 gatgtttcat tctatatctc gacaagtctt tctt

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

662

(B) LOCATION: 1..140

(D) OTHER INFORMATION: / Ceres Seq. ID 2053354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

5 Met Ala Ala Thr Phe Ala Thr Pro Ser Thr Val Ile Gly Leu Gly Gly
 1 5 10 15
 Ser Ser Ile Thr Thr Lys Pro Phe Ser Ser Ser Phe Leu Lys Pro Thr
 20 25 30
 Leu Ser Ala Lys Asn Pro Leu Arg Leu Ala Gly Ala Ser Gly Gly Arg
 35 40 45
 10 Val Thr Cys Phe Glu Arg Asn Trp Leu Arg Arg Asp Leu Asn Val Val
 50 55 60
 Gly Phe Gly Leu Ile Gly Trp Leu Ala Pro Ser Ile Pro Ala Ile
 65 70 75 80
 Asn Gly Lys Ser Leu Thr Gly Leu Phe Phe Asp Ser Ile Gly Thr Glu
 85 90 95
 15 Leu Ala His Phe Pro Thr Pro Pro Ala Leu Thr Ser Gln Phe Trp Leu
 100 105 110
 Trp Leu Val Thr Trp His Leu Gly Leu Phe Leu Cys Leu Thr Phe Gly
 115 120 125
 20 Gln Ile Gly Phe Lys Gly Arg Thr Glu Asp Tyr Phe
 130 135 140

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

30 (A) NAME/KEY: -

(B) LOCATION: 1..393

(D) OTHER INFORMATION: / Ceres Seq. ID 2055693

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

35 atgcaaaaac ctctctctct ctctcaattc acttctcttc cttcaatggc ttggcgcaac 60
 gcaggatctg ccgctcggtc tttcgtctcc gccaccgcaa gatcaccatc tctccgttct 120
 cccaccacgg cgcttctctg cctccgtcct cctcaatcct ccttacctag ccgctcgcttc 180
 accttctcat caccttccag gaatctagga gcacttggtt gcacacagtc gttcttgctt 240
 ctgtacagtg ttgtggctac ttctcaactc acatctcacc ttaacgttaa cttgcgagct 300
 40 ttctgcgagc tgtctaacgg gaattggaaa agatgggtga tgcactcgga ttttacgtcg 360
 ctggcaagag aatggtgctg cattgttccg tga

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 130 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

50 (A) NAME/KEY: peptide

(B) LOCATION: 1..130

(D) OTHER INFORMATION: / Ceres Seq. ID 2055694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

55 Met Gln Lys Pro Leu Ser Leu Ser Gln Phe Thr Ser Pro Pro Ser Met
 1 5 10 15
 Ala Trp Arg Asn Ala Gly Ser Ala Ala Arg Ser Phe Val Ser Ala Thr
 20 25 30
 Ala Arg Ser Pro Ser Leu Arg Ser Pro Thr Thr Ala Leu Pro Arg Leu
 35 40 45
 60 Arg Pro Pro Gln Ser Ser Leu Pro Ser Arg Arg Phe Thr Phe Ser Ser
 50 55 60
 Pro Ser Arg Asn Leu Gly Ala Leu Gly Cys Thr Gln Ser Phe Leu Pro
 65 70 75 80

663

Leu Tyr Ser Val Val Ala Thr Ser Gln Leu Thr Ser His Leu Asn Val
 85 90 95
 Asn Leu Arg Ala Phe Cys Glu Leu Ser Asn Gly Asn Trp Lys Arg Trp
 100 105 110
 5 Val Met His Ser Asp Phe Thr Ser Leu Ala Arg Glu Trp Cys Cys Ile
 115 120 125

Val Pro
 130

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..115

(D) OTHER INFORMATION: / Ceres Seq. ID 2055695

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Met Ala Trp Arg Asn Ala Gly Ser Ala Ala Arg Ser Phe Val Ser Ala
 1 5 10 15
 Thr Ala Arg Ser Pro Ser Leu Arg Ser Pro Thr Thr Ala Leu Pro Arg
 20 25 30
 25 Leu Arg Pro Pro Gln Ser Ser Leu Pro Ser Arg Arg Phe Thr Phe Ser
 35 40 45
 Ser Pro Ser Arg Asn Leu Gly Ala Leu Gly Cys Thr Gln Ser Phe Leu
 50 55 60
 30 Pro Leu Tyr Ser Val Val Ala Thr Ser Gln Leu Thr Ser His Leu Asn
 65 70 75 80
 Val Asn Leu Arg Ala Phe Cys Glu Leu Ser Asn Gly Asn Trp Lys Arg
 85 90 95
 Trp Val Met His Ser Asp Phe Thr Ser Leu Ala Arg Glu Trp Cys Cys
 100 105 110
 35 Ile Val Pro
 115

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..68

(D) OTHER INFORMATION: / Ceres Seq. ID 2055696

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Cys Lys Asn Leu Ser Leu Ser Leu Leu Leu Leu Gln Trp
 1 5 10 15
 Leu Gly Ala Thr Gln Asp Leu Pro Leu Val Leu Ser Ser Pro Pro Pro
 20 25 30
 Gln Asp His His Leu Ser Val Leu Pro Pro Arg Arg Phe Leu Ala Ser
 35 40 45
 55 Val Leu Leu Asn Pro Pro Tyr Leu Ala Val Ala Ser Pro Ser His His
 50 55 60
 Leu Pro Gly Ile
 65

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:

5 (A) NAME/KEY: -
 (B) LOCATION: 1..394
 (D) OTHER INFORMATION: / Ceres Seq. ID 2056405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

10 tcaatagctt atctagttct tgactgttca acgatcaatg gcaccatccg ctgcaatgct 60
 catactctca catcctctag ttagccacaa agctaagaat cagtctctgt catcgccgtc 120
 gtctgttaag tcgacacgtg tcttcggttt tctttggcct tggaaggcat tagacaatga 180
 ggatcattcc gcggttggtc tcggccggct ctttggcgat ccggctacta tcgagaagcg 240
 cttccaagaa gctcttgaac aaagctgttg gtaatttgta caatgtttgg ttgggtttat 300
 15 tgattgtttt tacgttaaaa tagcttttat aaattggaaa tggaagtact gtaaaatgta 360
 aaaattgact atatataatt aaaggtacat tatg

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

20 (A) NAME/KEY: peptide
 (B) LOCATION: 1..78
 (D) OTHER INFORMATION: / Ceres Seq. ID 2056406

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

30 Met Ala Pro Ser Ala Ala Met Leu Ile Leu Ser His Pro Leu Val Ser
 1 5 10 15
 His Lys Ala Lys Asn Gln Ser Leu Ser Ser Pro Ser Ser Val Lys Ser
 20 25 30
 Thr Arg Val Phe Gly Phe Leu Trp Pro Trp Lys Ala Leu Asp Asn Glu
 35 40 45
 Asp His Ser Ala Val Val Leu Gly Arg Leu Phe Gly Asp Pro Ala Thr
 50 55 60
 35 Ile Glu Lys Arg Phe Gln Glu Ala Leu Glu Gln Ser Cys Trp
 65 70 75

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

40 (A) NAME/KEY: peptide
 (B) LOCATION: 1..72
 (D) OTHER INFORMATION: / Ceres Seq. ID 2056407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

50 Met Leu Ile Leu Ser His Pro Leu Val Ser His Lys Ala Lys Asn Gln
 1 5 10 15
 Ser Leu Ser Ser Pro Ser Ser Val Lys Ser Thr Arg Val Phe Gly Phe
 20 25 30
 Leu Trp Pro Trp Lys Ala Leu Asp Asn Glu Asp His Ser Ala Val Val
 35 40 45
 Leu Gly Arg Leu Phe Gly Asp Pro Ala Thr Ile Glu Lys Arg Phe Gln
 50 55 60
 Glu Ala Leu Glu Gln Ser Cys Trp
 65 70

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 48 amino acids

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(B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 5 (ix) FEATURE:
 (A) NAME/KEY: peptide
 (B) LOCATION: 1..48
 (D) OTHER INFORMATION: / Ceres Seq. ID 2056408
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:
 10 Met Arg Ile Ile Pro Arg Leu Phe Ser Ala Gly Ser Leu Ala Ile Arg
 1 5 10 15
 Leu Leu Ser Arg Ser Ala Ser Lys Lys Leu Leu Asn Lys Ala Val Gly
 20 25 30
 15 Asn Leu Tyr Asn Val Trp Leu Gly Leu Leu Ile Val Phe Thr Leu Lys
 35 40 45
 (2) INFORMATION FOR SEQ ID NO:164:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 766 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: DNA (genomic)
 (ix) FEATURE:
 25 (A) NAME/KEY: -
 (B) LOCATION: 1..766
 (D) OTHER INFORMATION: / Ceres Seq. ID 2065747
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:
 acagtcgcct ccttcctgcg cgcgcgcgcg cgccgcgcgt accaccgcct cgcggccgcgc 60
 30 tgcggctccg cgtttccgca cggatttggg gaaggtttct tgaggctgag aacatgggtgc 120
 tgaagacgga actttgccgc ttcagcggcc agaagattta tcctgggaaa ggcattagat 180
 ttatccgtgc tgattctcag gtcttctttt ttgccaaactc gaaatgcaag cgctacttcc 240
 acaaccgcct gaagcctgca aagcttacct ggacagcaat gtacaggaag cagcacaaga 300
 aggatatcca tgctgaagcg gtaaagaaga ggcgcgcgcg caccaagaag ccatactcca 360
 ggtcaattgt ggggtgcttcc ttggaagtaa tccagaagaa gagagctgag aagccagagg 420
 35 tccgcgatgc tgctagagaa gctgctcttc gtgagatcaa ggagcgcac aagaagacca 480
 aggatgagaa gaaagcgaag aaggcggagg tgagcaagtc ccagaagacg cagacaaagg 540
 gtgcggtcca gaagggttcc aagggcccca agttgggagg cggtggtggg aagcgctgaa 600
 agaacttagt gtcgtttctc gacattgcag tcgttcctta gccaaagcca ctttcgtaga 660
 40 acctgtgttg aatttgcaag acttattcaa gcgttgcttg tgcgtgctaa ataccatggc 720
 aagagaacgg atttatattt atgcctgaaa aaaaatgacc gttcat
 (2) INFORMATION FOR SEQ ID NO:165:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 45 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: peptide
 (ix) FEATURE:
 (A) NAME/KEY: peptide
 50 (B) LOCATION: 1..161
 (D) OTHER INFORMATION: / Ceres Seq. ID 2065748
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:
 Met Val Leu Lys Thr Glu Leu Cys Arg Phe Ser Gly Gln Lys Ile Tyr
 1 5 10 15
 55 Pro Gly Lys Gly Ile Arg Phe Ile Arg Ala Asp Ser Gln Val Phe Leu
 20 25 30
 Phe Ala Asn Ser Lys Cys Lys Arg Tyr Phe His Asn Arg Leu Lys Pro
 35 40 45
 Ala Lys Leu Thr Trp Thr Ala Met Tyr Arg Lys Gln His Lys Lys Asp
 60 50 55 60
 Ile His Ala Glu Ala Val Lys Lys Arg Arg Arg Ala Thr Lys Lys Pro
 65 70 75 80

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	Tyr	Ser	Arg	Ser	Ile	Val	Gly	Ala	Ser	Leu	Glu	Val	Ile	Gln	Lys	Lys
				85						90					95	
	Arg	Ala	Glu	Lys	Pro	Glu	Val	Arg	Asp	Ala	Ala	Arg	Glu	Ala	Ala	Leu
			100						105					110		
5	Arg	Glu	Ile	Lys	Glu	Arg	Ile	Lys	Lys	Thr	Lys	Asp	Glu	Lys	Lys	Ala
			115					120					125			
	Lys	Lys	Ala	Glu	Val	Ser	Lys	Ser	Gln	Lys	Thr	Gln	Thr	Lys	Gly	Ala
			130				135					140				
10	Val	Gln	Lys	Gly	Ser	Lys	Gly	Pro	Lys	Leu	Gly	Gly	Gly	Gly	Gly	Lys
	145					150					155					160
	Arg															

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20 (ix) FEATURE:

(A) NAME/KEY: peptide

(B) LOCATION: 1..106

(D) OTHER INFORMATION: / Ceres Seq. ID 2065749

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

25	Met	Tyr	Arg	Lys	Gln	His	Lys	Lys	Asp	Ile	His	Ala	Glu	Ala	Val	Lys
	1				5					10					15	
	Lys	Arg	Arg	Arg	Ala	Thr	Lys	Lys	Pro	Tyr	Ser	Arg	Ser	Ile	Val	Gly
				20					25					30		
30	Ala	Ser	Leu	Glu	Val	Ile	Gln	Lys	Lys	Arg	Ala	Glu	Lys	Pro	Glu	Val
			35					40					45			
	Arg	Asp	Ala	Ala	Arg	Glu	Ala	Ala	Leu	Arg	Glu	Ile	Lys	Glu	Arg	Ile
		50					55					60				
	Lys	Lys	Thr	Lys	Asp	Glu	Lys	Lys	Ala	Lys	Lys	Ala	Glu	Val	Ser	Lys
			65			70					75				80	
35	Ser	Gln	Lys	Thr	Gln	Thr	Lys	Gly	Ala	Val	Gln	Lys	Gly	Ser	Lys	Gly
					85					90					95	
	Pro	Lys	Leu	Gly	Gly	Gly	Gly	Gly	Gly	Lys	Arg					
				100						105						

40

CLAIMS

What is claimed is:

1. An isolated nucleic acid molecule comprising a nucleic acid having a nucleotide sequence selected from the group consisting of

(i) a nucleotide sequence shown in SEQ TABLES 1 AND 2;

5 (ii) a nucleotide sequence complementary to one shown in SEQ TABLES 1 AND 2;

(iii) a nucleotide sequence which is the reverse complement of one shown in SEQ TABLES 1 AND 2;

10 (iv) a nucleotide sequence capable of hybridizing to a nucleotide sequence shown in SEQ TABLES 1 AND 2;

(iv) a nucleotide sequence capable of hybridizing to a nucleotide sequence complementary to one shown in SEQ TABLES 1 AND 2;

15 (vi) a nucleotide sequence capable of hybridizing to a nucleotide sequence which is the reverse complement of one shown in SEQ TABLES 1 AND 2;

whereby the hybridization in groups (iv) to (vi) allow said sequences to form a duplex at a temperature from about $T_m - 40^\circ\text{C}$ to about $T_m - 48^\circ\text{C}$.

2. An isolated nucleic acid molecule according to claim 1 that comprises a complete open reading frame.

3. An isolated nucleic acid molecule according to claim 1 that functions as a promoter or as a 3' end termination sequence or as a regulator sequence influencing the transcription rate, the transcript stability or RNA
5 translation rate in a host cell.

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4. The isolated nucleic acid of claim 3, comprising a sequence selected from the group consisting of a TATA box sequence, a CAAT box sequence, a motif of GCAATCG or a transcription-factor binding sequence.

5. An isolated nucleic acid molecule comprising a nucleic acid sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequences shown in SEQ TABLES 1 AND 2, a complementary nucleotide sequence to said
5 nucleic acid sequence that encodes said amino acid sequence selected from SEQ TABLES 1 AND 2, a reverse complementary nucleotide sequence to said nucleic acid sequence that encodes said amino acid sequence selected from SEQ TABLES 1 AND 2, and a nucleotide sequence that will hybridize to said nucleic acid
10 sequence encoding an amino acid selected from SEQ TABLES 1 AND 2 or said complementary sequence under hybridization conditions providing $T_m - 40^{\circ}\text{C}$ to $T_m - 48^{\circ}\text{C}$.

6. An isolated nucleic acid molecule comprising a nucleic acid sequence that encodes at least a part or a portion or a mutant or a fusion of an amino acid sequence selected from the group consisting of the amino acid sequences shown in SEQ
5 TABLES 1 AND 2, a complementary nucleotide sequence to said nucleic acid sequence that encodes said part or portion or mutant or fusion of an amino acid sequence selected from SEQ TABLES 1 AND 2, a reverse complementary nucleotide sequence to said nucleic acid sequence that encodes said part or portion or
10 mutant or fusion of an amino acid sequence selected from SEQ TABLES 1 AND 2, and a nucleotide sequence that will hybridize to said nucleic acid sequence that encodes said part or portion or mutant or fusion of an amino acid selected from SEQ TABLES 1 AND 2 or said complementary sequence or said reverse
15 complementary sequence under hybridization conditions providing $T_m - 40^{\circ}\text{C}$ to $T_m - 48^{\circ}\text{C}$.

7. An isolated nucleic acid molecule according to claim 1, having a nucleotide sequence selected from the group consisting of the nucleotide sequences shown in SEQ TABLES 1 AND 2, and a complementary nucleotide sequence to said
5 nucleotide sequence selected from SEQ TABLES 1 AND 2.

8. A chimeric DNA construct comprising (a) a promoter sequence capable of driving gene expression in plant cells and operatively linked to (b) a structural gene comprising an DNA molecule according to any one of claims 1, 2, 5 and 7.

9. A chimeric DNA construct comprising (a) a promoter that is a nucleic acid molecule according to claim 3 or 4 operatively linked to (b) a structural gene and, optionally, (c) an associated UTR.

10. An isolated DNA molecule comprising (a) a promoter sequence according to claim 3 or 4 and operatively linked to (b) a structural gene sequence according to any one of claims 1, 2, 5, 6 and 7.

11. A promoter according to claim 10, wherein said promoter is a specific promoter.

12. A promoter according to claim 11, wherein said promoter is a seed-specific promoter, an embryo-specific promoter, an ovule-specific promoter, a tapetum-specific promoter or a root-specific promoter.

13. A host cell transformed with a polynucleotide comprising the isolated nucleic acid molecule according to claim 1.

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14. An isolated polypeptide comprising an amino acid sequence encoded by a polynucleotide sequence shown in SEQ TABLES 1 AND 2, or one that is at least 75% identical thereto.

15. An isolated polypeptide according to claim 14, that is at least 85% identical to said amino acid sequence.

16. An isolated polypeptide, according to claim 15, that is at least 90% identical to said amino acid sequence.

17. A polynucleotide comprising a first polynucleotide sequence from SEQ TABLES 1 AND 2 or a fragment thereof, wherein said_first sequence is capable of regulating transcription or translation of second a polynucleotide comprising a coding
5 sequence in a host cell or *in vitro* system wherein the first and second polynucleotides are operatively linked.

18. The first polynucleotide of claim 17, which is capable of regulating transcription or translation in an *in vitro* system.

19. The first polynucleotide of claim 17, which is capable of regulating transcription or translation in a host cell.

20. The polynucleotide of claim 19, wherein said host cell is a plant cell.

21. A host cell of claim 13, wherein said isolated nucleic acid comprises a promoter and operatively linked structural gene and further wherein said promoter and structural gene are not heterologous to each other and are
5 exogenous to the host cell genome.

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22. A method of introducing an isolated nucleic acid into a host cell comprising:

(a) providing an isolated nucleic acid of any of claims 1-12;

5 (b) contacting said isolated nucleic acid with said host cell under conditions that permit insertion of said nucleic acid into said host cell.

23. A method of producing a polypeptide of any one of claims 14-16 comprising:

(a) providing a host cell of claim 13;

5 (b) culturing said host cell under conditions that permit transcription and translation of said structural gene to produce a polypeptide; and

(c) isolating said polypeptide.

24. An antibody capable of binding to a polypeptide of any one of claims 14-16.

25. An isolated nucleic acid comprising a promoter of a gene wherein said gene comprises a nucleic acid having the nucleotide sequence of claim 1.

26. An isolated polypeptide comprising an amino acid sequence selected from SEQ TABLES 1 AND 2, or one that is at least 75% identical thereto.

27. The isolated polypeptide according to Claim 26 that is at least 85% identical thereto.

28. The isolated polypeptide according to claim 26 that is at least 90% identical thereto.